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Table 4
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Top Hit Descriptor	RC3-HN0001-310300-011-b04 HN0001 Homo septens cDNA	qB9d01.xf NCI_CGAP_Co8 Homo septens cDNA clone IMAGE:1874689.3'	H. sapiens gene for immunoglobulin kappa light chein variable region A8 and A9	801306127F1 NIH MGC 39 Hamo septens cDNA clone IMAGE:3640420 5	Homo seplens hyeluronen synthese 2 (HAS2), mRNA	1948f01.s1 Scenes Infant brain (NIB Homo sepiens cDNA clone IMAGE:36639 3	Mas musculus phosphatidylinositol 4-phosphate 5-kinase, the 1 gamma (PicSk1c), mRNA	802124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE-4281611 5	802124743F1 NIH_MGC_56 Homo sepiens cDNA clone IMAGE:4281611 5	961611.xf NCI_CGAP_KkB Homo septens cDNA clone IMAGE:1863980 3' similar to gb:355700 HYDROXYMETHYLGLUTARYL-COA LYASE PRECURSOR (HUMAN):	9947N08 s.1 Strategere fetal epieen (#037205) Homo espiens CDNA clone INAGE:74367 3' eimiler to similer to ob:M01036 me2 HEMOSI OBIN GAMMAA AND CAMMA-C CHAINS FILIMAN	801883592F1 NIH MGC 57 Homo septems cDNA clone IMACE -4095814 F	Homo sepiens KIAA0764 gene product (KIAA0764), mRNA	Anolis opalinus isolate QS NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochandrial gene for mitochandrial product	Stansabdon vitreum 40S ribosomal protein S11 mRNA partial oris	Homo sepiene membrane-bound eminopeptidese P (XNPEP2) pene, complete cds	Homo septens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, trible LJM domain protein 6, and superpolinging protein.	complete ods; and L-type calclum channel a>	Mus musculus peptidoglycan recognition protein-like (Pahyrp-pending), mRNA	Mus musculus protein khase C, epston (Picce), mRNA	Homo sepiens Xq pseudosubsomal region; segment 1/2	xe63f08.x1 NCI_CGAP_Kid11 Homo sepiens cDNA clone IMAGE:2774343 31	Beleencotera physalus gene encoding attel nethuretic peptide	Rattus norvedicus Ce2+/celinodulin-dependent protein kinase II alpha si brant mRNA 3' imhanalatad sacion	Connected times. ALY-1 at PG gene for polycular orate hase, complete ora	PM1-ST0262-261199-001-g01 ST0262 Homo septens cDNA	Balaenoptera physakus gene encoding atrial natriuretic pectide	801594960F1 NIH_MGC_9 Homo sepiens cDNA clone IMAGE:3948734 5	Centagalo critiopoxvirus hemagglutinin gene, completa cds
Top Hit Detabase Source	EST_HUMAN F	EST_HUMAN o	E	EST HUMAN		T HUMAN		EST_HUMAN 6	EST HUMAN 8	EST HUMAN	1	Т		NT A		E	Σ¬				F	EST_HUMAN x	NT B	<u> </u>		HUMAN	N IN	EST_HUMAN OF	П
Top Hit Acession No.	3.1E-01 AW983549.1	8.1		2.1	388	-	0679322 NT	3.1E-01 BF696639.1	3.1E-01 BF608839.1	Ξ	,	1.7	12231	3.1E-01 AF294308.1	Γ			AF196779.1	10946623 NT	6755083 NT	5.1		3.0E-01 A.1006755.1	8.1	3.0E-01 AB030481.1				17
Most Similar (Top) Hit BLAST E Value	3.1E-01	3.1E-01	3.1E-01 X71887.	3.1E-01 BE73736	3.1E-01	3.1E-01 R45318.	3.1E-01	3.1E-01	3.1E-01	3.1E-01 AI24400	8.1E-01 T56325.	3.1E-01	3.1E-01	3.1E-01	3.16-01/	3.1E-01		3.1E-01	3.1E-01	3.0E-01	3.0E-01	3.0E-01 AW3004	3.0E-01	3.0E-01 AF23777	3.0E-01	3.0E-01 AW8177	3.0E-01	3.0E-01 B	3.0E-01 AF22924
Expression Signal	1.34	1.01	3.91	241	0.77	1.71	0.64	1.05	1.05	1.74	0.68	1.28	2.56	1.48	3.03	262		3.48	1.35	2.01	14.52	2.51	6.57	12	1.18	1.48	1.95	7.22	0.77
ORF SEQ ID NO:	32140	32203	32360	30545	33354	34381	35855	35818	35819	35893		36672	37430		-					25533	25896	26618	26830	27502		29234	29837	30702	30833
SEQ ID NO:				25061			22463	22815	22815	22877	22840	23428	24124	24623	24647	24729		24960	25347	15512	13056	13954	14241	14862	15969	16597	17212	18073	18152
Probe SEQ ID NO:	6374	6439	6583	6873	7579	8546	9802	2967	1968	10029	10201	10741	11524	12133	12165	12304		12680	12690	2	247	1202	1497	2132	3206	3846	4477	5267	5349

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Top Hit Descriptor	RC3-BT0333-180700-111-e03 BT0333 Homo sapiens cDNA	RC3-BT0333-180700-111-a03 BT0333 Homo sepiens cDNA	Mus musculus 129/sv Clara cell 10 kd protein (mCC10) gene, complete cds	Mouse cytokeratin 15 gene, complete cds	Strongylocentrotus purpuratus 34/67 kDe laminin-binding protein mRNA, pertial cds	Centagalo orthopoxytrus hemagglutirin gene, complete cds	Homo saplens chromosome 21 segment HS21C006	Was musculus midnolin (Midn-pending), mRNA	Streptococcus pneumoniae strain DBL5 PspA (pspA) gene, partial ods	Thermotoga maritima section 67 of 138 of the complete genome	Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 (Cleosfb), mRNA	801339079F1 NIH MGC 53 Homo septens cDNA clone IMAGE:3681594 5	Streotomyces suifoncfaciens iscoenicilian Neyathere (bcbC) cene partial ods	Homo septiens DKFZP586M0122 protein (DKFZP588M0122), mRNA	Anabaena PCC7120 cytosine-specific DNA methyltransferase (dnin8) gene, complete cds; putative	RC2-BN0074-240400-110-h12 BN0074 Home series only	602133271F1 NIH MGC 81 Homo septens oDNA clone IMAGE:4288336 51	Actinobecilius actinomycetemcomitans TadA (tadA), TadB (tadB), TadC (tadC), TadD (tadD), TadE (tadE), TadF (tadF), and TadG (tadG) genes, complete cds	Actinobacilius ectinomycetermoomitans TedA (tadA), TedB (tadB), TedC (tadC), TedD (tadD), TedE (tadE), TedF (tadF), and TedG (tadG) genes, complete eds	xe03d10 x1 Sogres, NFL, T, GBC, S1 Homo saplens cDNA clone IMAGE: 2606035 3	Aspergillus cryzae bipA gene for ER chaperone BIP, complete cots	602140133F1 NIH_MGC_46 Homo septens cDNA clone IMAGE:4301097 5	602140133F1 NIH_MGC_46 Homo septens cDNA clone INAGE:4301097 5	yp84b10.r1 Scenes fetal liver spieen 1NFLS Homo sepiens cDNA clone IMAGE:194107 5'	yp84b10.r1 Soares fetal liver spleen 1NFLS Hamo septens cDNA clane IMAGE:194107 5	Rattus nonegicus mRNA for glyceraldehyde-3-phosphate dehydrogenase type 2 (gapdh-2 gene)	Mus musculus ribose 5-phosphate isomerase A (Role), mRNA	Aquifex aecitious section 68 of 109 of the complete genome	Chrysodidymus synuroideus mitochandrian, complete genome	PM1-CT0326-171296-001-f12 CT0326 Homo sapiens cDNA
Top Hit Database Source	EST_HUMAN	EST_HUMAN	- L	 	F	Į.	LN			E		T HUMAN	Ī		Į.	T HI IMAN	HUMAN		Ę	T HUMAN		EST HUMAN	EST_HUMAN 0	EST_HUMAN y		F				EST_HUMAN F
Top Hit Acession No.	BE693575.1	BE693575.1	J01247.1	516313.1	J02369.1	3.0E-01 AF228247.1	9.2	10947007 NT	0.1	5.1	9910161 NT	3.0E-01 BE566083.1		7661685	1				85		Ξ	1.1				1.	TN 9877788			2.0E-01 AW754239.1
Most Similar (Top) Hit BLAST E Value	3.0E-01	3.0E-01 BE69357	3.0E-01 U01247.1	3.0E-01	3.0E-01 U02369.	3.0E-01	3.0E-01 AL 16320	3.0E-01	3.0E-01 AF07181	3.0E-01 AE00175	3.0E-01	3.0E-01	3.0E-01 AF14167	3.0E-01	\$ 0F-04 AF22050	3.0E-01	3.0E-01	3.0E-01 AF152598	3.0E-01 AF152598	3.0E-01 AW11811	3.0E-01 AB03023	3.0E-01 BF68384	3.0E-01 BF08384	3.0E-01 H51029.1	3.0E-01 H51029.1	3.0E-01 AJ297631	3.0E-01	2.8E-01	2.9E-01	2.0E-01
Expression Signal	3.94	3.94	4.77	3.06	0.61	0.85	0.71	277	1.37	1.3	2.97	1.32	0.51	0.8	0.81	43.84	1.26	0.49	0.49	0.84	1.88	0.73	0.73	1.05	1.95	2.52	5.51	1.43	1.16	2.73
ORF SEQ ID NO:	30924	30925	31142	32598	30567	32510	32770	32985	33159	33648		34207	34564		34972		35714	35908	32909	36155	36157	36179	36180	37694	37695			27481	27710	28658
Exam SEQ ID NO:	18216					19488	19713	19912	20078	20522	20965	21067	21420	21462	21806	22506	22518	22690	22690	22941	22043	22963	22963	24363	24363	25302	25345	14753	14973	16908
Probe SEQ ID NO:	5417	5417	5453	6732	6762	6827	7021	7227	7400	7827	8271	8374	87.28	8770	9118	8858	8988	10042	10042	10294	10298	10316	10316	11772	11772	12416	12803	848	2245	3248

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SEQ Expression (Top) Hit Top Hit Accession (Top) Hit Top Hit Accession (Top) Hit Top Hit Descriptor Signal BLAST E No. Source	4328 0.84 2.9E-01 AU160910.1 EST_HUMAN AU150910 NT2RP2 Homo septiens cDNA clone NT2RP20039013'	1.02 2.9E-01 AF225908.1 NT Arabidopsis thatlana suffonylunes receptor-like protein mRNA, complete cds.	0.65 2.8E-01 M22452.1 NT	0.76 2.8E-01 AJ248287.1 NT	0.76 2.9E-01 A.1248287.1 NT	1.93 2.9E-01 AF128843.1 NT	1.75 2.9E-01/V01394.1 NT	1.75 2.9E-01 V01394.1 NT		1.36 2.8E-01/AA8333/3.1 EST HUMAN	3.55 2.8E-01 AL 139078.2 INT	1.62 2.9E-01 U35025.1 NT	1.62 2.0E-01 U35025.1 NT	4.05 2.9E-01 AF082453.1 NT	1.86 2.9E-01 Y08937.1 NT	1.86 2.9E-01 Y08037.1 NT	1.7 28E-01 U67138.1 NT Rattus norvegicus A-kinsee enchoring protein AKAP150 mRNA, complete cds	1.01 2.8E-01 [28145.1 NT	3.69 2.8E-01 AF168050.1 NT	1.62 2.8E-01 BE313442.1 EST_HUMAN	1.62 2.8E-01 BE313442.1 EST_HUMAN	1.34 2.8E-01 D86550.1 INT	1.11 2.8E-01 AF076238.1 NT	2.04 2.8E-01 AW800020.1 EST_HUMAN	2.35 2.8E-01 ALO47620.1 EST_HUMAN	1.41 2.8E-01 AW611195.1 EST_HUMAN	2.04 2.8E-01 AE000494.1 NT	2.04 2.8E-01 AE000494.1 NT	2.8E-01 AL161 666.2 NT	0.97 2.8E-01 AB020975.1 INT	1.28 2.8E-01 AF179480.1 NT Toxoplesma gondii 30/Da heat-shock protein (HSP90) mRNA, pential cds	2.04 2.8E-01 Z14087.1 NT	2.04 2.8E-01 214037.1	1.13
	0.84	1.02	0.65	0.78	0.76	1.93	1.75	1.75		36.	3.55	1.02	1.62	4.05	1.86	1.86	1.7	1.01	3.60	1.62	1.62	1.34	1.11	204	2.35	1.41	2.04	204	1.89	0.97	1.29	2.04	2.04	1.13
ORF SEQ D. ID NO:	21186 34328	21515 34000		21876 35040				23784 37060	72770					24821 31024		25007 30974	13338					╛		[15193 27934	15284	15380 28118	15736			16132 28788
Probe Exan SEQ ID SEQ ID NO: NO:	8493 21					10810 23		11114 23	76.20		_									1264 140		┙	_	1720 14				_]		_l				3373 161

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	ſ						
Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3978	16728	29360	1.50	2.8E-01	AE001180.1	F	Borrelia burgdorferi (section 68 of 70) of the complete genome
4174	16914		1.95	2.8E-01	2.8E-01 At060868.1	EST_HUMAN	ov44g10.xt Source, testis, NHT Homo agplens cDNA clone IMAGE:1640228 3' similar to conteins Alu repetitive element; contains element MER22 repetitive element;
							Mus musculus chromosome X contigA; putative Magea9 gene, Celtractin, NAD(P) steroid dehydrogenase
4422	17158	ł		2.8E-01	2.8E-01 AL021127.2	Ę	and Zinc finger protein 185
4427	17163	29793	231	2.8E-01 P13615		SWISSPROT	RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN) (L PROTEIN)
4772	17504	30128	1.19	2.8E-01	2.8E-01 AF075238.1	Į.	Hepatitis G virus Isolate 80 (SZNAE12) polyprotein precursor, gene, partial cds
4777	17509	30131	2.67	28€-01	2.8E-01 AF030154.1	Ę	Boyine adenovirus 3 complete genome
4808	17539	30162	1.23	2.8E-01	2.8E-01 BF528188.1	EST_HUMAN	602042601F1 NCI, CGAP, Bm67 Hamo saplens cDNA clone IMAGE:4180129 5
4829	17580	30182	1.91	2.8E-01	2.8E-01 A 272889.1	EST HUMAN	qi50c11.x1 Soeres_NhHMPu_S1 Homo sepiene cDNA cione IMAGE:1876628 3' similar to contains Alu receditive element contains alement LTRS receditive element contains alement LTRS receditive element
5228	25084	30800	24.65	2.8E-01	-	EST HUMAN	EST57072 Infert brain Homo saciens cDNA 51 end
62218	18317	31218	3.07	28E-01	1.5	¥	Homo saplers OCTN2 dere, complete ods
6727	18519		0.95	2.8E-01	L	EST HUMAN	CM1-BN0024-150200-118-012 BN0024 Homo sersiens cDNA
							2/4/101.11 Source ovary furnor NbHOT Homo septems cONA done MAGE:72/4921 5' strater to contains Alu
5848 8	18635		0.63	2.8E-01	2.8E-01 AA404576.1	EST_HUMAN	repetitive element;
6083	25418		0.65	2.8E-01	2.8E-01 M36868.1	F	Bovine 680 bp repeated unit of 1.723 setalitie DNA
6123	18901	31869	1.53	2.8E-01	1.1	Z	Mesembryanthemum crystallinum fructose-biphosphate addiase mRNA, complete cds
6123	18901	31870	1.53	2.BE-01	14		Mesembryanthemum crystallinum fructose-biphosphate addlase mRNA, complete cds
9832	19394	32409	8.34	2.8E-01	2.8E-01 BF611215.1	EST_HUMAN	UI-H-BI4-acif-04-0-UI.s1 NCI_CGAP_Sub8 Hamo espiens aDNA alone IMAGE:30861823
7341	30033	·	7		2 OC 04 1 10 E022 4	Ŀ	Marsies quadrifolis ribuloss-1,5-bisphosphate carborylass/oxygenase large subunit (rbcL) gene, chloroplast
282	2000	22440	- 0	2000		i Ni	United and conditional parties of the conditional conditions of the conditions of th
		3	8	705-01			Concurrential your mistak for G. PDraging protein
7887	20686	33811	1.28	2.85-01	2.8E-01 Al346128.1	EST_HUMAN	qp48h01 x1 NCI_CGAP_Co8 Home saplens cDNA done IMAGE:1926289 3' similar to gb:X06323_cds1 MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
7981	20696	33812	8	285-04	2.8F-01 Al346126 1		9p48h01xf NCI_CGAP_Co8 Home septens oDNA clone IMAGE:1928289 3' similar to gb:X06323_cds1
8108	20802	33935	1.92	2.8E-01		Z	Homo sepiens lanosterol 14-alpha demethylase cytochrome P450 (CYP51) owns. Amm 5
						Т	of02h05.st NCI_CGAP_Co12 Homo sepiens cDNA clone IMAGE:1419993 3' similiar to ob;M87789 IG
8412	21105	34244	. 0.51	2.8E-01	1.1		GAMMA-1 CHAIN C REGION (HUMAN);
8888	21 188		7.34	2.8E-01	.1	T_HUMAN	602022987F1 NCL CGAP_Bm67 Homo sepiens cDNA clone IMAGE:4158525 5
8388	21941	35115	0.02	2.85-01			Neurospora crassa negative regulator suifur controller-2 (scon-2) gene, complete ods
<u>¥</u>	7528		0.88	2.8E-01 L13654.1			Lycoperation seculentum percediase (TPX1) mRNA, complete ods
9788	22439	35848	0.00	2.8E-01	2.8E-01 AF132728.1	Ę	Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds

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		~	_		_			_							_					_										_
	Top Hit Descriptor	Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds	Raffus norvegicus glycerol-3-phosphate dehydrogenase gene, promoters A and B and exons 1a and 1b; nuclear gene for mitochondrial product	Homo septens hypothetices protein (LOC5/319), mRNA	Fullnerni sercoma virus, complete genome	801654822R1 N#L MGC_57 Hano septens cDNA clane IMAGE:3839786 3'	601880794F1 NIH_MGC_55 Hamo saplens cDNA clone IMAGE:4109350 5	801880794F1 NIH MGC 55 Hamp saplens cDNA dans IMAGE:4100350 5	801852148F1 NIH_MGC_56 Hamo sepiens cDNA clone IMAGE:4076028 67	Oroeophila heteroneura fruitees (fru) gene, alternative spiice products, 5 flanking region, excns 1 through 7 and complete cds	802137418F1 NIH MGC 83 Homo septens cDNA clone IMA QF-4.0773853 F1	Carroylobacter jejuni NCTC11168 complete cenome: segment 1/8	Mus musculus DNA for prostaciandin D2 swithese complete of a	PM4-HT0606-030400-001-e07 HT0606 Homo septems cDNA	601673020F1 NIH MGC_21 Hamo sepiens aDNA dane IMAGE:3955888 5	Homo septens CDC42-binding protein kinase beta (DMPK-Ike) (CDC42BPB), mRNA	W498g05.x1 NCI_CGAP_K43 Homo septens cDNA clone MAGE:2527g28 3	Rettus norvegicus CDK104 mRNA	263910.s1 Sceres, total fetus Nb2HF8_9w Homo saplens cDNA clone IMAGE:788827 3' similar to contains Afu repetitive element:	Ipomoea purpurea transposable element Tip100 gene for transposase, complete cuts	Glamblia SR2 gene	2422/110.r1 Scenes_fetal_heart_NbHH19W Homo sepiens cDNA clone IMAGE:341443 5	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCL FOPROTEIN P40!	Rettus norveolous vesicular monoamine transporter hose 2 promotes randon and avvo.	Felme trimunodeficiency whus envigence include ITT0088PIU (M88), partial	te43o11.22 NCL_CGAP_Lu25 Homo septens cDNA clone IMAGE:2046836 3' similar to contains element L1 receittre element:	Mus musculus serine probase inhibitor 14 (Soi14) mRNA complete Als	CM1-HT0875-060000-385-e05 HT0876 Homo sepiens cDNA	Rattus norvegious Insulin receptor (Iner.), mRNA	wo92e11.x1 NCI_CGAP_Kid11 Homo septens cDNA clone IMAGE:2452828 3'
51 1100	Top Hit Detabase Source	LN	TN	N.	Z	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	Ĭ	EST HUMAN	LN LN	LZ LZ	EST HUMAN	EST HUMAN	E	EST_HUMAN	NT	EST HUMAN	¥	Į.	EST HUMAN	SWISSPROT	Ę	Z	EST HIMAN	Ų	EST HUMAN	Ę	EST HUMAN
	Top Hit Acession No.	2.8E-01 AF132728.1	2.8E-01 AF294393.1	7708163 NT	5826154 NT	2.8E-01 BE959727.2	2.8E-01 BF241062.1	BF241062.1	2.8E-01 BF695970.1		Γ	42		2.8E-01 BE178899.1	2.8E-01 BE900116.1	11433629	AW025400.1	1	2.7E-01 AA450061.1	2.7E-01 AB004908.1		2.7E-01 W58067.1		2.7E-01 AF047575.1	L	2.7E-01 Al310858.1	T	2.7E-01 BF088284.1	920	2.7E-01 AI928015.1
	Most Similar (Top) Hit BLAST E Value	2.8E-01	2.8E-01	2.8E-01	2.8E-01	2.8E-01	2.85-01	2.85-01	2.8€-01	2.8E-01	2.8E-01	2.8E-01	2.8E-01	2.8E-01	2.8E-01	2.8E-01	2.8E-01 AW0254	2.7E-01 Y17324.	2.7E-01	2.7E-01	2.7E-01	2.7E-01	27E-01	2.7E-01	2.7E-01 Y13868.	2.7E-01	2.7E-01	2.7E-01	2.7E-01	2.7E-01
	Expression Signal	0.66	0.52	3.35	1.47	9.0	2.42	242	3.83	1.33	4.51	17.65	15.41	422	1.77	2.52	1.49	3.97	3.25	213	1.58	3.5	2.56	2.25	10.01	4.07	12	2.63	0.68	1.97
	ORF SEQ ID NO:	35847	35700	35813		36109	36573	36574	36603	36719		37510		31013	31019			25890	28007	28654		27164	27242		27826	27914	28314		28683	28374
	Exen SEQ ID NO:	22439	22500	22608	22859			23335	23362	23477	806EZ	24192	24789	24861	24877	25306	25401	13249	13377	13987	14364	14465	14511	15586	15089	15175	15006	15740	16044	16740
	Probe SEQ (D NO:	9788	9850	0966	10211	10251	10644	10844	10671	10794	11247	11563	12406	12509	12632	12685	12806	484	500	1238	1617	1722	1700	2131	2367	2457	2899	2983	3283	3992

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Top Hit Descriptor	Drosophila buzzati alpha-esterase 6 (aE6) gene, pertial cds	Droscophile buzzati alpha-esterase 6 (aE6) gene, pertial cds	Homo sapiens DiGeorge syndrome critical region, telomeric end	RC1-CT0286-230200-016-603 CT0286 Homo septems cDNA	280801.r1 Strategene colon (#837204) Homo saplens cINIA clone IMAGE:511848 5' similar to gb:X85488_cds1 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HUMAN):	280a01.rf Strategene colon (#837204) Homo septens CDNA clone IMAGE:511848 5' stritter to ab:X85488 cds1 HETEROGENOUS NUCLEAR RIBONIK'S FORROTEIN 117H MANN:	HOMEOBOX PROTEIN HOX 44 (CHOX-1.4)	Astreopora myriophthalma mitochondrial cytb gene for cytochrome b, partial cds	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT)	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1) (TBANSFORMING GROWTH FACTOR BETA 1 BINDING PROTEIN 1 APAC 61 19 19 19 19 19 19 19 19 19 19 19 19 19	Archaeoglobus fulgicus section 13 of 172 of the complete necessity	Archaeoglobus fulgidus section 13 of 172 of the complete genome	FIBRILLIN 1 PRECURSOR	Drosophills melanogaster rfc40 protein, Rop protein (Rop), and small GTP binding protein (DRas2) genes, complete cds	MOBROBIAT NO! CGAP CLL1 Homo sablens cDNA clane MA GE: 2075/103 3'	HYPOTHETICAL 20,9 KD PROTEIN BOSS3.3 IN CHROMOSOME X	NITROGEN REGULATORY PROTEIN NUT1	NITROGEN REGULATORY PROTEIN NUT1	Bos taurus micromolar celcium activated neutral protesse 1 (CAPN1) gene, exons 11-20, and pertial cds	Bos taurus micromoler calcium activated neutral professe 1 (CAPN1) cens. acons 11-20, and partial cds	EST58740 Infant brain Homo sabiens cDNA 5' end similar to similar to myosin-binding protein H	EST58740 Infant brain Homo sabiens cDNA 5' end similar to similar to myosin-binding protein H	Orycholegus cuniculus UDP-glucuronosyftransferase (UGT2B13) mRNA, complete cds	2835011.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360957 3' similar to contains Alu repetifive element.
Top Hit Detaberse Source	Ę	NT	E E	EST_HUMAN	EST HUMAN	EST HUMAN	T	Г	SWISSPROT	TOGGSSIMS	7		ISSPROT	Į, į	EST HUMAN	Г	SWISSPROT	SWISSPROT	NT IN	NT B	EST HUMAN E	П	E L	EST_HUMAN IN
Top Hit Acession No.	2.7E-01 AF216214.1	2.7E-01 AF216214.1	2.7E-01 L77599.1	2.7E-01 AW858131.1	2.7E-01 AA100658.1	2.7E-01 AA100656.1		2.7E-01 AB033171.1	Q00918	870000	7		2.7E-01 Q61554		2.7E-01 AI540070.1	011070	Q01168	201168	2.7E-01 AF248054.1	2.7E-01 AF248054.1	2.7E-01 AA351121.1	Γ	2.7E-01 L01081.1	2
Most Similer (Top) Hit BLAST E Value	2.7E-01	2.7E-01	2.7E-01	2.11年-01	2.7E-01	2.7E-01	2.7E-01 P17277	2.7E-01	2.7E-01 Q00918	2 75 C	276-01	275-01	2.7E-01	275-01	27E-01	2.7E-01 Q11079	2.7E-01 Q01168	2.7E-01 Q01168	2.7E-01	2.7E-01	2.7E-01	2.7E-01	2.7E-01	2.7E-01 AA01314
Expression Signal	0.69	0.09	212	2.85	2.53	2.53	239	0.85	0.88	8	0.83	0.93	223	0.58	0.79	0.74	0.75	0.75	2.16	2.16	9.0	.0 9.0	0.71	0.68
ORF SEQ ID NO:	08888		78284		30339	30340	30509		31995	31000	32282	32283	32637	32689	-	33015	33225	33226	33363	33364	33411	33412	33472	33583
Exam SEQ ID NO:			16754	17703	17733	17733	17983	18202	19023	19023	19280	19280	19598	19653	19434	19940	20134	20134	20256	20256	20303	20303	20358	20459
Probe SEQ ID NO:	4005	4002	4008	4980	5011	5011	5185	5402	6249	6249	8615	6515	9681	6916	2982	7256	7461	7461	7688	7588	8892	7838	7894	7763

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	_			_			
Probe SEQ ID S NO:	Exen C	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7925	20620		0.53	2.7E-01	2.7E-01 AF048820.1	Ę	Ceraesius euratus pituitary adenylate cyclase activating polypeptide type 1 receptor precursor mRNA, complete cds
8086	20780	33909	0.51	2.7E-01	2.7E-01 R39257.1	EST_HUMAN	yc91h06.s1 Soares Infant brain 1NIB Homo sepiens cDNA clone IMAGE:23511 3'
8190	20884	34022	0.8	2.7E-01	2.7E-01 AL161552.2	Z	Arabidopsis theliens DNA chromosome 4, contig fragment No. 52
8657	21349	34494	0.59	2.7E-01	2.7E-01 Q14764	SWISSPROT	MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN)
8925	21616	34760	0.48	2.7E-01	2.7E-01 X03216.1	Z	Staphylococcus aureus transposon Tn554
9232	21911	35084	10.41	2.7E-01	2.7E-01 083800	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9232	21911	35085	10.41	2.7E-01 083809	083809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9235	21914		2	2.7E-01 P37928	P37928	SWISSPROT	FIMBRIAE W PROTEIN
0020	22384	35546	2	2 75.04	2 7E 04 Decem 4	ţ	Rathus norvegicus DNA for percedsome assembly factor-2, exen 4, 5, 6, 7, 8, 9, 10, 11,12, 13, 14, 15, 16, 17
9861	22820	35838	17.0	275-01	2.7E-01 AF001848 1		Oncholonia calmanulin C mRNA partial cris
10018	22888	35882	3.00	2.7E-01	2 7E-01 AF087434 1		Mas muscalus transcribiton factor NEATC tenform a (NEATCs) mRNA complete cie
10149	78722	36012	0.57	2.7E-01	2.7E-01 AF150639.1		Homo sepiens xeroderna plamentasum complementation croup C (XPC) cene intro 9
10149	22797	36013	0.57	27E-01	27E-01 AF150539.1		Homo saplens vandeme plamentosum complementation group C (XPC) gene, Intron 9
10714	23403	39842	1.62	2.7E-01	AV705043.1	EST HUMAN	AV705043 ADB Homo septeme aDNA clame ADBCOD05 5'
10714	23403	36643	1.62	2.75-01	2.7E-01 AV705043.1	HUMAN	AV705043 ADB Homo sepiens dDNA done ADBCOD05 5
10724	23412	36653	3.13	2.7E-01	2.7E-01 AJ133269.1	ŢN	Homo saplens cavedin-1/-2 locus, Config1, D7S522, genes CAV2 (exons 1, 2s, and 2b), CAV1 (exons 1 and 2)
11820	24406		4.6	2.7E-01 014181	014181	ISSPROT	PUTATIVE 60S RIBOSOMAL PROTEIN CAF8.06C
	25190		1.49	2.7E-01	2.7E-01 AB008782.1	Į.	Arabidoposis thaliana mRNA for eutliate transporter, complete ods
	24963		283	2.7E-01	2.7E-01 AF217491.1	LN	Homo saplens fragile 16D codo reductase (FOR) gene, excn 6
12811	25054	30929	1.95	2.7E-01	2.7E-01 AV742419.1	EST HUMAN	AV742419 CB Homo sepiens cDNA clone CBMAXF02 5*
457	15542	25883	203	2.0E-01 P78411	P78411	SWISSPROT	IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-2
	13254		1.38	2.0E-01 D16459.	D16459.1	٦	Bos teurus mRNA for mb-1, complete cds
	14120	26795	1.65	2.6E-01	2.6E-01 BE885087.1	T_HUMAN	601510838F1 NIH_MGC_71 Homo sepiens cDNA clone IMAGE:3912345 5
1417	14165	26848	1.14	2.05-01	2.6E-01 AB013290.1	Г	Olycine max pseudogene for Bd 30K
	14626	27335	4.33	2.0E-01	2.0E-01 AL1014722	IN	Arabidopsis fhallana DNA chromosome 4, contig fragment No. 2
1880	14626	27338	4.33	2.6E-01	2.6E-01 AL161472.2	١	Arabidopsis thallana DNA chromosome 4, contig fragment No. 2
		•					bb04d10.x1 NIH_MGC_14 Homo septens cDNA clone IMAGE:2958451 3' similar to db:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN); gb:M14630_cds1 Mouse surfeit locus surfeit 3 protein gene
1	14818		10.48	2.0E-01	2.0E-01 AW733152.1	T HUMAN	(MOUSE);
_1	14878	27613	3.7	2.0E-01	2.0E-01 M11844.1		Humen prealbumin gene, complete cds
2476	15194	_	1.62	2.6E-01	2.6E-01 Y12998.1	LN LN	B.marttmus rbcL gene

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	_		_						_																		_				
Top Hit Descriptor	Homo sepiens serine palmitry, transferase, subunit II gene, complete ods, and unknown genes	IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (IGA1 PROTEASE)	Aquifex aedicus section 12 of 109 of the complete genome	7h23d04.x1 NCI_CGAP_Co16 Home suppers cDNA done IMAGE:3316807 3' similar to SW:PRSB_XENLA 042896 268 PROTEASE REGULATORY SUBUNIT 6A	D.discoldeum (Ax3-K) panA gene	S.pambe sw/6 gene	Borine adenovirus 3 complete genome	Oryza longistaminata receptor kinase-like protein, family member D, and retrofit (geg/pol) genes, complete ods	H.suplens AGT gene, Pati fragment of Intran 4	Escherichia celi K-12 MG1655 section 202 of 400 of the complete genome	Raffus norvegicus mRNA for aichaB crystallin-related protein, complete ods	Arabidopsis theliana DNA chromosome 4, contig fragment No. 85	Hepetitis C virus genomic RNA for polyprotein, complete cds	wo33d05x1 NCI_CGAP_Ges4 Homo saplens cDNA clone IMAGE:2457129 3	wo33405x1 NCI_CGAP_Ces4 Homo septems cDNA clone IMAGE:2457129 3'	Glycine max mRNA for mitatic cyclin b1-type, complete cds	Mus musculus Wm protein (Wm) gene, complete cds	Mus musculus Wm protein (Wm) gene, complete ods	Gallus gallus brain-derhed neurotrophic factor (BDNF) gene, 5' end	Branchipetoma floridae mRNA for calmodulin 2 (caM2 gene)	7154404.x1 NCI_CGAP_B116 Homo septens cDNA clone IMAGE:3338503 3' stmiler to SW:SFR4_HUMAN Q08170 SPLICING FACTOR, ARGININESERINE-RICH 4 ; contains element TAR1 TAR1 repetitive element		Drosophwa mekanogastar poda MAP Khase gene, complete cos	Homo sepiens HSPC142 protein (HSPC142), mRNA	AV733787 cdA Homo sepiens cDNA clone cdAADE11 5	wc62c11.x1 NC_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2323220 3' skniker to gb.,103494	PROCOLLAGEN ALPHA 2(1) CHAIN PRECURSOR (HUMAN);	Bos taurus guanylyl cyclase-activating protein 2 (guos2) mRNA, complete cds	yySSo11.r1 Soares_multiple_solerosis_ZNB-HMSP Homo sepiens cDNA clone IMAGE:277460 6	Mus musculus DXImx48e protein (DXImx48e) mRNA, complete cds	Tetrahymens themophila macronuclesr gene encoding ribosomal protein L3, exons 1-2
Top Hit Database Source	Z	SWISSPROT	NT.	EST HUMAN	Z	¥	LA	Z	¥	۲	F	Z	N	EST HUMAN	EST HUMAN	Z	Z	F	Ę	¥	A V V V V V V V V V V V V V V V V V V V	L'ALLINGUE I	Z	F	EST_HUMAN		EST HUMAN	NT	EST_HUMAN	LN	IN
Top Hit Acession No.	2.4E-01 AF111168.2	P45384	2.4E-01 AE000680.1	2.4E-01 BF002171.1	230534.1	2.4E-01 X71783.1	2.4E-01 AF030154.1	2.4E-01 U72728.1	X74209.1	2.4E-01 AE000312.1	2.4E-01 D29980.1	2.4E-01 AL161589.2	2.4E-01 D00944.1	2.4E-01 AI925707.1	-		2.4E-01 AF001216.1	2.4E-01 AF001218.1		2.4E-01 AJ133836.2	P occurred to the state of		Al-Woo46.1	661801	2.4E-01 AV733787.1		2.4E-01 Al698989.1			2.4E-01 AF229644.1	
Most Similar (Top) Hit BLAST E Veitue	2.4E-01	2.4E-01 P45384	2.4E-01	2.4E-01	2.4E-01 Z38534.1	2.4E-01	2.45-01	2.4E-01	2.4E-01 X74209.1	2.4E-01	2.4E-01	24E-01	245-01	2.4E-01	2.4E-01 AI925707	2.4E-01 D50871.1	2.4E-01	2.4E-01	2.4E-01	2.4E-01	1000	2010		2.4E-01	2.4E-01		24E-01/	2.4E-01 LA3001.1	2.4E-01 N48732.1	2.4E-01	24E-01
Expression Signel	1.1	1.44	2.28	1.38	2.48	2.16	2.84	2.04	1.48	67.0	0.74	1.09	96.0	96.0	96.0	8.0	8.16	8.16	0.77	0.00	6	77	3	2.83	0.67		223	9.5	0.65	0.84	1.01
ORF SEQ ID NO:	27594		27725	27843	27994	28213	28234		28554	29131	<u> </u>		30317	30865	30886	30891	31275	31276			24500	21000	2102/	31741	31793		32208	33004	33163	33400	34078
SEQ ID NO:	14864		14985	15104	15254	15470	15494		15909	16496	18756	17610	17712	18175	18175	18197	18308	18366	18392	25078	7070	1000	1000	18790	18830		19200	19928	28 88 87	20291	20941
Probe SEQ ID NO:	2134	2165	2258	2382	2539	2785	2789	3129	3145	3743	4010	4883	4989	5375	6376	5397	5569	6560	5597	5799	S C	400	3	8685 87	9090		444	7243	404	7825	8247

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Top Hit Descriptor	801877878F1 NIH_MGC_55 Hamo septems cDNA clane IMAGE:4108288 5	602086188F1 NIH_MGC_83 Hamo sepiens cDNA clane IMAGE:4250372 5	Campylobacter jejuni NCTC11168 complete genome; segment 4/6	Cempylobacter Jejuni NCTC11168 complete genome; segment 4/8	wd43e02.x1 Soares_NR_T_GBC_S1 Homo sepiens cDNA clone IMAGE:2330906 3' similar to contains MER22.b1 TAR1 repetitive element :	Drosophilla melangasatar SKPB gene, complete cds	Drosophila melanogaster SKPB gene, complete cds	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR	Arabidopsis thallene DNA ohromosome 4, contig fragment No. 6	Mus musculus type 1 sigms receptor gene, complete cds	P. aslatica mosaic virus genomic RNA	601441421T1 NIH_MGC_65 Hamo septens aDNA clone IMAGE:3845836 3'	Homo sapiens fragile 16D oxido reductase (FOR) gene, exon 6	Arabidopsis thaliana ethylene-tneensitive3-like1 (EIL1) mRNA, complete cds	Mus musculus mRNA for putative mo? protein (mo? gene)	Gallus gallus gene coding for e-actin	801842848F1 NIH_MGC_54 Homo sepiens cDNA clone IMAGE:4083739 5	Homo sepiens chromosome 21 segment HS21C081	aromatase [Posphila guttata≂zabra finches, ovary, mRNA, 3188 nt]	Mycoplasma genitalium section 35 of 51 of the complete genome	Metherrococcus Janneschii section 138 of 150 of the complete genome	601142073F1 NIH_MGC_14 Hamo suplens aDNA olane IMAGE:3505818 5	Yershite peats HmeH (hmeH), HmeF (hmeF), HmeR (hmeR), and HmeS (funsS) genes, complete cds	Brassica napus sig gene for S-locus glycoprotein, cutiffixer T2	Mus musculus odh5 gene, econ 1, partial	Homo septens partial intron 3 of the wild type AF-4/FEL gene	601175562F1 NIH_MGC_17 Homo sepiens oDNA clone IMAGE:3531015 5	Human erythropoletin gene, complete cds	Merinilabilia ageroxorans gyrB gene for DNA gyrase subunit B, pertial cds, strain:IFO 14957	no16d08.s1 NCI_CGAP_Phe1 Hame septens cDNA done IMAGE:1100843.3' stimiter to contains Alu repetitive element;contains element THR repetitive element;	yh21b07.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:130357.37
Top Hit Database Source	EST HUMAN 8018	EST_HUMAN 002	1	NT		NT	_	SWISSPROT COL	Г		SB'd LN	T_HUMAN	NT Hom	NT Arab		NT COLIN	EST_HUMAN 6018		NT		NT Med	EST HUMAN 6011	NT Yers	NT Brass	NT	Hom	EST_HUMAN 6011	NT Hum	NT	EST_HUMAN repel	П
Top Hit Acession No.	BF242794.1	BF678275.1	77	2	2.4E-01 Al693515.1		<u>:</u>	2.4E-01 Q03892	2.4E-01 AL161494.2	2.4E-01 AF030199.1		2.4E-01 BE617638.1 E		1.1		2.4E-01 V01507.1	2.4E-01 BF184542.1	1.2			2.3E-01 U67598.1	2.3E-01 BE311893.1 E	2.3E-01 U22837.2 N	2.3E-01 AJ245480.1		2	2.1	2.3E.01 M11319.1 N	2.3E-01 AB015033.1 N	2.3E-01 AA601379.1	
Most Similar (Top) Hit BLAST E Value	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	246-01	24E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.4E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	235-01	2.3E-01	2.3E-01	2.3E-01	2.3E-01	2.3€-01	2.3E-01	2.3E-01
Expression	1.02	0.47	0.40	0.49	7.01	0.88	0.88	1.68	4.8	1.39	2.09	1.32	1.75	234	2.74	1.97	2.08	3.96	1.06	5	33.31	4.19	1.12	123	2.74	1.51	2.86	1.59	3.38	1.36	7.07
ORF SEQ ID NO:	34332		34874	34875	35181	35441	35442	36202	36598	39671		37765	37801						25810		26069	26341		27035	27063		27903	28105	26789	28379	
Exon SEQ ID NO:	21189	21244	21720	21720	22013	22256	22256	22984		i i						25162					13430	13680	14305	14345	14374	14772		15367	14114		Ш
Probe SEQ ID NO:	8497	8552	9030	9030	9463	9603	9603	10337	10667	10739	11158	11840	11891	12019	12080	12287	12400	12720	380	622	662	913	1558	1599	1628	2038	2447	2057	2827	2963	3082

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Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Vatue	Top Hit Acession No.	Top Hit Databese Source	Top Hit Descriptor
3363	16122	28780	1.14	2.3E-01	H69836.1	EST_HUMAN	yr97h10.r1 Soares fetal liver splean 1NFLS Homo sapiens aDNA clone IMAGE:213283 51
3821	16573	20202	1.01	2.3E-01	\$82821.1	ĖN	GSTA5-glutathione S-transferase Yc2 subunit (5 region, Intron 1) [rats, Morris hepatoma ceil line, Genomic, 2212 nt, segment 1 of 3]
3914	18864		6.22	2.3E-01	7862133 NT	Ę	Homo sepiens KIAA0450 gene product (KIAA0450), mRNA
4316	17055	29680			2.3E-01 R82252.1	EST_HUMAN	1/17/01.11 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:149017 5"
4368	17106		1.98	23E-01		M	Mus musculus renin (Ren-1c) gene, promoter region
4417			1.03	2.3E-01	2.3E-01 D90999.1	Z	Synechocystis sp. PCC8803 complete genome, 1/27, 1-133859
4454	17190	29816	2.51	2.3E-01	2.3E-01 AF092535.1	M	Homo sepiens mitogen-ectivated protein kinase p38delta (PRKM13) mRNA, complete cds
4517	17252	18862	6.19	23E-01	5031984 NT	N.	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA
4988	17711	30316	0.84	2.3E-01	1	¥	Mus musculus tulip 1 mRNA, complete cds
5221	18028	30654	2.53	2.35-01	2.3E-01 AB040945.1	Z	Homo sepiens mRNA for KIAA1612 protein, pential cds
1							7/30b08.x1 NCI_CGAP_OV18 Home septens cDNA done INAGE:3476699 3' similar to SW;GAG_SMSAV prospection for the property of the p
5343	18146	30825	208	2.3E-01	2.3E-01 BF058381.1	EST HUMAN	PROSSE GAG POLITRO I EIN (CONTAINS) CORE PROTEIN 715; INNER COAT PROTEIN 715; CORE SHELL PROTEIN P36; NUCLEOPROTEIN P461;
5443	18242	31130		2.3E-01		Z	C.familiants rom1 gone
5563	18380		0.94	2.3E-01		Į.	Vitariorma comeum emell subunit ribosomal RNA gene
5665	18460	31374	0.76	2.3€-01		M	23S rRNA [Leuconosioc carnosum, Genomic, 2866 nt]
5851	18638	31575	1.50	2.3E-01		EST HUMAN	as27e12.xi Barstead acrta HPLRB6 Home septens cDNA clone IMAGE:2318446.3' similar to gc:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN)
							as27e12.x1 Barsteed acrta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446.3' similar to gb:X13238
5851	18638	31576	1.59	2.3E-01	2.3E-01 AI708840.1	EST_HUMAN	CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
655B	10323	02268	80 0	2 2E 04	2 3E-04 AE408089 4	5	Oryctolegus cuniculus cytochrome addase subunit VIa (catVIa2) mRNA, complete ods; nuclear gene for mitochonetal product
			1				8942/12x1 Bersteed acts HPLRB6 Homo serviers cONA clone IMAGE: 2319887 3' strailer to contains Altu
6778	19522	32549	4.33	2.3E-01	2.3E-01 AI718148.1	EST_HUMAN	repositive element;
7011	19703	32759	1.08	2.3E-01	923323	Į.	Homo saplens hypothetical protein FLI20345 (FLI20345), mRNA
7188	19874	32947	6.0	2.3E-01	2.3E-01 AF000227.1	Ę	Secale cereale amega seculin gene, complete ods
7315	19998	33077	3.14	2.3E-01	1	F	Glycine max resistance protein LM17 precursor RNA, pertial cds
7318		33079	0.64	2.35-01	-	EST_HUMAN	AV719881 GLC Homo sepiens aDNA clane GLCDGB08 5'
7318	20001	33080	0.64	2.3E-01	2.3E-01 AV719681.1 EST	EST_HUMAN	AV719881 GLC Homo sepiens aDNA clane GLCDGB08 5'
7508			2.94	2.35-01			Mus musculus myosin XV (Myo15), mRNA
7513		33278	1.38	2.3E-01	.1	HUMAN	801511573F1 NIH_MGC-71 Homo saplens cDNA clone IMAGE:3912859 5
7652			2.73	2.3E-01	2.3E-01 N80983.1	T HUMAN	2x12x08.r1 Soares fetal liver spleen 1NFLS Homo expiens cDNA clone IMAGE:292358 51
7750	20446	33569	0.71	2.3E-01	2	N	Anabidopsis thallans DNA chromosome 4, contig fragment No. 58

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Probe SEQ ID NO:	SEO ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similer (Top) Hit BLAST E Vælue	Top Hit Acession No.	Top Hit Defabese Source	Top Hit Descriptor
7892	20587	33717	2.16	2.3E-01	2.3E-01 M68831.1	¥	Oxytricha nova macronuclear telomere-binding protein alpha subunit (tel-alpha atanine version) gene, complete cds
8391	21084	34217	25.0	2.3E-01	2.3E-01 U57999.1	Z	Mus musculus prosaposin (peapISGP-1) gene, complete cds
8671		34510	0.56	2.3E-01	2.3E-01 AW090541.1	EST_HUMAN	xx90e06.x1 NCI_CGAP_Bm35 Homo sepiens cDNA clone IMAGE:2591554 3'
8786			0.45	2.3€-01	2.3E-01 AW864460.1	EST_HUMAN	EST378533 MAGE resequences, MAGH Homo septens cDNA
9039	21729	34883	1.02	23E-01	2.3E-01 AA372164.1	EST_HUMAN	EST84081 Phabdomyoearcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X63368)
8038			1.02	2.3E-01	2.3E-01 AA372164.1	EST_HUMAN	EST84061 Rhebdomyosarcoma Homo sepiens cDNA 5' end straiter to DnaJ homotog (GB:X83388)
9480	22133	35313	0.62	2.3E-01	0679318 NT	F	Mus musculus phosphatidylinositol 3-kinase catalytic subunit detta (Pit3cd), mRNA
8008	22262	i	29'0	2.3E-01	2.3E-01 U77974.1	F	Tribolitum castaneum transcription factor homolog (To-eve) gene, complete cds
8296	22281	35471	9.0	2.3E-01	2.3E-01 BE277880.1	EST_HUMAN	801120110F1 NIH_MGC_20 Hamo septens cDNA clane IMAGE:2886739 5'
9682	22334	35529	0.59	2.3E-01	2.3E-01 AW964460.1	EST_HUMAN	EST376533 MAGE resequences, MAGH Homo septens cDNA
9731	22382	35584	1.02	235-01	2.3E-01 X52124.1	<u> </u>	Heemophilus influenzae genee for Hincil restriction-modification system (Hincil methytransferase (EC 2.1.1.72) and Hincil endomiclesse (EC 3.1.2.1.4.1)
9767	22418	35625	0.56	2.3E-01	2.3E-01 AW364633.1	EST HUMAN	PM2-DT0036-281299-001-f04 DT0036 Homo sapiens cDNA
9834	22485		2.45	236-01	2.3E-01 BE173080.1	EST_HUMAN	MR0-HT0559-240400-014-g11 HT0559 Homo sapiens cDNA
9802			2.76	2.35-01	2.3E-01 AJ283261.1	N FN	Rhizobium leguminosarum partial genomic DNA for exceptionsechante biosynthesis genes
10340		36205	0.84	2.3E-01	2.3E-01 AF201929.1	N	Murine hepatitis whus strain 2, complete genome
10351	22998		5.11	2.3E-01	2.3E-01 BF133577.1	EST_HUMAN	601646155R2 NIH_MGC_50 Hamo septens cDNA clane IMAGE:4102062 3'
10937	23617	36867	1.40	2.3E-01	2.3E-01 AF004833.1	NT	Mus musculus tissue factor pethway inhibitor (TFPI) mRNA, complete cds
10937	23617	36868	1.49	2.3€-01	2.3E-01 AF004833.1	IN	Mus musculus fissue factor pathway inhibitor (TFPI) mRNA, complete cds
<u>+</u>	23811	37092	1.77	2.3E-01	2.3E-01 AJ250189.1	NT	Mus musculus pertial mRNA for muscle protein 534 (mg534 gene)
<u> </u>	23811	37003	1.77	2.3E-01	1	TN	Mus musculus pertial mRNA for muscle protein 534 (mg534 gene)
11324	24015	37318	3.03	2.3E-01	2	ŅŢ	Chlemydophlia pneumoniae AR39, section 4 of 94 of the complete genome
11815	24483		1.75	2.3E-01	2.3E-01 AV709736.1	EST_HUMAN	AV709736 ADC Homo sepiens cDNA clone ADCAGH01 5'
44055	06770			100			Homo septems Integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor) (ITGA3), transcript
2	2 2	1	1.33	2.35-01	2000010	LA.	Verkerit b., mid V.A.
128	24239		4.47	2.35-01		Ę	Borrella burgdorferi 2.8-6 locus, ORF-A-D genes, complete ods and REP+ gene, partial ods
12088 88	24583		4.88	23E-01		EST_HUMAN	HCOEST44 HT29M8 Hamo expiers aDNA clare HCoE44 6
12120	24612		1.62	2.3E-01	2.3E-01 AW863940.1	EST HUMAN	PM4-SN0012-030400-001-b06 SN0012 Homo sepiene cDNA
12173	25319	30711	288	235-01/	2.3E-01/AW303623.1	EST HUMAN	xxZ1d07.x1 Sogree_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:2813773 3' similar to TR:Q9Z175 O9Z175 I YSY1_OXIDASE-RFI ATED PROTEIN 2 : contable pTR5 to 1AB1 requirities alegant 1
12208	25366	30613	8.63	2.3E-01		7	601507202F1 NIH MGC 71 Homo septems cDNA clone MAGE-3008689 5
12255	24701		2.51	2.3E-01	2.3E-01 BF883319.1	EST HUMAN	60214459F1 NIH MGC 48 Homo saplens cDNA clone IMAGE 4297719 5
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Probe SEQ:ID NO:	Econ SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
12303			2.35		AJ006519.1	N	Rattus norvegicus mRNA for eold gated ion channel
12398	24784		1.76		U49645.1	N N	Pleurodeles wallt distal-less like probin PwDix-3 (PwDix-3) mRNA, complete ods
12403	24728		1.55		2.3E-01 AJ008519.1	LN	Raftus nonegicus mRNA for acid gated ion channel
12647	24952		2		2.3E-01 BF473611.1	EST HUMAN	nec38h12x1 Lupeki_sokatic_nerve Homo saplens cDNA clone MAAGE:3385950 3' similar to contains element. MER38 repetitive element :
88	l	25562	8,1		1 -	EST HUMAN	oz14er10.x1 Scense_febal_Rver_splean_1NFLS_S1 Homo saplens cDNA done IMAGE:1676290 3' similar to TR:013040 013040 ATP-BINDING CASSETTE PROTEIN:
1557	14304	20883	1.04	2.2E-01	2.2E-01 AF187850.1	N _T	Homo septens PPAR delta gene, promoter region
2082	14814	27547	252	2.2E-01	2.2E-01 M34840.1	LN L	Fresh-water sponge Emf1 alpha collegen (COLF1) gene
2402		27880	6.3		2.2E-01 BF677538.1	EST_HUMAN	602085608F1 NIH_MGC_83 Hamo sepiens cDNA clone IMAGE:4249999 5'
2594		28044	2.02	2.2€-01	2.2E-01 BE018258.1	EST HUMAN	601462628F1 NIH_MGC_67 Hamp septens cDNA clane IMAGE:3966190 5'
2594		28045			2.2E-01 BE618258.1	EST HUMAN	801482829F1 NIH_MGC_67 Hano sepiens aDNA clone IMAGE:3898190 5
7887		28294	4.36		2.2€-01 BE165625.1	EST_HUMAN	PM2-HT0363-281299-003-#12 HT0363 Homo sepiens cDNA
2884	15651	28295	4.36	2.2€-01	2.2E-01 BE155625.1	EST_HUMAN	PM2-HT0353-281289-003-412 HT0353 Homo septems cDNA
2021	15887		1.57	2.2€-01		Ę	Homo sapiens FRA3B common fractile region, diadenosine triphosohate hydrolese (FHIT) nerve, evon 5
3387	16146		1.97	225-01	7	TN	Arethdopsis thelens DNA chromosome 4, config fregment No. 52
3794			1.12		2	Z	Xphophorus maculatus truncated RexT retrotransposon reverse transcriptase (RT) pseudogene
4105	16848		0.72			LN.	Mus musculus breestloverien cencer susceptibility protein (BRCA1) mRNA, complete cds
4404	16045	208.82	W 4	20.00		l t	Mus musculus mbed lineage kinase 3 (MII3) and two pare domain K+ channel subunit (Konkd) genes,
1232	L	20507	244	225.04	-	L	We miss the MAD Whee kinese these 1 (Mat/A) mDNA Amadata Ale
4232	L	29598	211	275-01		LN	Muse musculus MAP kinase kinase kinase 1 (Mekr.) mRNA, complete cds
4323	L	29689	1.21	22€-01		LN	Human scRNA (BC200 beta) pseudogene
4323	17062	29690	1.21	2.2€-01	2.2E-01 U01307.1	E	Human scRNA (BC200 bets) peeudogene
4775	17507		1.38	2.2E-01	2.2E-01 D50604.1	ΙN	Human beta-cytoplesmic actin (ACTBP9) pseudogene
4779	17511	30133	2.1	2.2E-01	2.2E-01 AA211216.1	EST_HUMAN	2487005.r1 Stratagene INT neuron (#937233) Homo saplens cDNA clone IMAGE:648968 5
4082			1.1	2.2E-01		TN	Mus musculus vincuiin gene, exan 3
2062			0.93	2.2€-01	2.2E-01 S57565.1	NT	histernine H2-receptor (rata, Genomic, 1928 nt)
5140	17858	30474	264	2.2€-01	5835974 NT	TN	Vidua chalybeata mitochondrion, complete genome
2850	- [31368	2.07	2.2E-01	5803002 NT	F	Homo sepiene diaphenous (Drosophile, homolog) 2 (DIAPH2), transcript variant 156, mRNA
98895 288895			4.5	2.2€-01			Synechocyatis sp. PCC8803 complete genome, 19/27, 2392729-2538999
<u>8</u>	_1	31646	0.56	2.2€-01			Gestus galius T-box containing protein (Ch-TbxT) mRNA, complete cds
5910	18604	31647	0.58	22E-01	2.2E-01 U67087.1	NT.	Gallus gallus T-box containing protein (Ch-TbxT) mRNA, complete cds
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Top Hit Descriptor	Homo sepiens gene for fulstifn, complete ods	AV756238 BM Homo septens cDNA clone BMFAHC06 5'	Streptococcus pyogenee phosphotidylylycerophosphate synthese (pgsA) and ABC transporter ATP-binding protein (stpA) genes, complete cds; and unknown genes	Streptococcus pyogenes phospholidylghcerophosphate synthase (pgsA) and ABC transporter ATP-binding	protein (stpA) genes, complete cas; and unknown genes	Human alvocation B sense excent	Mycoplesma pneumoniae M129 section 45 of 63 of the complete genome	Bacilius halodurans DNA, complete and partiel cds, strain: C-125	Mus musculus nm23-M1 gene, promoter region	E. coli sepA and sepB genes	Pen troglodyles MeCP2 gene 3'UTR	Thermotoga maritima section 25 of 136 of the complete genome	PMS-CT0263-241299-009-b07 CT0263 Homo sapiens cDNA	Mus musculus deformed epidermal autoregulatory factor 1 (Drosophila) (Deaf1), mRNA	MR1-TN0045-110900-006-002 TN0045 Homo septens cDNA	za04f08.r1 Soares melanocyte ZNbHM Homo sapiens cDNA clone IMAGE::291591 5'	LARGE PROLINE-RICH PROTEIN BATZ (HLA-B-ASSOCIATED TRANSCRIPT 2)	Xenopus laevis mRNA for kinesin-like protein 3 (xktp3)	Mus musculus osteoblest specific factor 2 (OSF-2), mRNA	Brachydento rerio eperidyntin beta end gemme cheine (Epd) gene, complete ods	CYCLIC NUCLEOTIDE GATED CHANNEL, ROD PHOTORECEPTOR, ALPHA SUBUNIT (CNG CHANNEL 3) (CNG-3) (CNG3)	Funaria hygrometrica chloroplast-localized small heat shock protein (CPsHSP21) mRNA, complete ods;	nuclear gane for chloroplast product	601809724F1 NIH_MGC_19 Hamo septens cDNA clone IMAGE:4100189 5'	Human herpesvirus 5, complete genome	yb63d08.rl Strategene overy (#637217) Homo septens cDNA clone IMAGE:75855 5	yod3d08.r1 Strategene overy (#837217) Homo sepiens cDNA clane IMAGE:75855 5'	Pseudomonas aeruginosa quinoprotein ethenol defrydrogenase (easA) gene, partial cds; cytochrome c550 preoutsor (easB), NAD+ dependent acetaldehyde dehydrogenase (easC), and pyrroloquinoline quinone senthesis A (parts) participated and participated of participated and participated participated and participated partic	Mus musculus PHR1 (Phr1) gene, perfect cds
Top Hit Detabase Source	FZ	EST_HUMAN	Į,	ļ	Z	L	¥	NT	TN	IN	TN	TN	EST_HUMAN	TN	EST_HUMAN	EST_HUMAN	SWISSPROT	M	NT	IN	SWISSPROT		M	7.1 EST HUMAN	NT	EST_HUMAN	EST_HUMAN	5	Į.
Top Hit Acession No.	1	2.2E-01 AV756238.1	+-		2.2E-01 AF-082/38.1		7	-	1		1	2.2E-01 AE001713.1	1.1	393247	.1	2.2€-01 W02988.1		2.2E-01 AJ009839.1	7667428 NT	2.2E-01 M89643.1			2.2E-01 AF197941.1	2.2E-01 BF206507.1	9825871			F POCHAULT	
Most Similar (Top) Hit BLAST E Value	2.2E-01	22E-01	2.2E-01	100	225-01	275-01	2.2E-01	2.2€-01	2.2€-01	2.25-01	2.2E-01	22€-01	2.2E-01	2.2€-01	2.2€-01	2.2€-01	22€-01	2.2E-01	2.2€-01	2.25-01	2.25-01 090880		2.25-01	2.25-01	2.25-01	2.2E-01 T59472.1	2.2E-01 T59472.1	2.25.01	2.2E-01
Expression Signal	0.73	10.21	1.28	2	87. 8	38	0.63	0.68	2.04	1.01	0.54	3.53	4.35	1.45	1.04	1.36	13.43	0.08	0.81	3.95	0.58		3.4	1.85	0.95	9.0	0.5	89 C	0.61
ORF SEQ ID NO:		32708	32777	92206	32//8	32951	33144	33402			34279	34632		34853	34952	35024	35250	35104	35185	35200	35358		35564	35703	35941	36092	36093	36428	
Exan SEQ ID NO:	19369	19862	19721	100	12/81	19877	20066	20294	20614	20682	21141	21486	21611	21703	21786	21859	22086	21931	22017	22030	22174		888 828	22503	- 1	22880	22880	22916	22988
Probe SEQ ID NO:	6806	6926	7029	7	7194	7191	7386	7628	7919	7987	8440	8794	8920	9013	8606	9189	0207	9252	9263	9276	9521		9716	88 53	10078	10232	10232	10268	10341

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Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acessian No.	Top Hit Detabase Source	Top Hit Descriptor
10387	Ц		0.6	2.2€-01	2.2E-01 AE0015621	N	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
10387	23033	36248	9.0	2.2E-01	2.2E-01 AE001562.1	N _T	Helicobacter pykari, strain J99 section 123 of 132 of the complete genome
10520		36394	0.48	2.2E-01	2.2E-01 AF049720.1	NT	Homo saplens neuronal nitric codde synthase (NOS1) gene, alternative exons 11 and AS
11070	23740	37014	1.56	2.2€-01	AF257772.1	LN	Homo sepiens RNA binding protein MCG10 gene, complete cds, afternetively spliced
11164				2.2€-01	2.2E-01 AB021083.1	F	TT whus ORF1 gene, isolate TS4-II, pertial cds
11399	24005	37309	4.83	2.28-01	2.至-01 X01918.1	ΝT	Droeophila 68C glue gene cluster
11438	23205	36437	27.5	2.2€-01	7706215 NT	LN	Homo sepiens H-2K binding factor-2 (LOC61580), mRNA
11935	24493		1.66	2.2€-01	2.2E-01 BE870959.1	EST_HUMAN	601446957F1 NIH_MGC_65 Hamo septems cDNA clane IMAGE:3850670 5'
							Homo sapiene chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12
12040	25380		221	2.2E-01	2.2E-01 U82671.2	<u> </u>	(MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), cattractin ((CALT), NAD(P)H defividionanase-like protein (NSDH:), and LI>
12123	L		2.19	225-01	2.2E-01 AF188843.1	Į,	Vitts whifers cultivar Pinot Noir plesma membrane aquaportn (PIP1a) mRNA, complete cds
12225	17904	30591	3.87	2.2€-01	2.2E-01 AW381098.1	EST HUMAN	RC1-CT0249-141199-021-g04 CT0249 Homo sepiens cDNA
12226	24681		1.6	22€-01	2.2E-01 AW661922.1	EST_HUMAN	htt7b02.xt NCI_CGAP_GU1 Homo sepiens oDNA done IMAGE:2972523 3'
12731	25371		2.58	2Æ-01	2.2E-01 AV694801.1	EST_HUMAN	AV694801 GKC Homo sepiens cDNA clone GKCAHB02 5
950	13718		212	2.15-01	2.1E-01 AA589280.1	EST_HUMAN	nm31e11.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:1061804
953	13718	26384	22.0	2.16-01	2.1E-01 AL161504.2	Į,	Arabidopsis theliana DNA chromosome 4, contig fragment No. 16
1102			2.75	2.1E-01	2.1E-01 AE002314.2	F	Chlamydia mundarum, section 45 of 85 of the complets genome
1178	13920	26593	1.15	2.1E-01	6754290 NT	۲	Mus musculus interferon (alpha and beta) receptor 2 (lifner2), mRNA
1176	13929	26594	1.15	2.1E-01	6754299 NT	۲	Mus musculus interferon (eipha end beta) receptor 2 (finer2), mRNA
ano)	14847	2364.6	200	0.45.04	2.4E 04 A4000824 4	MANUTAL TOTAL	ok73e02.s1 NCI_CGAP_GC4 Homb septens cDNA done IMAGE:1519610 3' strutter to gb:K02765
2152	1	L		2.1E-01 BF69507	BF695073.1	Т	602083129F1 NIH MGC 81 Hamp septemb cDNA clone IMAGE:4247503 51
2485	ļ		1	2.1E-01 H73988.	H73968.1	Т	yu04f07.s1 Soures fetal liver splean 1NFLS Homo saplens cDNA clone IMAGE:232837.31
2485	15598	27943	-	2.1E-01 H73968.	H73968.1	HUMAN	yu04f07.s1 Soares fetal liver spleen 1NFLS Homo sepiens cDNA clone IMAGE:232837 3'
2558	15270		0.91	2.1E-01	2.1E-01 AF022814.1	L	Fugu rubripes transcription factor (SLP-1) and home-axygenase genes, complete cds
2825	15891	28335	23	2.1E-01	6912445 NT	TN	Homo septens potassium voltage-gated channel, subfamily H (eag-related), member 4 (KCNH4), mRNA
3786	16538		6.08	2.1E-01	9838361 NT	F	Beta vulgaris mitochondrion, complete genome
4032	16777		- -	2.1E-01 P11675	i	SWISSPROT	MANEDIATE-EARLY PROTEIN IE180
4032		29409	1.1	2.1E-01 P11675	P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4343			1.77	2.1E-01 AB03304	1.1	NT	Homo saplens mRNA for KIAA1215 protein, partial cds
4537			1.23	2.1E-01 AB01027	3.1		Homo sepiens pshsp47 gene, complete cds
5013	17734	30341	1.4	2.1E-01 Q01338	201338	SWISSPROT	ALPHA-2A ADRENERGIC RECEPTOR (ALPHA-2A ADRENOCEPTOR) (ALPHA-2AAR)

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Probe SEQ ID NO:	Exam SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Vatue	Top Hit Acession No.	Top Hit Databerse Source	Top Hit Descriptor
9090	17809	30425	1.09	2.1E-01	AE001528.1	N	Helicobacter pylori, strain J99 section 87 of 132 of the complete genome
5218		05908	624	2.1E-01	2.1E-01 BF672695.1	EST_HUMAN	802152001F1 NIH_MGC_81 Hamo septens cDNA clane IMAGE:4293001 5'
6787	19531	32559	1.4	2.1E-01	2.1E-01 AJ223392.1	N	Doto fragilis mitochondrial 16S rRNA gene, partial
6798	19459	32481	1.92	2.1E-01	2.1E-01 U04642.1	N	Human offectory receptor (OR17-2) gene, partial ods
7306	19989	33065	0.65		2.1E-01 Q01956	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIIID)
7306	19989	33066	0.65		2.1E-01 Q01956	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIIID)
7317			238		AE000972.1	N FN	Archaeoglobus fulgidus section 135 of 172 of the complete genome
7608	20272	33380	1.94	2.1E-01	2.1E-01 AF000949.1	N.	Canis familiaris keretin (KRT9) gene, complete cds
7651	20315	33425	1.22	2.1E-01	2.1E-01 AF068887.1	ĽN	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial ods
7051	20315	33426	771	2.1E-01	2.1E-01 AF008687.1	Ę	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene excoding mitochondrial protein, partial ods
7971			121	2.1E-01	TN 0505057	닏	Mus musculus enythrocyte protein band 4.1-like 3 (Epb4.1i3), mRNA
							Heemophilus Influenzae hmdD, putative heemodin processing protein (hmcC), putative ABC transporter (finncB), putative heemochi structural protein (hmcA), and heemochi (mmunity protein (hmci) genes, complete
8400		34229	4.44	2.1E-01	U68309.1	Ę	spo
8696		34531	98.0		2.1E-01 AL040537.1	EST_HUMAN	DKFZp434H0614_r1 434 (synonym: htes3) Homo septens cDNA clone DKFZp434H0614 5'
9698		34532	0.86	2.1E-01	2.1E-01 AL040537.1	EST_HUMAN	DKFZp434H0614_r1 434 (syncrym: hbss3) Hamo septens cDNA clane DKFZp434H0614 5
8857	21548		0.45	2.1E-01	2.1E-01 AB022524.1	F	Homo saplens APCL gene, exon 9
8935	21626	34768	5.58	2.1E-01 Z35786.	235786.1	NT	S.cerevisies chromosome II reading frame ORF YBL025w
9404		35237	0.57	2.1E-01	2.1E-01 N42536.1	EST_HUMAN	yy11e10 r1 Soares mekanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270854 5'
9404		35238	0.67	2.1E-01 N42538	N42538.1	EST_HUMAN	yy11910.r1 Sceres melanocyte ZNbHM Homo sapiens cDNA clone IMAGE:270954 5
9413		35262	2.31	2.1E-01 X97378.	X97378.1	IN	A.thallana mRNA for AtRanBP1b protein
9518		35354	1.13	2.1E-01 AB0365	AB036529.1	NT.	Homo sapiens p53R2 gene for ribonucleotide reductase, exon 6
10227	22875	30088	1.47	2.1E-01 Z97067.	297067.1	NT.	Beta wigaris mRNA for elongation factor 1-beta
10258	22906	36116	25	2 1E-01 P59824	P69694	TORGREIWE	DIACYLGLYCEROL KINASE, DELTA (DIGLYCERIDE KINASE) (DGK-DELTA) (DAG KINASE DELTA)
10264	<u> </u>	36122	26.0	2.1E-01 BF5742	BF574254.1	Т	602131427F1 NIH_MGC_81 Homo septens cDNA clone IMAGE:4270831 5
11554	24153		2.10	2.1E-01	11036647	Z	Homo sapiens pencreatic polypeptide 2 (PPY2), mRNA
11572	24171	37487	1.59	2.1E-01 BE18042	2.1	EST HUMAN	RC3-HT0622-040500-013-b11 HT0622 Homo sepiens cDNA
11870			1.38	2.1E-01 X57624.		NT	Drosophile melanogaster ALA-E6 DNA, repeat region
12377			2.07	2.1E-01	20.1	NT	Homo sapiens fragile 16D oxido reductase (FOR) gene, excrs 8, 9, and partial cds
12578	_ 1		1.47	2.1E-01 L32588.	L32588.1		Human granulin gene
12635	24935		1.42	2.1E-01 BE6221	BE622149.1	EST_HUMAN	601440712F1 NIH_MGC_72 Homo septens cDNA clane IMAGE:3915675 5
						•	

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	Top Hit Descriptor	THE CONTRACT OF THE CONTRACT O	Section of the control of the contro	CHELLIS GRINGS THY OVER THE COMPRESS COST	Homo eaplens CGI-18 protein (LOC51008), mRNA	O.cunniculus germline IgH heavy chain V-H pseudogene, allotype VHa2	Mus musculus Major Histocompatibility Locus class II region	Synechocyetis sp. PCC8803 complete genome, 7/27, 781449-920915	Homo saplens chromosome 21 segment HS21C013	Homo saplens rac1 gene	PM1-HT0422-291299-002-c06 HT0422 Homo sapiens cDNA	Plum pox virus strain M, complete genome, isolate PS	Homo saplens dystrobrewn, alpha (DTNA), mRNA	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0505	Homo sepiens acdium/fodide symporter mRNA, partiel cds	Human bradykinin B1 receptor (bradyb1) gene, complete cds	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene	Methenococcus jannaschili section 67 of 150 of the complete genome	601449441F1 NIH_MGC_65 Hamo saplens cDNA clone IMAGE:3853330 5'	601440441F1 NIH_MGC_65 Homo septens cDNA clone IMAGE:3853330 67	H.sepiens Na+-D-glucose cotransport regulator gene	xp15b02.x1 NCI_CGAP_HN9 Homo sapiens dDNA clone IMAGE:2740395 3' similar to contains element	MENAL Impentive mement;	Homo seciens chromosome 21 secreed HS21C004	Sus scrofe	QV4-EN0032-190500-223-e03 EN0032 Homo sepiens cDNA	Homo sapiens hypothetical protein ASH1 (ASH1), mRNA	HOMEOBOX PROTEIN GLABRA2 (HOMEOBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10)	Rat SOD-2 gene for manganese-containing supercide dismutase	Homo saplens dual addase-like domains 2 (DUOX2), mRNA	F.rubripes DNA encoding for vely-tRNA synthetiese	Saccharomyces cerevisiae Hal5p (HAL5) mRNA, complete cds	Human hepatocyte growth factor gene, excn 1	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
	Top Hit Database Source	TANK IN FOR	TOWNIA TOWNIA	Ž	L'N	TN	· LN	NT	LN LN	TN.	EST HUMAN	Ę	LN FN	IN	LN.	N.	N.	TN.	EST_HUMAN	EST_HUMAN	LN		EST HUMAN	L	NT.	5.1 EST_HUMAN	Į.	SWISSPROT	LN	NT.	N	NT	TN	SWISSPROT
)	Top Hit Acession No.	0 4E 04 DE020000 4	DEG SOOT	Z.UE-U1 ABU1/43/.1	7705601 NT	M77085.1	AF027865.1	D90906.1	AL163213.2	4J132695.5	2.0E-01 AW384937.1	2.0E-01 AJ243957.1	4503408 NT	4B007974.1	2.0E-01 AF260700.1	J22346.1	4F111170.3	J67525.1	2.0E-01 BE871330.1	2.0E-01 BE871330.1	(82877.1		1.600	242	7,46906.1	BE826165.1	8922080		(56800.1	11432540 NT			A75967.1	02467
	Most Similar (Top) Hit BLAST E Value	245 04	A 15-01	Z.UE-01	2.0E-01	2.0E-01 M77085.	2.0E-01 AF02786	2.0E-01 D90906.	2.0E-01 AL16321	2.0E-01 AJ13269	2.0E-01	2.0E-01	2.0E-01	2.0E-01 AB00797	2.0E-01	2.0E-01 U22346.	2.0E-01 AF11117	2.0E-01 U67525.	2.0E-01	2.0E-01	2.0E-01	70.0	2.0E-01 AW 23800	205-01	2.0E-01 Z46006.1	2.0E-01	2.0E-01	2.0E-01 P48807	2.0E-01 X56600.1	2.0E-01	2.0E-01 X91858.1	2.0E-01 U15300.1	2.0E-01 M75967.1	2.0E-01 P02467
	Expression Signal	7	9,-	247	3.11	1.24	2.19	1.00	2.47	1.77	1.63	1.52	14.63	1.97	1.01	1.4	1.67	4.33	1.12	1.12	1.63	- 7	0.71	1.12	0.78	8.40	5.26	0.8	263	1.94	0.76	6.3	0.73	0.79
	ORF SEQ ID NO:	Caoooc		DC0C7				28414	28519	26651	28708	-	28904	26977	28983	27132			27329	27330			79087	29206	29327		30309	28803	30845	31363	31464	31712		31943
	Exem SEQ ID NO:	25040	1	SOUS	13305			13753	13960	13981	14035	14190	14217	14290	14296	14438	14455	14494	14620	14620	15070	10010	18210	16574	18888	17263	17702	16237	18161	18450	18542	18751	18860	18968
	Probe SEC ID	40758	3 2	2	221	883	792	8	1103	1232	1285	1443	1470	1544	1550	1692	1712	1752	1883	1883	2347	4440	2800	3822	3838	4528	4979	2000	5359	2992	5750	5969	6081	6192

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Top Hit Descriptor	segene	Homo saplens cDNA	Isozyme (Pfkc) gene, exons 3 through 7	SE PRECURSOR	xbin (Y2)	G1 and G2 precursor, gene, partial cds		ns cDNA clane IMAGE:3677794 5'	Dictyostellum discoldeum rendom slug cDNA19 protein (rec19) mRNA, pertial cds	dc2) gene, complete cds	the complete genome			cmplete cds	ntrol protein (PIN2) gene, complete cds	ntrol protein (PIN2) gene, complete cds	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12	(jedd		complete cds	complete cds	enome	enome	Pimephales prometas Iver glucose-& phosphate-1-dehydrogenase mRNA, partial cds	mRNA, complete ods	Homo sepiens cDNA	spiens cDNA clone IMAGE:1843610 3'	83) mRNA, partial ods	i3k), mRNA	Rattus norvegicus Aryl hydrocarbon receptor nuclear translocator 1 (Amtr), mRNA	pe allele, 3' region, partial cds	Homo sapiens lambda/fota protein kinase C-Interacting protein mRNA, complete cds	Homo sapiens lambda/fota protein kinase C-Interacting protein mRNA, complete cds
	M.auratus mu class gluterthione transferase gene	PM1-CT0247-141099-001-g06 CT0247 Homo saplens cDNA	Mus musculus phosphofnuctoldnase-1 Clsozyme (Pfl.c.) gene, exons 3 through 7	GAMMA-GLUTAMMLTRANSPEPTIDASE PRECURSOR	Mouse germ line gene coding for beta-globin (Y2)	Andes virus strain Ol23133 glycoprotein G1 and G2 precursor, gene, partial cds	M.musculus scp2 gene excn 14	601344648F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677794 5'	Dictyostelium discoldeum random slug of	Arabidopsis pyruvate decarboxylase-2 (Pdc2) gene, complete cda	Chlamydla trachomatis section 5 of 87 of the complete genome	DAUGHTERLESS PROTEIN	DAUGHTERLESS PROTEIN	Homo sapiens filamin 2 (FLN2) mRNA, complete cds	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds	Arabidopsis thallans root gravitropism control protein (PIN2) gene, complete ods	Homo sapiens cAMP specific phosphodia	Homo sapiens cAMP specific phosphodia	D.melanogaster DNA mobile element (hoppel)	R.norvegicus mRNA for NTR2 receptor	Salvelinus pluvius mRNA for transferrin, complete cds	Selvelinus pluvius mRNA for transferrin, complete cds	Chlorella vulgaris chloroplast, complete genome	Chlorella vulgaris chloropiast, complete genome	Pimephales prometas Ilver glucose-6-pho	Homo sapiens ninein-Lm isoform (ninein) mRNA, complete cds	EST387405 MAGE resequences, MAGN Homo sapiens cDNA	ov80a10.s1 Soares_beetis_NHT Homo sapiens cDNA clone IMAGE:1643610 3	Homo sepiens Ku70-binding protein (KUB3) mRNA, partial ods	Mus musculus fructosamine 3 kinase (Fn3k), mRNA	Rattus norvegicus Aryl hydrocarbon recei	Mus musculus pale ear (ep) gene, wild type allele, 3' region, partial cds	Homo sapiens lambda/lota protein kinase	Homo sapiens lambda/fota protein kinase
Top Hit Detabase Source	Į.	EST_HUMAN	Į,	SWISSPROT	INT	LN	LN.	EST_HUMAN	LN LN	NT	LN	SWISSPROT	SWISSPROT	LN.	Ę	¥	NT	TN	LN	TN	N TN	TN	NT	M	₽N	TN	Γ	EST_HUMAN	LN	L'A			NT	LN
Top Hit Acession No.	1	20E-01 AW360865.1	1.1			2.0E-01 AF028028.1		BE562247.1	1	1	78.1			2.0E-01 AF146682.1			4.1	4.1	l l			1	7524759 NT	7524759 NT	7.2	3.1	97.1	<u>.</u>	2.0E-01 AF078164.2	11528495 NT	7549743 NT	1.9E-01 AF004353.1		
Most Similer (Top) Hit BLAST E - Value	2.0E-01 X61033.	20E-01	2.0E-01 AF25037	20E-01 P54422	2.0E-01 V00726.1	2.0E-01	2.0E-01 X91151.1	2.0E-01 BE56224	2.0E-01 U82511.	2.0E-01 U71122	20E-01 AE00127	2.0E-01 P11420	20E-01 P11420	2.0E-01	2.0E-01	2.0E-01	20E-01 AF15781	2.0E-01 AF15781	2.0E-01 X78368.	2.0E-01 X97121.1	2.0E-01 D89088.1	2.0E-01 D89088.	2.0E-01	2.0E-01	2.0E-01 AF20663	2.0E-01 AF30277	2.0E-01	2.0E-01 A1023502	2.0E-01	2.0E-01	1.9E-01	1.9E-01]	1.9E-01 U32581.2	1.9E-01
Expression Signal	3.2	4.02	1.28	0.68	78.0	5.8	2.95	0.99	0.82	0.68	4.97	0.65	0.65	2.11	1.98	1.98	0.68	0.68	0.69	2.78	1.58	1.56	1.4	1.4	1.51	1.39	1.36	3.58	2.68	1.87	3.0	6.86	1.43	1.43
ORF SEQ ID NO:		32200	32954		33452		33925		35103	35129			35494		35792	35793	35833	35934		38167	38674		37530	37531			30894	30085		30978		25781	25058	28059
SEQ ID NO:	19105	19203	19880	20026	20339	20548	20794	21316	21930	21957	22006	86727	22298	22442	22589	22589	27715			22952	L_		24207	24207	24762	25210	25139	24950	24824	71002	12920		13420	13420
SEQ ID NO:	6335	6435	7194	7345	7675	7853	0018	8624	1526	8280	9456	9846	9646	9791	1400	1706	10067	10067	10114	10305	10744	10744	11609	11609	12358	12545	12556	12594	12618	12753	108	342	041	641

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					5	101 - 1007 all	Single Lyon Flores Lynessed in Digit
Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
848	13427	28088	5.97	1.96-01	1.9E-01 BE070801.1	EST HUMAN	RC3-BT0502-251199-011-d01 BT0502 Hamo eaplens cDNA
949	13427		8.46	1.9E-01	1.9E-01 BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-401 BT0502 Homo septems aDNA
596	13730		1.73	1,95-01	7305180 NT	N	Mus musculus interieukin 2 receptor, gamma chain (IIZrg.), mRNA
1082	13840	26499	13.43	1.9E-01	1.9E-01 AA358813.1	EST_HUMAN	EST67784 Fetal king II Homo septens cDNA 6' end
1349	14097	20172	1.76	1.95-01	1.9E-01 AF061282.1	N	Sorghum blooks 22 kDe keffrin duster
1414	14162		251	1.9E-01	1.9E-01 AF184623.1	NT	Plasmodium wwax reticulocyte binding protein-2 (rbp-2) gene, complete cds
2380	15102		3.61	1.95-01	IN 8822583 NT	NT	Homo septens hypothetical protein FLJ10681 (FLJ10681), mRNA
2923	15689	58333	3.43	1.95-01	1.9E-01 U66066.1	TN	Sigmodon hispidus p63 gene, perdel cds
2830	15704		2.68	1.96-01	1.9E-01 J00922.1	NT	Gellus gellus overburnin (Y) gene, complete cds
3002	15788	28417	96'0	1.05-01	1.9E-01 U25148.1	TN	Rattus norvegicus brush border myosin-I (BBMI) mRNA, pertial ods
3390	16149		4.26	1.9E-01	1.9E-01 D13197.1	TN	Mouse gene for immunoglobulin diversity region D1
3473	16229	28883	4.44	1.9E-01	1.9E-01 R16467.1	EST_HUMAN	y42/10.r1 Soares fetal liver epieen 1NFLS Homo sepiens cDNA clone IMAGE:129547 5
3816	18668	29199	1.33	1.9E-01 P39768	P39768	SWISSPROT	PAIR RULE PROTEIN ODD-PAIRED
3973	16722	28358	3.15	1.9E-01	1.9E-01 AB006784.1	LN TN	Schizosaccharomyces pombe DNA for cytopleamic dynein heary chain, complete cds
4063	16808		1.28	1.9E-01	1.9E-01 AW754106.1	EST HUMAN	CM3-CT0315-271199-045-b11 CT0315 Homo sapiens cDNA
4206	16947	29573	1.09	1.9E-01	1.9E-01 BE834943.1	EST HUMAN	MR1-FN0010-290700-007-d04 FN0010 Homo sepiens cDNA
4950	17677		1.05	1.95-01	1.9E-01 AF223642.1	LN	Rattus norvegicus chemoidne receptor CXCR3 mRNA, complete cds
							xf29e07.x1 NCI_CGAP_Utf Homo sepiens cDNA clone IMAGE:2619444 3' similar to gb:M73779 RETINOIC
2	18815			1,96-01	1.0E-01 AW130149.1	EST HUMAN	AGD RECEPTOR ALPHA-1 (HUMAN);
5558			'	1.95-01	1.9E-01 AF127937.1	LN L	Homo septens DNA polymerase epellon cetalytic suburit protein (POLE1) gene, econ 1a
5749	I	31463	İ	1.95.01	1.9E-01 AF091216.1	N	Mus musculus Wm protein (Wm) gene, complete cds
5795	18586			1.95-01	1.9E-01 AU133116.1	EST_HUMAN	AU133116 NT2RP4 Hamo septens cDNA clane NT2RP4001328 5
6235	19009	31985	0.75	1.9E-01	1.9E-01 AI762391.1	EST_HUMAN	wi54h02.x1 NCI_CGAP_Co16 Hamo sepiens aDNA clane IMAGE:2394099 3'
6294	19067	32050	1.03	1.95-01	1.9E-01 AW148452.1	EST_HUMAN	xf14c08.xf NCI_CGAP_Kk8 Homo septens cDNA clone IMAGE:2618030 3' similar to gb:X03559 ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR (HUMAN);
							yg09e12.s1 Soeres infant brain 1NIB Homo sapiens dDNA done IMAGE:31663 3' similar to contains MER13
8876	17952	30548	1.00	1.9E-01		EST HUMAN	repetitive element;
0000	19638	32682	. 0.69	1.95-01	.1	IN	Homo saplens tubby like protein 1 (TULP1) gene, expns 9-11
0000	19638	32683	0.60	1.0E-01	0.1	LN	Homo saplens tubby like protein 1 (TULP1) gene, expns 9-11
7160	19847	32917	0.62	1.9E-01	1.9E-01 U73848.1	INT	Drosophila melanogaster teatis-specific RWA-binding protein (bruno) mRNA, complete ods
7391	20070	33149	1.38	1.9E-01		NT .	Arabidopeis frailana sermethrecnine protein phosphatase type one (TOPP8) gene, complete cds
7436	20113	33201	3.11	1.9E-01	1	TN	Zea mays starch branching enzyme I (sbe1) gene, complete cds
7885	20580	33709	1.46	1.9E-01	1.9E-01 AL161557.2	INT	Arabidopeis thallana DNA chromosome 4, config fragment No. 57
8586	21278	34417	10.77	1.9E-01	1	NT	Homo saplens mRNA for KIAA1198 protein, partial cds

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Table 4
Single Exon Probes Expressed in Brain

Chiga Lycros Lycrosco. III Digiti	Most Similar Top Hit Acession Top Hit Acession Top Hit Acession Top Hit Detablese No. Squrce Value Value	34881 1.24 1.9E-01 M14588.1 INT Mersupiel cet bete-globin gene mRNA, partiel cds	34682 1.24 1.9E-01 M14568.1 INT Marsupial cat bela-globin gene mRNA, partial cds	NALL TOO 1 PROCESSES TO DO 1	0.85 4 OE 04 DEBANARS 4	0.85 1.9E-01 BE830353.1 FST HUMAN	2.48 1.9E-01 AL161503.2 NT	2.48 1.8E-01 AL161503.2 NT	2.09 1.0E-01 AF223391.1 NT	o89602.sr1 NCI_OGAP_PNS1 Home saplens cDNA clone IMAGE:1537467.3' similar to gb:L21095_cds1 1.34 1.9E-01 AA912490.1 EST_HUMAN PROTHYMOSIN ALPHA (HUMAN);contains element OFR repetitive element;	1.34 1.8E-01 AA912480.1 EST HUMAN	1.53 1.9E-01 M22253.1 NT	277 1.9E-01 AJ243213.1	1.8 1.9E-01 L07344.1 NT	1.3 1.9E-01 AF287263.1 NT	1.67 1.0E-01[AF055000.1 NT	2.61 1.8E-01 U73200.1 NT	25700 0.9 1.8E-01 AB022090.1 INT Mus musculus Cotg gene for chaperonin contehing TCP-1 gennne subunit, pertial ods	1.7e 1.8E-01 4502532 NT	26158 1.01 1.8E-01 AB021480.2 NT Oryzdes helipes gene for membrane guarnyl cycless OlGC1, complete cds	0.94 1.8E-01 AISH2212.1 EST_HUMAN	1.63 1.8E-01 AF000580.1 NT	8.26 1.8E-01 AL117189.1 NT	1.97 1.8E-01 6753947 NT	1.97 1.8E-01 6753947 NT	1.2 1.3E-01 4505036 NT Homo explens latent transforming growth factor beta binding protein 4 (LTBP4) mRNA	A1733708.1 EST HUMAN
	ORF SEQ Express ID NO: Signs	34881	34682	35.832				36471	36583	36915	36916	37399	37845	37673	37772			25700	25802	26158		26485		26925	26926		
- - -	SEQ ID	44 21636	14 21536	30438	L	┸	<u> </u>	123237	56 23346	36 23861	36 23861	17 24088						3 15539	13159		Ц		14015		14239	9 14577	14697
	Probe SEQ ID NO:	8844	8844	0775	10142	10142	10540	10540	10655	10986	10986	11487	11726	11752	11847	12399	9	253	361	729	961	1069	1266	1492	1402	1839	1850

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Top Hit Descriptor	Mus musculus Scyat), Scyat16-ps, Scyat5 genes for small inducible cytoidne A6 precursor, small inducible cytoidne A9 precursor, scyat16 pseudogene, small inducible cytoidne A5 precursor, complete ode	QV3-DT0018-081289-036-g04 DT0018 Hamp septens cDNA	Jonopskidum acaule LEAFY protein (LEAFY2) gene, partial cds	x41a03.x1 Soares_NFL_T_GBC_S1 Homo sepiens cDNA done MAGE:2859758.3'	QV0-BN0041-070300-147-c04 BN0041 Homo septiens oDNA	145601.s1 Soeres placenta Nb2-IP Homo septens cDNA done IMAGE:151704.3' similar to contains Alu repetitive element;	1/45601.s1 Soares placenta Nb2-IP Homo sepiens cDNA done IMAGE:1517043' similar to contains Alu repetitive element;	Bowne NB25 mRNA for MHC class II (Bd A-DQB), complete cds	Arabidopeis thallana DNA chromosome 4, contig fragment No. 56	Mus musculus Scyat), Scyat 6-ps, Scyat genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, sowat6 pseudosens, small inducible cytokine A5 precursor, combiets ods	S.tuberosum mRNA for alcohol dehydrogenese	MR3-ST0203-151289-112-g06 ST0203 Homo sepiens cDNA	an 28g07, y5 Gessler Wilms fumor Homo septens cDNA clone IMAGE: 1700028 5'	Mesocricetus auratus Ne-taurocholate cotransporting polypeptide mRNA, partial cds	Arabidopsis theliana DNA chromosome 4, contig fragment No. 90	yc38h08.r1 Soares malanocyte ZNIDHM Homo sapiens cDNA clone IMAGE:264063 5	Mus musculus Tnf receptor-associated factor 8 (Traf8), mRNA	Mus musculus Trif receptor-associated factor 6 (Traf6), mRNA	FORKHEAD BOX PROTEIN E3	yyd2h02.r1 Soeree_multiple_eclerosis_2NbHMSP Homo sepiens cDNA clone IMAGE:278163 5'	Officulius lamatus mRNA for weus, complete cds	Citrulius lanatus mRNA for weus, complete cds	Bacillus halodurans genomic DNA, section 5/14	Human cellular DNA/Human papiliomarinus provinal DNA	Bacterlophage Ike, complete genome	inh02s05.s1 NCL CGAP_Thy1 Homo septens cDNA clone IMAGE:943088 similar to contains L1.t3 L1 repetitive element;	AMP NUCLEOSIDASE
Top Hit Database Source	Ę	EST_HUMAN	LN FA	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN			<u> </u>		EST_HUMAN	EST HUMAN	Ę	NT IN	EST_HUMAN			SWISSPROT	EST_HUMAN	Ę	LN TN	Ę	Ę		EST HUMAN	П
Top Hit Acessian No.	.8E-01 AB051897.1	AW935728.1	1.8E-01 AF184589.1	1.8E-01 AW182300.1	1.8E-01 AW995178.1	1.8E-01 H03369.1	H03309.1	037954.1	1.8E-01 AL 161558.2	1.8E-01 AB051897.1	X92179.1	1.8E-01 AW814270.1	1.8E-01 AI792382.1	1.8E-01 AF181258.1	1.8E-01 AL161594.2	N28620.1	5678428 NT	6678428 NT	29QY14	N94853.1	1.8E-01 AB018581.1		4P001511.1	M73258.1	9626232 NT	1.8E-01 AA493751.1	o15272
Most Similar (Top) Hit BLAST E Value	1.8E-01	1.8E-01 AW9357	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01 H03369.	1.8E-01 D37954.	1,8E-01	1.8E-01	1.8E-01 X92179.	1.8E-01	1.8E-01	1.8E-01	1.8E-01	1.8E-01 N28629.	1.8E-01	1.8E-01	1.8E-01 Q9QY14	1.8E-01 N94853.	1.8E-01	1.8E-01	1.8E-01 AP00151	1.8E-01	1.8E-01	1.8E-01	1.8E-01 P15272
Expression Signal	1.75	236	1.89	1.20	1.78	0.88	0.88	1.43	5.94	2.0	Q.	2.03	1.06	4.66	0.82	0.68	1.18	1.18	1.15	2.06	1.18	1.18	2.0	1,23	1.22	0.5	0.94
ORF SEQ ID NO:	27355		_	28319	28628	20005	28006	-	29888	30087	30114	30311	30325	30367	31431	31558	31777	31778	32185		32689	32890	33103	35091	35198		35305
Exan SEQ (D NO:	14645	15406	15665	15670	15886	16363	16363	17038	17254	17463	17486	17707	17722	17754	18510	1	18817	18817	19187	19230	19644	19644	20027	21921	22028	22053	22126
Probe SEQ ID NO:	1908	2697	2898	2004	3121	3610	3610	4289	4519	4724	4754	4984	0661	2032	5718	5835	6037	6037	6419	6463	9089	6906	7348	8242	8274	9391	8473

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					·	Old	III Descriptions of the Property of the Proper
Probe SEQ ID NO:	SEQ ID	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Veitue	Top Hit Acession No.	Top Hit Darbabase Source	Top Hit Descriptor
8473	22126	35306	0.94	1.85-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
9514	22167	35348	16'0	1.8E-01	1	Ę	S.commune orolidine-S'-phosphate decarboxylase (URA1) gene, complete cds
9514	22167	35349		1.8E-01	4	ZĮ.	S.commune crotidine-51-phosphate decarboxylase (URA1) gene, complete ods
8298	22331		0.75		P08123	SWISSPROT	COLLAGEN ALPHA 2(1) CHAIN PRECURSOR
9683	22335	35530	77.0	1.85-01	U67548.1	¥	Methanococcus jannaschil section 90 of 150 of the complete ganome
10033	22681		87.0		4 8E-04 AE-000-69 4	5	Aquarius emplus cytochrome addese subunit I (COI) gene, partial cds; mitochondrial gene for mitochondrial
10266	22914	38124	1.48			Ž	M.musculus mRNA for P/9-orden tyrosine chosobaixes
10533	23230	38465	3.08	Ì			A thatlans mRNA for ribonucleotide reductase R2
10577	23272	90908	7.28		_	5	Bacterlophage rit integrase, repressor protein (rro), dUTPase, holin and lysin genes, complete cds
10637	19644	32689	2.61	1.8E-01	1.8E-01 AB018561.1	Z	Citrulius laneitus mRNA for waus, complete ods
10637	19844	32890	2.61	1.85-01	1.8E-01 AB018681.1	Ę	Citrulius Ismarlus mRNA for weues, complete cds
10638	23329	36567	5.69			Z	Dictyostellum discoldeum unknown (DG1041) gene, complete cds
10942	23621	36870	2.64	1.8E-01	1.8E-01 M59257.1	Ŋ	Human carcinoembryonic antigen (CEA) gene, exon 4
11439	23206	36438	404	1.8E-01	1.8E-01 X57033.1	٦	B.teurus mRNA for potessium channel
11787	24358	37691	3.45	1.8E-01	8394421 NT	Z	Rettus nonegicus Thrombosene receptor (Tbxa.2r), mRNA
11967	24514		1.59	1.8E-01	10086561 NT		Bovine ephemeral fever virus, complete genome
12025	24553	31111	2.04	1.8E-01	1.8E-01 BF348623.1	EST_HUMAN	602019928F1 NCI_CGAP_Bm67 Homo septens cDNA clone IMAGE:4155318 51
12476	24839		3.28	1.8E-01 Q96382		SWISSPROT	DNA TERMINAL PROTEIN (BELLETT PROTEIN) (PTP PROTEIN)
12585	24908		1.91	1.8E-01 R24494.		EST_HUMAN	yr48h10_r1 Scenes placenta Nb2HP Homo septens cDNA clone IMAGE:133027 51
12628	24931		2.3	1.8E-01		IN	E.disper mRNA for hexoldnese (hold)
12745	25324		1.61	1.85-01	1.8E-01 X18635.1	攴	Rattus nonegicus CeBPSk gene
563	13345	25972	1.57	1.7E-01	1.7E-01 BE385164.1	EST_HUMAN	601274604F1 NIH_MGC_20 Homo septiens cDNA done IMAGE:3615768 5
787	13550	26221	2.32	1.7E-01	1.7E-01 X53330.1	L L	P. dumerilli histone gene cluster for core histones H2A, H2B, H3 and H4
g	13708		221	1.7E-01 P35616		SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
1036	13796	26455	1.80	1.7E-01	1.7E-01 AF081810.1	ĽΝ	Lymantria dispar nucleopolyhadrovirus, complete genome
1036	13796	26456	1.89	1.7E-01	1.7E-01 AF081810.1		Lymantria dispar nucleopolyhedrowns, complete genome
1974	14710		2.6	1.7E-01	1.7E-01 AF255051.1	NT	Homo sepiens BNIP3H (BNIP3H) gene, complete cds; nuclear gene for mitochondrial product
8	-				-		Vibrio cholerae hypoxamithine phosphoribosyftransferase (hpt) gene, pertial ods, hemagglutinin/protesse
7863	19631	28275	7.28	1.7E-01 AF00071	6.1	LN	regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds

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Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similer (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2863	15631	28276	2.28	1.7E-01	AF000716.1	<u> </u>	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemaggjutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds.
2927	15693	28338	1,55	1.75-01	1.7E-01 AA336909.1	EST HUMAN	EST41651 Endometrial tumor Homo septens cDNA 5' end
2995				1.7E-01		Z	Naja naja atra obe1 gene, exons 1-3
2005			1.33	1.7E-01	1.7E-01 AJ238736.1	Z	Neje neje atte cti<1 gene, exons 1-3
3103	15868	28508	1.24	1.75-01	1.7E-01 AF081514.1	F	Taxus canadensis gerany/geranyl diphosphata synthasa mRNA, complete cds
3430	16195	28845	7.1	4 7/E-04	1 7E.01 A 1280505 1	5	Anabaena sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpB gene, edpC gene, adpD gene, adpE
3695	1			1.75-01		Į.	Homo sepiens hard complete CDS
3616	16369			1.7E-01	1.7E-01 5031886 NT	Ę	Homo saplens LIM domain-containing preferred translocation partner in Iboma (LPP) mRNA
3918	16968	20306	4.84	1.7E-01	2	Ę	Homo sapiens derivative 11 breakpoint fragment partial intron 10 of the ALL-1/ML/HRX gene fused to intron 5 of the AF-4/FEL gene
4522	17257			1.75-01		F	Schistocerce gregaria alpha repetitive DNA
4787	17518	30140	1.08	1.7E-01	1.7E-01 AI247635.1	EST HUMAN	qh57e09.x1 Soares_fetaj_kver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848808 3' similar to contains OFR bit OFR repetitive element:
5054	47773		1.11	1.7E-01		N	Zee mays starch branching erzyme IIb (ae) gene, complete cds
5122	17840	30456	0.75	1.7E-01		NT	Rattus norvegicus mRNA for MIBP1 (c-myc infron binding protein 1), complete ads
6323	18128	30785	2	1.7E-01	1.7E-01 AA470888.1	EST_HUMAN	ne13e02.s1 NCL_CGAP_Co3 Homo sepiens cDNA clone IMAGE:881066 3' similar to gb;M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
6323	18126	30786	2	1.7E-01	1.7E-01 AA470888.1	EST HUMAN	net3e02.s1 NCI, CGAP. Co3 Homo sapiens cDNA clone IMAGE:881066 3' similer to gd:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN):
5506	18304		0.62	1.7E-01		Т	Brugle pehengi microfilarial sheath protein SHP3 (shp3) gene, complete cds
6237	19011	31986	13.23	1.7E-01	1.7E-01 H72118.1	EST_HUMAN	ys02g06.s1 Scenes fetal liver spleen 1NFLS Hamo septens cDNA clone IMAGE:213658 3'
6293	19066		76.0	1.7E-01	1.7E-01 AI370978.1	EST_HUMAN	ta:28c11.x1 Soares_fetal_htng_NbHL19W Homo septens cDNA clone IMAGE:20454923*
6203	19068	32040	76.0	1.7E-01	1.7E-01 AI370976.1	EST_HUMAN	ta29c11.x1 Soeres_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:2045492.3
6753	17922	30557	0.65	1.7E-01		EST_HUMAN	600944067T1 NIH_MGC_17 Homo sepiens cDNA clone IMAGE:2360248 3'
6780	19524		2.28	1.7E-01	2.3	NT	Mesocricelus auratus oviductin precureor (OVI) gene, complete ods
8007	19640		0.88	1.7E-01 Z92910.1		NT	Homo saplens HFE gene
7120	19808		1.1	1.7E-01	2.1	NT	Escherichia coii 0157:H7 genomic DNA, Sakai-VT2 prophage inserted region
7197	19883		8.8	1.7E-01	79.1		601569022F1 NIH_MGC_21 Homo sepiens aDNA clane IMAGE:3843964 6"
380	20080		1.37	1.7E-01 P16724			PROBABLE PROCESSING AND TRANSPORT PROTEIN ULSG (HFLF0 PROTEIN)
8	26112		0.71	1.7E-01 Q01955		/ISSPROT	COLLAGEN ALPHA 3(IV) CHAIN PRECURSOR
7700	20456	33580	1.32	1.7E-01	73.1	NT	Homo sapiens homogentisate 1,2-dioxygenese gene, complete cds

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Table 4
Single Exon Probes Expressed in Brain

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Table 4
Single Exon Probes Expressed in Brain

Probe Exon SEQ ID SEQ ID NO: NO: 12268 25167 12552 24889	S C	Expresi	Most Similar (Top) Hft BLAST E Valve 1.7E-01	Similar pp) Ht Top Ht Acession 4ST E No. setue 1.7E-01 AI824404.1 1.7E-01 U01317.1	Top Hit Database Source Source EST_HUMAN NT	Top Hit Descriptor 569905.x1 NCI_CGAP_Utf Home sepiens cDNA clone IMAGE:2274872.3° similar to gb:M73779 RETINOIC ACID RECEPTOR ALPHA-1 (HUMAN); Human beta globin region on chromosome 11
لللا			1.6E-01 1.6E-01	2 2	EST_HUMAN EST_HUMAN	Homo septens mevalonate kinase gene, exch 6 and 7 yin76712_r1 Soares placenta Nb2HP Homo septens cDNA clone IMAGE:135599 57 inf28d12_s1 NCI_CGAP_Co11 Homo septens cDNA clone IMAGE:1014839 3'
		3.82 1.86 1.51	1.6E-01 AF2981 1.6E-01 P22083 1.6E-01 U10334 1.6E-01 X94232	17.1	7	Homo sepiens homeobox protein OTX2 gene, complete eds AXONIN-1 PRECURSOR (AXONAL_GLYCOPROTEIN TAG-1) Crassostrea gigas RNA polymerase II largest subunit mRNA, partial cds H.sepiens mRNA for novel T-cell activetion protein
	28307 28308 28308 7 29019		1.8E-01 1.8E-01 1.8E-01 1.8E-01		5555	Homo septens mRNA for KIAA1308 protein, partial cds Homo septens cytochrome P450 3A4 (CYP3A4) gene, promoter region Homo septens cytochrome P450 3A4 (CYP3A4) gene, promoter region Populus trichocerpe cv. Trichobel ABI3 gene Populus trichocerpe cv. Trichobel ABI3 gene
3982 16730 4294 17033 4423 17159 4431 17167 4869 17596	29661	9.42 9.42 3.07 4.36	1.6E-01 AE0044 1.6E-01 AW968 1.6E-01 AW968 1.6E-01 1.6E-01 P40631	601.1 601.1 6753319	NT NT EST HUMAN NT SWISSPROT	Vibrio cholerae chromosome II, section 70 of 83 of the complete chromosome Homo sepiens apelin gene, complete cds EST380677 MAGE resequences, MAGJ Homo sepiens cDNA Mus musculus chaperonin subunit 3 (gamms) (Cct3), mRNA MICRONUCLEAR LINKER HISTONE POLYPROTEIN (MIC LH) [CONTAINS: LINKER HISTONE PROTEINS ALPHA, BETA, DELTA AND GAMMA]
			1.0E-01 1.0E-01 1.6E-01	56.1 56.1 56.1		284H06.st Strategere colon (#637204) Homo explens cDNA clone IMAGE:511361 3' similar to TR:E221955 E221966 38,865 BP SEGMENT OF CHROMOSOME XIV.; Lycopersion esculerulum Risal fragment 2, safelitie region Lycopersion esculerulum Risal fragment 2, safelitie region Lycopersion esculerulum Risal fragment 2, safelitie region Plasmodium falcipenum (strain Dd2) variant-specific surface protein (var-1) cone, complete ods
			1.6E-01 1.6E-01	6.1		xm43f01.xt NCI_CGAP_GC8 Homo sepiens cDNA clone IMAGE:2686969 3' similar to TR:075984 075984 HYPOTHETICAL 127.6 KD PROTEIN; xm43f01.xt NCI_CGAP_GC8 Homo sepiens cDNA clone IMAGE:2686969 3' similar to TR:075984 075984 HYPOTHETICAL 127.6 KD PROTEIN; Rathus marveglous CCAAT/enhancer binding protein epsilon (cebpe) gene, complete cds
5438 18720 6162 18939 6162 18939	31909	0.83 0.71 0.71	1.8E-01	1.6E-01 BE/25803.1 1.6E-01 BF183584.1 1.6E-01 BF183584.1	EST HUMAN EST HUMAN	RC3-EN0034-310800-113-h01 BN0034 Homo septems cDNA 601809725R1 NIH_MGC_18 Homo septems cDNA clone INA/QE:4040335 3' 601809725R1 NIH_MGC_18 Homo septems cDNA clone INA/GE:4040335 3'

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	Most Similar Top Hit Acession Top Hit Detablese Signal BLASTE No. Source	2.37 1.6E-01/AL161588.2 INT Arabidopsis theliana DNA chromosome 4, contig fragment No. 84	2.37 1.6E-01 AL161588.2 NT Arebidopsis thelians DNA chromosome 4, config fragment No. 84	0.55 1.6E-01 AA398047.1 EST_HUMAN	6.32 1.6E-01 AW 291215.1 EST_HUMAN UI-H-BIZ-401-D-08-0-UI.s1 NOI_CGAP_Sub-I Homo appiens dDNA done IMAGE:2724418 3'	50.1 EST_HUMAN	5.1 EST HUMAN	1.81 1.6E-01 LA9349.1 NT Gorilla gorilla enchogen receptor gene, pertiel exon	0.51 1.6E-01 BE244087.1 EST_HUMAN cone TCBAP0607	Bacteroidee vulgatus beta-lactamese (cfxA) gene, complete cds and mobilization protein (mobA) gene,	1 RE-01 700110 1 NT	1.6E-01 R13673.1 EST HUMAN	1.6E-01 L36861.1	1.0E-01 Z49501.1 NT	1 AE 01 AE111167 2 NIT	1.0E-01 BF375171.1 EST HUMAN	1.8E-01 Z49501.1 NT	0.97 1.6E-01 BE165884.1 EST_HUMAN PM2-HT0353-270100-004-f11 HT0353 Homo saplens cDNA	3.3 1.0E-01 AW 650863.1 EST_HUMAN IL3-CT0220-111199-029-G01 CT0220 Homo sapiens cDNA		1.59 1.6E-01 014647 SWISSPROT CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)	1.55 1.0E-01 BE259849.1 [EST_HUMAN 601145783F1 NIH MGC_19 Homo sepiens cDNA clone IMAGE:3161183 5	AF106064.1 NT	7.28 1.6E-01 6871552 NT Mus musculus adaptor-related protein complex AP-1, beta 1 subunit (Ap151), mRNA	1.26 1.9E-01 BF527237.1 EST_HUMAN 602039465F2 NCI_CGAP_Bm67 Homo septens_cDNA clone IMAGE:4177073 57	6679466 NT	5.28 1.6E-01 AV719585.1 EST_HUMAN AV719585 GLC Homo sapiens cDNA clone GLCEMF07 5/		1.5 1.8E-01 AW839711.1 [EST_HUMAN RC1-LT0074-120200-014-h01_1 LT0074 Homo septens cDNA	287.78 1.6E-01 AB046310.1 INT Cucumis sativus KS mRNA for ent-kaurene synthese, complete cds	2.4 1.6E-01 AK024496.1 NT Homo sapiens mRNA for FLJ00104 protein, perfei cds
	Expression (Top) Signal BLAS	L																											,		
	ORF SEQ ID NO:	32092	32083	32641	30539	33453		33589		3384		L		34708			35301		36486			36852		37296			37273	31052		_	
	Exem SEQ ID NO:	19104	19104	19602	17944	20340	20368	20484	20619	20713	L	L	L.	L	2,690		L	<u> </u>	23249			23603	23729	23094			24538	24721	24740	25149	24901
ſ	Probe SEQ ID NO:	6334	6334	6685	6867	7676	7703	7768	7924	8018	8530	8725	8831	8870	000	9551	9554	9589	10553	10918	10918	10923	11059	11388	11706	11886	12002	12292	12321	12418	12574

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ORF SEQ Expression (Top) Hit Accession O.Signel BLASTE No. Source Source	1.72 1.6E-01 AF297344.1 NT product	30992 1.7 1.6E-01	1.52 1.0E-01 BF672698.1 EST HUMAN	25889 1.4 1.5E-01 BE710087.1 EST HUMAN	25890 1.4 1.5E-01 BE710087.1 EST_HUMAN	8.31 1.5E-01 AV711696.1 EST HUMAN	25198 1.09 1.3E-01 AL163284.2 NT	28487 1.01 1.5E-01 AJ009735.1 NT	28481 2.75 1.5E-01 A.251885.1 NT	1.42 1.5E-01 L36125.1 NT	28810 0.82 1.5E-01 AW195516.1 EST_HUMAN	28868 2.96 1.5E-01 D26535.1 NT	26669 2.96 1.6E-01 D26535.1 NT	28901 1.86 1.5E-01 AF117340.1 NT	27347 1 1.5E-01 AW 444451.1 EST HUMAN	28162 1.98 1.5E-01 BF685381.1 EST_HUMAN	1.16 1.6E-01 AW672616.1 EST HUMAN	28459 0.74 1.5E-01 078687 SWISSPROT	28761 5.06 1.5E-01 AAG35040.1 EST HUMAN	28777 0.82 1.5E-01 223104.1 NT	28778 0.82 1.5E-01 223104.1 NT	29126 2.11 1.5E-01 U09964.1 INT Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds	29140 0.74 1.5E-01 7108359 NT	29236 2.65 1.5E-01 AW 965963,1 EST HUMAN	29405 1.1 1.5E-01 AW 300059.1 EST HUMAN	29530 8.35 1.5E-01/AL163284.2 NT	30046 1.57 1.5E-01 BF887665.1 EST_HUMAN	28162) 1.92) 1.5E-01 BF095381.1 EST_HUMAN	30487 1.55 1.5E-01 Z72608.1 NT
ORF SEQ ID NO:												26668	26699			28162		28459			28778	29126	28140	20236	29405	29530	30048	28162	30467
D SEQ ID NO:	34 24961	37 24073	35046	13050	Ц	15517			76 13833				14001		14638	6 15423	15680	8 15814	7 16106	16120	15120	8 16491	10504	16599	8 16773	1 16901	17410	1	17850
Probe SEQ ID NO:	12861	12687	12796	241	241	673	766	1070	1075	1091	1194	1252	1252	1465	1901	2716	2914	3048	3347	3361	3361	3738	3752	3848	4028	4161	4676	2 2	5132

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Probe SEQ ID S NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signel	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5145	17864	30480	1.05	1.6E-01	1.5E-01 AF056313.1	NT	Morone savatilis gonedotropin-releasing hormone type II gene, complete cds
5175	17964	30499	2.18	1.5E-01	1.5E-01 P07996	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5203	18011	30632	1.15	1.5E-01	1.5E-01 AF258852.1	۲	Calman crocodifus MHC class II beta chain (hclibeta) gene, complete cds
87.45	18057		603	1 AF-01	1 4E-01 (014108	EWISSDROT.	SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX STEROID-BINDING PROTEIN)
5451	18250	31139	5.08	1.50	1.5E-01 AW850754.1	EST HUMAN	IL3-CT0219-160200-064-F10 CT0219 Homo septems cDNA
5482	18291	31188	8.42	1.5E-01	1.5E-01 U65018.1	Ę	Mus musculus transforming growth factor alpha (TGFa) mRNA, complete cds
5482	18291	31189	8.42	1.55-01	1.5E-01 U65016.1	Ę	Mus musculus transforming growth factor alpha (TGFa) mRNA, complete cds
5915	18700	31653	3.00	1.5E-01	6753659 NT	Z	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
5915	18700	31864	3.09	1.5E-01	6753659 NT	Ę	Mus muscalus DNA methyltransferase 2 (Dnmt2), mRNA
5952	18734	31663	1.93	1.55-01	AJ276505.1	Ę	Mus musculus genomic fragment, 279 Kb, chromosome 7
6102	18880	31847	3.1	1.5E-01	1.5E-01 BE727858.1	EST_HUMAN	601584322F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833981 5'
6162	18929		1.77	1.5E-01	4508398	4506396 NT	Homo sepiens RAD64 (S.cerevislee)-like (RAD64L) mRNA
6251	19025	31999	2.09	1.5E-01	1.5E-01 AF134907.1	Ę	influenza B virus (BNemchang/480/94) NB protein gene, complete cds; and neuraminidase gene, partial cds
6400	25089	32176	22	1.5E-01		Ę	Archaeoglobus fugidus section 68 of 172 of the complete genome
6437	19205	32201	4.89	1.5E-01	11417236 NT	Ę	Homo saplens chromosome 5 open reading frame 3 (C5ORF3), mRNA
6448	19216	32214	3.95	1.5E-01	1.5E-01 P48508	SWISSPROT	GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYLCYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN)
6463	19259	32280	2.35	1.5E-01	0.28462	SWISSPROT	AMELOGENIN
6585	19348	32361	1.25	1.5E-01	1.5E-01 AA714750.1	EST_HUMAN	my30d10.s1 NCI_CGAP_GCB0 Hamo septens cDNA done IMAGE:12419713'
6812	19375	32380	1.08	1.5E-01	P30143	SWISSPROT	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORFS)
6882	17958	30554	6.82	1.5E-01	1.5E-01 AW970295.1	EST_HUMAN	EST382376 MAGE resequences, MAGK Homo sapiens cDNA
8048	25.400		200	17.	4 KE 04 A A B 4 4 K 4 K 4	NV#NIT LOD	ob/3802.s1 NCI_CGAP_GCB1 Homo sepiens dDNA clone IMAGE:1337019 3' similar to contains element
7115	19803	1	2.07	1.56-01	T	NT.	Homo sepiens HARP (HARP) gene, evan 17 and complete cds
7290	19973	33051	2.96	1.5E-01	Γ	EST HUMAN	w52208x1 NCI CGAP Ut1 Homo septems dDNA done IMAGE:2491310 3'
7490	20162	33254	204	1.5E-01	1.1	N	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
	20162	33266	2.04	1.5E-01	1.5E-01 AF299073.1	Ę	Bos taurus Niemenn-Pick type C1 disease protein (NPC1) mRNA, complete cds
	20171	33262	2.04	1.5E-01	1.1	EST_HUMAN	UI-HF-BNO-ekk-4-05-0-UI.r1 NIH_MGC_50 Hamo septens cDNA clane IMAGE:3077409 5
I	20171	33263	2.04	1.5E-01	1.1	EST HUMAN	UHHF-BNO-ekk-d-05-0-ULM NIH_MGC_50 Homo septens cDNA clone IMAGE:3077409 5
t	20306	33414	0.81	1.5E-01	F:		Saccharomyces cereviales weak multicopy suppressor of los1-1 (SOL3) gene, complete ods
7957	20052	33775	0.96	1.5E-01 P21303		SWISSPROT	MEROZOITE RECEPTOR PK00 PRECURSOR (00 KD PROTECTIVE MINOR SURFACE ANTIGEN)

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Probe SEQ ID 8 NO:	Econ SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
11119	19973	33051	1.58	1.05-01	Al973157.1	EST_HUMAN	wr52c08.x1 NCI_CGAP_Ut1 Homo septens cDNA clone MAGE:2491310 3'
11625	24222		1.56	1.55-01	1.5E-01 AI193704.1	EST HUMAN	qe72e01.x1 Soares_fetal_jung_NbHL19W Homo septens cDNA done IMAGE:1744536 3' similar to gb:M17887 eos ACIDIC RIBOSOMAL PROTEIN P2 (HUMAN);
11969	25202		11.07	1.6E-01	1.6E-01 BF700682.1	Γ	602/128753F1 NIH_MGC_66 Hamo espiens aDNA clane IMAGE:4285549 5
12320	24739		1.37	1.5E-01	1.5E-01 AF030358.2	TN	Rattus norvegicus chemokine CX3C mRNA, complete cds
12324	24743		1.77	1.5E-01	1.5E-01 AJ238332.1	Ę	Mus musculus mRNA for death inducer-obliterator-1 (Dio-1)
12369	24771		5.35	1.55-04	1.5E-01 AB026898.1	NT	Homo septions DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 gence, complete cds)
12385	25220		9.87	1.5E-01 R83077.		T_HUMAN	yp87e04.r1 Sceres fetal liver spleen 1NFLS Homo sepiens cDNA clone IMAGE:194430 5'
12472	25241		2.53	1.5E-01	2.1	EST_HUMAN	AV741272 CB Homo sepiens cDNA clone C8DAGD04 5
12573	25150	26808	2:6	1.5€-01	1.5E-01 AL139074.2	TN	Campylobacter jejuni NCTC11168 complete genome; segment 1/6
12783	25036	30965	1.89	1.55=-01			Sus scrafa mRNA for sodium lodide symporter
202	13098		1.72	1.4E-01	1.4E-01 AF009863.1		Homo saplens T cell receptor beta locus, TCRBV8S5P to TCRBV21S2A2 region
830	13659		3.62	1.4E-01 D78638.	1	TN	Xenopus leevis mRNA for DNA (oytosine-5-)-methyttransferese, complete cds
1236	13985		2.48	1.4E-01	1.4E-01 T91864.1	EST_HUMAN	yd34c01.s1 Soares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:112032.3'
1742	14484		1.5	1.4E-01	6879980	NT	Mus musculus growth differentiation factor 5 (Gdf5), mRNA
1745	14487	27196	1.71	1.4E-01	0.1		Thermotoga maritima section 22 of 136 of the complete genome
1898	14635		96.0	1.4E-01	1.4E-01 AW135741.1		UI-H-BI1-ecf-e-09-0-UI:s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2714009:3'
1978	14714		9.33	1.4E-01	1.4E-01 AA720815.1	\neg	ny72d07.s1 NCI_CGAP_GCB1 Homo sepiens cDNA clone IMAGE:1283821 3'
2478	15196	27835	1.38	1.4E-01 P30708	P30706	SWISSPROT	GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT)
2795	15500	28241	4.23	1.4E-01	1.4E-01 A1933498.1		wm74d01.x1 NCI_CGAP_Uiz Homo sapiens cDNA clone IMAGE:2441665 3'
	16829	29267	96.0	1.4E-01 R59232.	1		yg97a03.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:41467 5'
	16829	29268	96'0	1.4E-01 R59232.1			yg97a03.r1 Scares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:41467 5'
4153	16895	29524		1.4E-01	7.	EST HUMAN	b58c02.x1 NCI_CGAP_Lu24 Hamo sepiens cDNA clane IMAGE:2273570 3'
4153	16895	20525	8.69	1.4E-01	1.4E-01 AI699094.1		b58c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4212	16953	29577	3.73	1.4E-01	0.1	LN	Thermotoga maritima section 22 of 138 of the complete genome
5014	17735	30342	0.94	1.4E-01 U12283.		L	Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds
5223	18030	30856	5.48	1.4E-01 T90677.1		T_HUMAN	ye15c11.s1 Strategene lung (#937210) Homo sapiens cDNA clone IMAGE:1178123
5246	18052	30679	4.6	1.4E-01	1.4E-01 AB004556.1	IN	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenese, complete ods
5246	18052	30680	4.6	1.4E-01	1.4E-01 AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete ods
6205	18980	31959	3	1.4E-01	li	EST_HUMAN	hr67c02.xt NCI_CGAP_Kid11 Homo sepiens cDNA clone IMAGE:3133538 3'
6391	19160	32160	9.9	1.4E-01			AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
6391	19160	32161	5.6	1.4E-01	1.4E-01 AU117147.1		AU117147 HEMBA1 Homo septiens cDNA clone HEMBA1000769 5'
6477	19244	32244	3.14	1.4E-01	1.4E-01 AW082798.1	EST_HUMAN	xb71d12X1 Sogres_NFL_T_GBC_S1 Hamo sapiens cDNA clone IMAGE:25817513'

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Probe Exon			Most Similar			
_	ORF SEQ	Expression		Top Hit Aceasion	Top Hit Database	Top Hit Descriptor
NO:			Value		Source	
		1.64	1.4E-01	1.4E-01 BE286536.1	EST_HUMAN	601103523F1 NIH_MGC_7 Hamo sapiens cDNA clone IMAGE:3537581 5
6509 19274	32275	2.45	1.4E-01		EST_HUMAN	QV1-UM0038-080300-103-d09 UM0036 Homo sepiens cDNA
7026 19718	1	0.65	1.4E-01	1.4E-01 AL118568.1	EST_HUMAN	DKFZp761A0910_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A0910 5
7284 19967		1.51	1.4E-01 AW0153		EST_HUMAN	UHH-BIO-eart-c-09-0-UI.s1 NCI_CGAP_Sub1 Homo sepiens cDNA clone IMAGE:2710289 3'
	33283	1.18	1.4E-01 U85845.1		NT	Oryctolegus cuniculus fructose 1,6, bisphosphete aidolase (AIdB) gene, complete cds
7863 20317	33427	86.0	1.4E-01	1.4E-01 Al305192.1	EST_HUMAN	q190b12.xt Soares_NHHMPu_S1 Homo saplens cDNA clone IMAGE:1879583 31
8373 21066	1	1.23	1.4E-01	1.4E-01 AV659047.1	EST_HUMAN	AV650047 GLC Homo septens cDNA dane GLCFSH08 31
8683 21375		750	1 4F-01 A1436092	A1436093 1	EST HUMAN	trazb12x1 Soeres NSF F8 9W OT PA P S1 Homo sepiens dDNA done IMAGE:2126111 3' similar to TR-002710 002710 GAG POLYPROTEIN
	34650	4.18	1.4E-01 AA30707	3.1	EST HUMAN	EST178192 Colon carcinoma (HCC) cell line Homo sepiens cDNA 5' end
L.,	34722	0.59	1.4E-01	36.1	Г	df68b03.y1 Morton Fetal Coohlee Homo sepiens cDNA clone IMAGE:2487485 5'
9021 21711	34864	26.0	1.4E-01 R62746.1		HUMAN	W10H05.r1 Sources placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5
9021 21711	34865	26.0	1.4E-01 R62746.1	Г	EST_HUMAN	y10h05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IWAGE:138873 5'
9085 21774	34638	8.81	1.4E-01	1.4E-01 BF310959.1	EST HUMAN	601895485F1 NIH_MGC_19 Hamo septens cDNA clane IMAGE:4124824 57
						2d94a04.r1 Sceres fetal heart_NbHH19W Homo sapiens cONA clone IMAGE:357102 5' similar to contains
\perp		124	1.4E-01 W93411		HUMAN	element KER repetitive element;
_1		0.48	1.4E-01 X73283.			M. vermielt genee rport, rpod end rpoA
		0.46	1.4E-01 X73293.			M.vermielli genes rpdH, rpdB and rpoA
╝		1.46	1.4E-01 Y10196.1		NT	Homo sepiens PHEX gene
9258 21937	35112	1.48	1.4E-01 Y10198.	1	M	Homo septems PHEX gene
	33541	1.96	1.45.01	AF121361.1	!	Drosophila melanogaster signal transducting adaptor protein (STAM), serine threcraine kinase ial (IAL), and zinc finger protein (DNZ1) genes, complete cds
9704 22356		0.97	1.4E-01 X88092.1		Ę	C.perfringens ORF for putsitive membrans transport protein
9887 22537	35732	1.26	1.4E-01 AF02381	3.1	Į	Macromitrum levetum email ribosomal protein 4 (rps4) gene, chloroplest gene encoding chloroplest protein, pertial ods
9988 22638	35846	0.56	1.4E-01/	8.1	EST HUMAN	d/20h08.y1 Mortan Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485084 5
	35847	0.56	1.4E-01/	1.4E-01 AW021908.1	EST_HUMAN	d/23h08.y1 Martan Fetal Coohlea Horno septiens cDNA clone IMAGE:2485094 5'
10157 22805	36022	0.81	1.4E-01		EST HUMAN	MR3-ST0216-211289-013-e08 ST0218 Homo sapiens cDNA
157 22805	38023	0.81	1.4E-01		Г	MR3-ST0218-211289-013-408 ST0218 Homo sepiens cDNA
10360 23007		0.57	1.4E-01 T84283.		EST_HUMAN	yd47d03.r1 Soares febal fiver spleen 1NFLS Home sepiens cDNA clone IMAGE:111365 61
10499 23145	36372	0.62	1.4E-01 Z99117.1		NT	Bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870
		1.84	1.4E-01	1.4E-01 AA811480.1	EST_HUMAN	oesset3.s1 NCI_CGAP_GCB1 Homo septens cDNA clone IMAGE:1320384 3'
		3.24	1.4E-01 R53400.1			1/370c05.r1 Soarse breest 2NbHBst Homo saplens cDNA clone IMAGE:154088 51
10954 23631	36879	1.31	1.4E-01	82.1	EST_HUMAN	xd73ef0.x1 Source_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:2603274 3

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Table 4
Single Exon Probes Expressed in Brain

	Top Hit Descriptor	ye47g10.r1 Soares fetal liver spleen 1NPLS Homo sapiens oDNA clone IMAGE:120830 5'	ye47g10.r1 Scares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120930 5	INTEGRIN ALPHA-5 PRECURSOR (FIBRONECTIN RECEPTOR ALPHA SUBUNIT) (INTEGRIN ALPHA- F) (VIA-5) (CD40E)	C.perfringens ORF for putative membrane transport protein	UI-H-BIO-est-c-09-0-UI.\$1 NCI_CGAP_Sub1 Homo sepiens cDNA done IMAGE:2710289 3'	Borrella burgdorferi giyoeraldefryde-3-phosphaia defrydrogenase (GAPDH), phosphogiyoerate kinase (PGK), thosephosphate isomerase (TPI) genes, complete cds	M.mueculus p16K gene for 16 kDa protein	Mus musculus neuromedin U precursor (Nmu) gene, pertiel cds; tPhLP (Tphlp) gene, pertial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pft27) gene, complete cds; and HSAR (HSar) gene, complete cds	hi14h08.x1 NCL CGAP_GU1 Homo sepiens cDNA clone IMAGE:2072319 3'	hti 4h08.xt NCI_CGAP_GU1 Homo sepiens cDNA clone IMAGE;297.2319 \$'	Ephydatta fluviatilis mRNA for adddase, partial cds	P. saline plactid gene sec Y	Rattus novegicus desmin (Des), mRNA	601315638F1 NIH_MGC_8 Homo septens cDNA clone IMAGE:3634329 5	Fugu rubripes putative neurotransmitter receptors, YDR140w homolog, and ghoinsmide ribonucleotide transformytese (GART) genes, complete ods	Synechocystis sp. PCC8803 complete genome, 23/27, 2868767-3002865	TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN ABL	Mus musculus mRNA for prolidese, complete ods	MR0-HT0208-221289-204-c08 HT0208 Homo sepiens cDNA	Homo sapiens G protein-coupled receptor 30 (GPR50) mRNA	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA	Homo sapiens gene for NBS1, complete cds	Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK	Human calicivirus HUALV/Girfington/93/UK RNA for capsid protein (ORF2), strath HUALV/Girfington/93/UK	P.dumerili histone gene cluster for core histones H2A, H2B, H3 and H4	Rattus norvegicus A-kinase anchor protein mRNA, complete cds	Botrytis cinerae strain T4 cDNA library under conditions of nitrogen deprivation
- -	Top Hit Database Source	EST HUMAN	EST_HUMAN	SWISSPROT		EST_HUMAN	Ę		Ā	EST_HUMAN	EST_HUMAN	Г	Į.	Ł	EST_HUMAN	- N		SWISSPROT	님	EST_HUMAN	Į.		Ę	NT	<u> </u>	攴	ᅜ	F
	Top Hit Acession No.	T96102.1	196102.1	208648	Γ	1.4E-01 AW015373.1	128780.1			1.4E-01 AW684572.1	1.4E-01 AW684572.1	1.4E-01 AB000800.1	1	11968117	3E513802.1	1.4E-01 AF083221.1	1	210447		1.4E-01 AW377998.1	3467	4758467 NT	19.1	06.1,	1.3E-01 AJZ77606.1	1	1.3E-01 AF139518.1	
	Most Similar (Top) Hit BLAST E Value	1.4E-01	1.4E-01 T96102	1.4E-01 P08648	1.4E-01 X86092	1.4E-01	1.4E-01 U28780.	1.4E-01 X52102	1.4E-01 AF14677	1.4E-01/	1.4E-01 /	1.4E-01	1.4E-01 X74773.	1.4E-01	1.4E-01 BE5138	1.4E-01	1.4E-01 D64004	1.4E-01 P10447	1.4E-01 D82983	1.4E-01 /	1.3€-01	1.3E-01	1.3E-01 AB01313	1.3E-01 A.227780	1.3E-01	1.3E-01 X53330.	1.3E-01	1.3E-01
	Expression Signal	1.3	1.3	2.35	1.88	1.41	237	1.82	8.	1.31	1.31	1.98	203	22	2.84	1.35	297	3.15	6.26	237	3.12	3.12	2.8	1.05	1.05	0.92	1.8	1.31
	ORF SEQ ID NO:	36975	36976	38979	37215		36445		37661	37747	37748	30904	31049					-			25758	25757	25832	28035	26036	26264	26313	26425
	Exon SEQ ID NO:	23707	23707	23709	23924	19967	23213		24335	24411	24411	25172	24708	24714	25383	24794	24801	25407	25221	25033	13118	13118	13300	13400	13400	13594	13643	13765
	Probe SEQ ID NO:	11036	11036	11038	11282	11301	11448	11512	11743	11827	11827	12213	12261	12275	12318	12413	12425	12500	12708	12779	314	314	518	129	621	824	874	1005

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Single Exon Probes Expressed in Brain

						.9	
Probe SEQ ID NO:	SEQ ID	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Detabese Source	Top Hit Descriptor
1105	13862		26		1.3E-01 AL115285.1	TN.	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1193	13945	26809	1.13		1.3E-01 AV712467.1	EST_HUMAN	AV712467 DCA Homo sapiens cDNA clone DCAAFF05 5
1425	14172		1.18		1.3E-01 AF146277.1	L	Homo sapiens adapter protein CMS mRNA, complete cds
1850	14588	27303	76.0	1.3E-01	TN 2560999	N _T	Mus musculus procollagen, type XI, alpha 1 (Cd11a1), mRNA
1952	14687	27400	2.18		1.3E-01 AL117078.1	LN L	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2167	14898	ı	122		1.3E-01 A.1243578.1	Ę	Rhodopseudomonas acidophila pucB5, pucA5, pucB6, pucA6, pucB7, pucA7, pucB8, pucA8 and pucC penes and ORF151
2288	15013		12		1.3E-01 AW812104.1	EST HUMAN	RC4-ST0173-191099-032-d12 ST0173 Homo saplens cDNA
2379	15101		3.34		1.3E-01 AE001016.1	IN.	Archaeoglobus fulgidus saction 91 of 172 of the complete genome
2592	15306	28042	4.76		1.3E-01 M86918.1	F	Cerassius auratus keratin type I mRNA, complete cds
3065	15831	28474	1.01		1.3E-01 AL163207.2	TN	Homo sepiens chromosome 21 segment HS21C007
3443	16199	28849	96:0		1.3E-01 M21572.1	LN	Bovine branched chain alpha-keto acid difrydrolipoyl transacylase mRNA, complete cds
3969	16718		1.43		1.3E-01 AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
4117	16859		1.27	1.3E-01	1.3E-01 AF020713.1	LN.	Bactertophage SPBc2 complete genome
4137	16879		4.24		1.3E-01 AW364341.1	EST_HUMAN	QV3-DT0018-081299-036-903 DT0018 Homo saplens cDNA
4145	16887	29518	2.03		1.3E-01 AF026805.1	NT	Schistosoma mansoni fructose bisphosphate aldolase mRNA, complete cds
4163	16903	29532	18.52		1.3E-01 AWZ73741.1		xx23f10.x1 Scares_NR_T_GBC_S1 Homo explens cDNA clone IMAGE:281396531
4257	16998	29627	0.99		AV752279.1	HUMAN	AV752279 NPD Hano septens aDNA dane NPDAZE02 5
4257	16998	20628	0.99		1.3E-01 AV752279.1	EST HUMAN	AV752279 NPD Homo septens cDNA clone NPDAZE02 5'
4279	17018		12.78		1.3E-01 AL163280.2	N	Homo sapiens chromosome 21 segment HS21C080
4445	17181	28806	0.77	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid difrydrolipcyt transacylase mRNA, complete cds
4407	17233	20863	2.68		1.3E-01 BE272330.1	EST_HUMAN	601126086F1 NIH_MGC_9 Hamo saplens aDNA alone IMAGE:2990063 5
4963	17688		0.74		1.3E-01 BF091980.1	EST_HUMAN	RC4-TN0077-180800-012-005 TN0077 Homo septens cONA
							ha07b06x1 NCL_CGAP_Kid12 Homo sepiens cDNA clone IMAGE:2872979 3' similiar to contains L1.51 L1
5242		30677	0.83		1.3E-01 AW468988.1	EST HUMAN	L1 repeditive element;
6278	18083	30739	2.23		1.3E-01 AW804417.1	EST_HUMAN	QV0-UM0083-100400-189_e08 UM0083 Homo expiens oDNA
5414	18213		71.0		1.3E-01 AF107783.1	NT	Emericalle niculans DNA-dependent RNA polymenase II RPB140 (RPB2) gene, partial cds
5497	18295	•	0.75		1.3E-01 AF056880.1	NT	Hepatitis C virus 68_CL10 genome polyprotein gene, partial cds
5638	18433	31348	0.97		1.3E-01 BF210620.1		801874501F1 NIH_MGC_54 Homo septens cDNA clone IMAGE:4101119 5'
5896	18681	31628	0.57	1.3E-01	1.3E-01 BF527281.1	EST_HUMAN	602038337F2 NCL_CGAP_Bring7 Hamo eaplens cDNA clane IMAGE:4177233 5
5896	18681	31629	0.57	1.3E-01	1.3E-01 BF527281.1	EST HUMAN	602039337F2 NCI_CGAP_Bm67 Hamo seplens cDNA clane IMAGE:4177233 5
6392	19161	32162	15.12		1.3E-01 AB031328.1	NT	Schizosaccharomycas pombe gene for Alp41, complete cds
6474	19241	32241	1.95		1.3E-01 X88891.1	N	Cjacchus Intron 4 of visual pigment gene (red allele)
6691	19608		0.75		1.3E-01 W26367.1	EST_HUMAN	26f3 Human retine cDNA randomly primed sublibrary Homo septens cDNA

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	ORF SEQ Expression (Top) Hit Acession ID NO: Signal BLAST E No. Source	0.99 1.3E-01 BF529560.1 EST_HUMAN 602044345F1 NCI_CGAP_Bm67 Homo septems cDNA clone IMAGE:4181888 5"	1.3E-01 H48664.1 [EST_HUMAN y/33d02.r1 Soares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:207075 5	BE272339.1 EST_HUMAN	33694 1.34 1.3E-01 11423294 NT Homo saplens PRO0611 protein (PRO0611), mRNA	BF69052	EST_HUMAN	1.3E-01 11421556 NT	4.47 1.3E-01 274102.1 NT S.cerevisiee chromosome N reading frame ORF YDL054c	4.44 1.3E-01 8923919 NT Homo septens core historie meand+12A2.2 (MACROH2A2), mRNA	34258 1.02 1.3E-01 BF690522.1 EST_HUMAN 60218701671 NIH_MGC_49 Homo septens oDNA done IMAGE:4299074.3'	34683 0.58 1.3E-01 R11172.1 EST_HUMAN SP:RL28_RAT P26316 60S RIBOSOMAL PROTEIN;	y89g11.1 Sources fetal fiver spleen 1NFLS Home achiens cDNA done IMAGE:129284 6' similar to 34894 0.58 1.3E-01 R1172.1 EST HUMAN SP:RL2B RAT P29316 60S RIBOSOMAL PROTEIN:	0.61 1.3E-01 11068003 NT	0.61 1.3E-01 11068003 NT	1.3E-01 AF023129.1 NT	0.56 1.3E-01 N86348.1 EST HUMAN RECEPTOR ASSOCIATED PROTEIN (BAP) 29	0.99 1.3E-01 8393940 NT Rattus norvegicus peptidyl erginine deiminese, type IV (Pdi4), mRNA	35894 0.85 1.3E-01 AW 851 599.1 EST_HUMAN MR2-CT0222-201099-001-601 CT0222 Homo septens cDNA	36151 1.1 1.3E-01 AL163246.2 NT Homo sepiens chromosome 21 segment HS210046	0.84 1.3E-01 AU121237.1 EST_HUMAN	36347 0.62 1.3E-01 AW247836.1 EST_HUMAN 2820637.3prime NIH_MGC_7 Homo septens cDNA chore INAGE;2820637.3	2.93 1.3E-01 BF330000.1 EST_HUMAN MR4-BT0358-130700-010-h08 BT0358 Homo sepiens cDNA	1.56 1.3E-01 H01883.1 EST_HUMAN	AF119117.1 NT	3871745 NT	37263 1.42 1.3E-01 BF577328.1 EST_HUMAN 902087045F1 NIH_MGC_83 Home sapiens cDNA clone IMAGE:4261346 5	1.42 1.3E-01 BF677328.1 EST_HUMAN	4.28 1.3E-01 BE279449.1 EST_HUMAN	37840 1.94 1.3E-01 BE618384.1 [EST_HUMAN 601473369F1 NIH_MGC_88 Hamo sapiens cDNA clone IMA GE:3876208 6	37676 1.44 1.3E-01 BF683565.1 EST_HUMAN 902139760F1 NIH_MGC_46 Home sepiens cDNA clone IMA GE:4300963 5	
Eben SEQ ID NO:			-		33694	33727		33998			34258	34683	34684	34973	34974	35120			35894	36151	36290	36347		36701	36980		37263	37264	37504	37840	37676	04000
	Exen SEQ ID NO:	<u>L</u> .	l					L					<u> </u>	L	Ĺ	L.		L		Ш	Ц											

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Top Hit Descriptor	Cellus gallus scyc1 gene for lymphotectin, exons 1-3	R.novegicus crp2 gene for cystatin related protein 2	Ephydatia fluviatilis mRNA for sALK-6, complete cds	wu24d09.x1 Soares. Dieckgraefe_colon, NHCD Homo sepiens cDNA clone IMAGE:2520977 3' similar to TR:0e0287 0e0287 KIAA0539 PROTEIN.	#39b02.x1 NCI_CGAP_Bm23 Homo sapiens cDNA done IMAGE:2098539 3' similar to gb:U05760_ma1 ANNEXIN V (HUMAN);	Dictyostellum discoldeum ORF DG1016 gene, pertiel cds	Homo septens colon cancer entigen NY-CO-45 mRNA, partial cds	AU149148 NT2RM4 Homo septens cDNA clone NT2RM4001691 3'	AU149146 NT2RM4 Hamo saplens cDNA clone NT2RM40016913'	AV735249 cdA Hamo sapiens cDNA clone cdAAJB11 5	a48e09.s1 Sosres_NFL_T_GBC_S1 Hamo septens cDNA olone IMAGE:1480584 3' similar to TR:Q16871 Q16871 ANTHMULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR.;	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL TRANSCRIPTION FACTOR	NFAT3) (NF-ATC4) (NF-AT3)	gride/tob.x1 NCI_CGAP_Eso2 Home septens dDNA clone IMAGE:1880553 3	H. sapiens DNA for endogenous retrovinal like element	UI-H-BI3-akt-e-10-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734554 3'	601821567F1 NIH_MGC_62 Hamo sepiens cDNA clane IMAGE:4046224 5	Homo sapiens chromosome 21 segment HS21C013	QV3-BN0048-220300-129-f10 BN0046 Homo sepiens cDNA	ts18g07.xt NCL_CGAP_Pen1 Homo septens cDNA done IMAGE;2228688 3' striller to TR:Q14048 Q14048 COLLAGEN VI ALPHA-2 ALTERNATIVE C-TERMINAL DOMAIN. [1] ;contains element PTR3 repetitive	Harmon Edit and an example to the Control of the Control of the	as80009x1 Berstead colon HPLRB7 Homo septens cDNA clone IMAGE:2335024 3' similar to gb:L05095	60S RIBOSOMAL PROTEIN L30 (HUMAN);	Humen creatine kinase-B mRNA, complete cds	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)	QV1-BT0259-261099-021-d05 BT0259 Homo sapiens cDNA	Methanococcus jannaschii section 142 of 150 of the complete genome	Bacillus subtilis complete genome (section 15 of 21); from 2795131 to 3013540	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
Top Hit Detabese Source	Į.	LN	LN LN	EST HUMAN	EST HUMAN	Ľ L×	N	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN		SWISSPROT	EST HUMAN	NT	EST_HUMAN	EST_HUMAN	FZ	EST_HUMAN		ES L HOMAN		EST_HUMAN	LN	IN	EST_HUMAN	ΝΤ	LN	N.
Top Hit Acession No.	1.3E-01 AJ242780.1	13894.1	1.3E-01 AB026829.1	W001114.1	U421744.1	166912.1	1.2E-01 AF039442.1	1.2E-01 AU149146.1	1.2E-01 AU149146.1	1.2E-01 AV735249.1	\A897474.1		214934	1285402.1	089211.1	1.2E-01 AW449368.1	1.2E-01 BF248490.1	1.2E-01 AL163213.2	(W908558.1		140040 4	200	1720470.1	116364.1		W370668.1	167600.1		(56882.1
Most Similer (Top) Hit BLAST E Value	1.3E-01	1.3E-01 Z13994.1	1.3E-01	1.3E-01 AW00111	1.2E-01 A1421744	1.2月1	1.2E-01	125-01	1.2E-01/	1.2E-01	1.2E-01 AA897474		1.2E-01 Q14934	1.2E-01 AI285402	1.2E-01 X89211.1	1.2E-01	1.2€-01	1.2E-01	1.2E-01 AWGO855	į	4 DE 04 1140040 4		1.2E-01 AT720470	1.2E-01 M16364.1	1.2E-01 X56882.1	1.2E-01 AW37066	1.2E-01	1.2E-01 Z99118.1	1.2E-01 X56862.1
Expression Signal	4.43	1.51	1.43	2.26	8.42	1.05	4.33	3.22	3.22	4.36	1.23		28	2.81	20.17	1.03	1.75	1,2	1.40	,	1.12	3	2.5	2.92	76.0	1.59	1.12	0.8	0.82
ORF SEQ ID NO:					25844			26778	26779				27062	27082			27642	27748	28047		20100	707	28318	28350	28418	28641			28921
Exen SEQ ID NO:	24695	24713	24915	24936	13199	12826	13317	14103	14103	14110	14243		14373	14382	14504	14650	14910	15009	15311	7.69	15645	2	13669	15701	15770	15987	16014	16228	16267
Probe SEQ ID NO:	12247	12274	12806	12636	374	415	3 8	1355	1355	1362	1496		1827	1848	1762	1913	2181	2284	2597	Î	7790		2903	2835	3004	3224	3252	3472	3511

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					·	AIR	Origin Lybors Expressed in Diam
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E	Top Hit Acession No.	Top Hit Detabase Source	Top Hit Descriptor
8623	21315		0.62	1.2E-01	1.2E-01 X15191.1	NT	M.musculus DNA fragment of Apolipoprotein B gene
1748	22080	35252	2.83	1.2E-01	1.2E-01 X77981.1	L	S.carevislae HXT5 gene
9066	22555	35750	1.59	1.2E-01	1.2E-01 AV710857.1	EST_HUMAN	AV710857 Cu Homo sepiens cDNA clone CuAAKE08 5"
10811	23305	36543	1.38	1.2E-01	1.2E-01 BF314481.1	EST HUMAN	601900763F1 NIH_MGC_19 Hamo septens cDNA clone IMAGE:4130103 5'
10801	23484		217		D28184.1	LN	Yeast MPT5 gene for suppressor protein, complete cds
10889	23672		3.18		1.2E-01 BE962324.2	EST_HUMAN	601655578R1 NIH_MGC_85 Homo sepiens cDNA clone IMAGE:3846283 3'
11094	23764		1.58	1.25-01	1.2E-01 BF314481.1	EST_HUMAN	601900763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
11220	23883	37168	2.61	1.2€-01		NT	Homo sepiens dynein Intermediate chain DNA11 (DNA11) gene, econ 17
11283	23944	37238	1.65	1.2E-01 R40249.	R40249.1	EST_HUMAN	y/80c02.s1 Scenes Infant brain 1NIB Homo sapiens cDNA clone IMAGE:28880 3'
11492	24093		1.67	1.2E-01 M65109.	1	N	Rabbit glycogen-associated protein phosphatase regulatory subunit (RG1) mRNA, complete ods
11892	24462		2.53	1.2至-01		EST_HUMAN	AV658033 CLC Hamo sepiens cDNA clane GLCFIB123'
12230	24683		3.52	1.2E-01	1.2E-01 AJ271736.1	LN	Homo sepiens Xq pseudoautosomal region; segment 2/2
12305	25351	30808	2.87	1.2至-01	ZE-01 Q04912	SWISSPROT	MACROPHAGE STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW136) (CD136 ANTIGEN)
	·						Drosophila melanogaster strain Oregon R potential RNA-binding protein gene, complete cds; and syntaxin
12417	24796		3.16	1 社	2.1	Ę	gene, pertial cds
12419	13317		3.19	1.2€-01	21	NT	Homo seplens colon cancer antigen NY-CO-45 mRNA, partial cds
12525	24872		2.11	1.2€-01		NT	R.norvegicus NF88 gene for 68kDa neurofilament
12586	25364		1.44	1.2E-01	1.2E-01 BE061418.1	EST_HUMAN	QV4-BT0234-111199-031-g10 BT0234 Homo sepieme cDNA
12810	24917	31007	5.86	1.2€-01	1.2E-01 AI29903.1	EST_HUMAN	qn20g05x1 NCL_CGAP_Lu5 Homo saplens oDNA olone IMAGE:1898840 3'
12632	24932		2.83	1.2€-01	1.2E-01 L10187.1		Xenopus laevis integrin alpha 3 subunit mRNA, pertial cds
12638	25289		7.95	1.2E-01 098433	098433	SWISSPROT	LNCXXX
12663	24962	30980	1.39	1.25-01	1.2E-01 AE004428.1	NT	Vibrio cholerae chromosome II, section 85 of 93 of the complete chromosome
12800	16228		1.81	1.2E-01	299118.1	INT	Bacillus subtilis complete genome (section 15 of 21); from 2795131 to 3013540
12812	25372		1.38	1.25-01	9845282 NT	LN	Mus musculus protein (16kOs) similar to human SYK interacting protein (p16k), mRNA
551	13334	72064	8.0	1.1E-01	1.1E-01 Al581003.1	EST_HUMAN	In18d08.x1 NCI_CGAP_Bm25 Hamo sepiens cDNA clane IMAGE:2167983 3'
56	13379	26010	1.65	1.1E-01	1.1E-01 AA569006.1	EST_HUMAN	nm08g11.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1059620 3' striiter to gb:X06985_me1 HENE OXYGENASE 1 (HUMAN);
1032	13792	28452	2.03	1.1E-01	1.1E-01 BF697308.1	EST HUMAN	602129847F1 NIH_MGC_56 Homo sepiens cDNA clone IMAGE:4286771 5'
1063	13821		1.3	1.1E-01		Γ	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
1136	15561	28552	4.62	1.1E-01		EST_HUMAN	EST384142 WAGE resequences, MAGL Homo sapiens cDNA
1227	13977	28648		1.1E-01			Synechocystis sp. PCC6803 complete genome, 23/27, 2868767-3002965
1511	14257	28943		1.1E-01	1.1E-01 AU140363.1	T HUMAN	AU140363 PLACE2 Homo sepiens aDNA done PLACE2000403 5'
2312	15037		1.85	1.1E-01	8755215 NT	NT	Mus musculus pre T-cell antigen receptor alpha (Ptora), mRNA

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Single Exon Probes Expressed In Brain

					5	אום דייטייו ו ויסד	Origin Lyons Lyboxed III Diani
Probe SEQ ID NO:	Exam SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similer (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Detabese Source	Top Hit Descriptor
2540	15530		١ -	1.1E-01	LN 9296269	LN	Rettus norvegious Procellagen II alpha 1 (Col2s1), mRNA
2572	15286		1.17	1.1E-01	1.1E-01 AW821909.1	EST_HUMAN	RC0-ST0379-210100-032-g04 ST0379 Hamp saplens cDNA
3030	15796	28442	0.82	1.1E-01 F03265	F03265.1	EST_HUMAN	HSC1RF022 normalized infant brain cDNA Homo septens cDNA clone ≎1rf02.3'
3336	16096		1.78	1.1E-01	F753231 NT	F	Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (Cacna1g), mRNA
3415	16173	28822	211	1.1E-01	BE393186.1	EST_HUMAN	601308679F1 NIH_MGC_44 Homo saplens cDNA clone IMAGE:3627088 5'
3444	l		1.21	1.1E-01	1.1E-01 X62135.1	IN	C.reinhardti nuclear gene on linkage group XIX
3570	16325	28972	0.77	1.1E-01 Y07695	Y07695.1	Ŋ	A.immersus gene for transposase
3688	16441		7.0	1.1E-01 P97384	P97384	SWISSPROT	ANNEXIN XI (CALCYCLIN-ASSOCIATED ANNEXIN 50) (CAP-50)
3696	16450	22080	1.47	1.15-01	1.1E-01 X52708.1	L	Ggallus gene encoding non-histone chromosomal protein HMG-14b, exons 4 and 5
4090	16833		1.28	1.1E-01	1.1E-01 AW819412.1	EST_HUMAN	MR3-ST0290-290100-025-g07 ST0290 Homo septems cDNA
4090	16833		1.28	1.1E-01	1.1E-01 AW819412.1	EST_HUMAN	MR3-ST0290-290100-025-g07 ST0290 Homo septems cDNA
4228	16967		8.78	1.1E-01	1.1E-01 AF157088.1	ΝŢ	Drosophila melanogaster ideraicht protein (Mar) mRNA, complete cds
4224	16995	29624	0.77	1.1E-01	1.1E-01 AW802058.1	EST HUMAN	L5-UM0070-020500-068-e08 UM0070 Homo sapiens cDNA
	<u> </u>	L					Tapa-1≓integral membrane protein TAPA-1 [mice, B cell lymphoma tine 38C13, Genomic, 1973 nt, segment 1
4594			0.96	1.1E-01	1.1E-01 944957.1	NT	(L)
4780	17512	30134	1.2	1.1E-01	1.1E-01 Y07695.1	NT	A.immersus gene for transposase
							Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial cds;
							Notch4, PBX2, RAGE, lysophatidic acid acyl transferase-alpha, palmitroyi-protein thioesterase 2 (PPT2),
4957	16839		0.85	1.1E-01	1.1E-01 AF030001.1	점	CREB-RP, and tensecin X (TNX) genes, complex
5077	17796	30412	1 1	1.1E-01 P70281	P70281	SWISSPROT	SYNAPTONEMAL COMPLEX PROTEIN 3 (SCP-3 PROTEIN)
							nx78ac3.s1 NCI_CGAP_Ew1 Homo sapiens cDNA done IMAGE:1288140 similar to contains Atu repetitive
5584				1.1E-01	1.1E-01 AA747218.1	EST HUMAN	element,contains element MERSS repetitive element;
5853				1.1E-01	1.1E-01 AF020927.1	ΝŢ	8 Homo saplens discrylgyceral kinese 3 (DAGK3) gene, exan 6
5687				1.1E-01	1.1E-01 AL110985.1	NT	Botrytts cineres strain T4 cDNA library under conditions of nitrogen deprivation
5745	18537		1.81	1.1E-01	1.1E-01 X88851.1	NT	S.pombe ste8 gene encoding protein kinese
5781	18572	31500	5.31	1.1E-01	1.1E-01 M86533.1	NT	Providencia rettgeri penicillin G emidase gene
5936			1.67	1.1E-01	1.1E-01 AJ007873.1	NT	Homo saplens LGMD2B gene
5955	18737	31696	1.75	1.1E-01	1.1E-01 BE780152.1	EST_HUMAN	PM3-FT0024-130800-004-f12 FT0024 Hamo septens cDNA
5975		31719	9.4	1.1E-01 AW853(AW853699.1	EST HUMAN	RC3-CT0264-280999-011-401 CT0254 Homo septems oDNA
6330	L			1.1E-01	1.1E-01 AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
6338		32098	1.25	1.1E-01	AF035746.1	EST_HUMAN	AF035746 Human salivary gland cell fine HSG Homo sapiens cDNA cione RL43
6381	19150		0.72	1.1E-01	1.1E-01 AI216307.1	EST_HUMAN	qg78d08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:18410993'
6512		32278		1.1E-01	1.1E-01 069635	SWISSPROT	ACETYL-COENZYME A SYNTHETASE (ACETATE-COA LIGASE) (ACYL-ACTIVATING ENZYME)
8604	19367		3.03	1.1E-01	1.1E-01 AF032922.1	Į.	Homo septens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds

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Probe SEQ ID	Exon SEQ ID	ORF SEQ	Expression	Moet Similar (Top) Hit BLAST E	Top Hit Acessian No.	Top Hit Detabase	Top Hit Descriptor
ö	ö			Vatue		Source	
6697	19814	32865	2.81	1.15-01	11432372 NT	NT	Homo saplens phosphatidylmostidi glycan, class B (PIGB), mRNA
8948	19430	32445	2.0	1.1E-01	1.1E-01 AE002155.1	NT	Ureaplasma urealyticum section 50 of 59 of the complete genome
8948	19430		2.0	1.1E-01	1.1E-01 AE002155.1	NT	Ureaplasma urealyticum section 58 of 59 of the complete genome
7087			0.89	1.1E-01	1.1E-01 BF382758.1	EST_HUMAN	601816624F1 NIH_MGC_66 Homo septens cDNA clone IMAGE:4050653 5'
7203	25107	32964	0.84	1.1E-01	1.1E-01 AP000006.1	N	Pyrococcus harikoshii OT3 genamic DNA, 1166001-1485000 nt. position (6/7)
7435	20112	33100	7.18	1.1E-01	1.1E-01 BF684628.1	EST_HUMAN	602140976F1 NIH_MGC_46 Homo sepiens cDNA clone IMAGE:4302019 5'
7435	20112	33200	7.18	1.1E-01	1.1E-01 BF684628.1	EST_HUMAN	602140976F1 NIH_MGC_46 Homo septens cDNA clone IMACE:4302019 5'
7555	20225	33329	1.83	1.1E-01 P41067	P41067	SWISSPROT	TRABPROTEIN
7505	20263	33374	335	1.15.01	1 1E.01 AA788794 1	EST HIMAN	ah31b08.s1 Source pereffyrold_tumor_NbHPA Homo sapiens cDNA clone 1240403 3' similar to gb:J03483_CHROMOGRANIN A PRECURSOR (HUMAN):
888	20563		0.5	1.1E-01	U67492.1	LN	Metherococcus jerneschil section 34 of 150 of the complete genome
8107	20801		1.7	1.1E-01	1.1E-01 AA483574.1	EST HUMAN	nh04g10.s1 NCI_CGAP_Thy1 Hamo septens cDNA clone IMAGE:943362
8107	20801		1.7	1.1E-01	1.1E-01 AA493674.1	EST_HUMAN	nh04g10.s1 NCI_COARP_Thy1 Hamo septens cDNA clane IMAGE:943362
8153	20847	33979	1.15	1.1E-01	1.1E-01 X91233.1	LN.	H.saplens IL15 gene
8183	20887		1.14	1.1E-01	1.1E-01 AW817918.1	EST_HUMAN	PM1-ST0270-080200-001-009 ST0270 Homo saplens cDNA
8240	20943	34081	1,45	1.1E-01	1.1E-01 AL134340.1	EST_HUMAN	DKFZp547P194_rt 647 (synonym: hfbrt) Hamo sapiens cDNA clane DKFZp547P194 5
							Pediococcus additactici H plannid pSMB74 pediocin AcH production (pap) gene cluster papA, papB, papC
6717	21409	34552	2.08	1.1E-01	1.1E-01 U02482.1	NT	and papD genes, complete cds
3				10 LV 4	7 7 27 2001 4	TOTAL TOTAL	wf48c01.x1 Source_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:2358816 3' similar to contains Alu
DL88	╛			1.15	1.TE-01 AI80/4/4.1	ES! NOIMEN	בות הבי מניוומו ל
8008				1.1E-01	1.1E-01 AF050081.1	Į.	Homo septens C16ort3 large protein mRNA, complete ods
1408	21632			1.1E-01	1.1E-01 AA192153.1	EST_HUMAN	zp83b12.r1 Stratagene muscle 837209 Homo saplens cDNA clone IMAGE:627743 5
8941	21632	34776	5.04	1.1E-01	1.1E-01 AA192153.1	EST_HUMAN	zp83b12.r1 Stratagene muscle 937209 Homo sapiens oDNA clone IMAGE:627743 5
9033	21723	34877	0.74	1.15-01	1.1E-01 Y12727.1	NŦ	P. furiosus partial dah5 gene and argF gene
				1			yd19h03.s1 Sogres fetal liver spieon 1NFLS Homo sepiens cDNA clone IMAGE:108725.3' similar to
8063	21762	34912		1.1E-01	1.1E-01 T72675.1	EST HUMAN	germenter southwaren Assignation in Californian,
0606			9.0	1.1E-01	1.1E-01 BE883250.1	EST_HUMAN	601436972F1 NIH_MGC_72 Hamo septens cDNA clone IMAGE:3922048 5
8322	21989		88.0	1.15-01	1.1E-01 BE142305.1	EST_HUMAN	CM3-HT0142-271089-028-g11 HT0142 Hamo seplens cDNA
9686	22058		7	1.1E-01	1.1E-01 BF085149.1	EST_HUMAN	MR2-GN0027-040900-005-a08 GN0027 Homo sapiens cDNA
9810	22461		9.0	1.1E-01	1.1E-01 AL161543.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 43
10017	22065		97'0	1.1E-01		EST_HUMAN	601140231F1 NIH_MGC_9 Hamo sepiens cDNA clane IMAGE:3049543 5'
10106	22764		1.67	1.1E-01	1	EST_HUMAN	y96a09.s1 Scares placenta Nb2HP Homo saplens cDNA clone IMAGE:147064.3'
10235	22883		1.26	1.1E-01	4	1	Ceretitis capitata yoyo retrotransposon gag-like, pol-like and env-like genes, complete cds
10708	15796	28442	202	1.1E-01	1.1E-01 P03265.1	EST_HUMAN	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1n02 3'

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- Top Hit Descriptor	Carassius auratus activin beta A precursor, mRNA, complete ods	yh39f12.r1 Soares placenta Nb2HP Homo septens dDNA done IMAGE:131759 5' similier to contains Alu repetitive element;	Rattus norvegicus Phosphofructokinasa, Iiver, B-type (PRI), mRNA	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation	M.musculus cytokine gene	Z.mobilis tot and itg genes encoding tRNA guentne transplycosylase and DNA ligase	Zimobilis tet and lig genes encoding tRNA guanine transphoosylase and DNA ligase	SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)	Arabidopeis thaliana DNA chromosome 4, config fragment No. 23	zps3b12.r1 Stratagene muscle 937209 Homo saplens cDNA clone IMAGE:627743 5'	RC2-NT0112-120600-014-f03 NT0112 Home sapiens cDNA	601680651R2 NIH_MGC_83 Hamo sepiens cDNA clane IMAGE:39506043	801908350F1 NIH_MGC_54 Homo septens oDNA clone MAGE:4134085 6'	DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOWAL DNASE II)	ws08d01.x1 NCI_CGAP_Kd11 Homo saplens cDNA done IMAGE:2498577 3' similar to contains MER7.t3	MER7 repetitive element;	Arabidopsis theliana DNA chromosome 4, config fragment No. 16	UI-H-BIS-elc-4-07-0-UI.s1 NCI_CGAP_Sub5 Homo sepiens cDNA clane IMAGE:2738420 3'	601456301F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3859849 67	601908489F1 NIH_MGC_54 Homo septens cDNA clone IMAGE:4134071 5	Escherichia coli enterotoda EspC (espC) gene, complete cds; and unknown genes	Escherichia cdii entarotoxin EspC (espC) gene, complete cds; and unknown genes	QV2-NT0048-160800-316-605 NT0048 Hamo septens cDNA	an32c04.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700358 5'	Drosophila melanogastar tyroeine khase p45 isoform (fer) mRNA, complete cds	EST364414 WAGE resequences, MAGB Homo septens cDNA	zhdZh04,s1 Soares_felal_liver_splean_1NFLS_S1 Homo saplens cDNA clone IMAGE:410095 3	Homo sapiens mRNA for FLJ00085 protein, partial ods	Homo sepiens growth factor receptor-bound protein 7 (GRB7) gene, complete cds	2v41g10.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone MAGE:756258 3' similer to contains L1.3 L1 repeditive element;	zu67c12.s1 Soeres_testis_NHT Hamo septens aDNA alone IMAGE:743062.31
Top Hit Database Source	NT	EST HUMAN		NT	IN		אַן	SWISSPROT	TN	EST_HUMAN			EST HUMAN	SWISSPROT		T_HUMAN	¥	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	NT.	EST_HUMAN	EST_HUMAN	Ę		THUMAN		Ę	EST HUMAN	T
Top Hit Acesskan No.	1.1E-01 AF169032.1	R23708.1	BB81351 NT	AL 110985.1	X70058.1	211910.1	211910.1	P47437	AL161511.2	1.1E-01 AA192153.1	1.1E-01 BE767023.1	1.1E-01 BE974558.1	1.1E-01 BF239753.1	062855		1.0E-01 AI985499.1	1.0E-01 AL161504.2	1.0E-01 AW451365.1	1.0E-01 BF033001.1	BF239818.1	1.0E-01 AF297061.1	1.0E-01 AF297061.1	1.0E-01 BP365703.1	1.0E-01 AI792349.1	J50450.1	44.1	Į.	1.0E-01 AK024472.1	AF274875.1	4A481879.1	1.0E-01 AA406039.1
Most Similar (Top) Hit BLAST E Value	1.15-01	1.1E-01 R23708.	1.1E-01	1.1E-01 AL 11098	1.1E-01 X70058.	1.1E-01 Z11910.	1.1E-01 Z11910.1	1.1E-01 P17437	1.1E-01 AL18151	1.1E-01	1.1E-01	1.1E-01	1.1E-01	1.0E-01 O62855		1.0E-01	1.0E-01	1.0E-01	1.0E-01	1.0E-01 BF23981	1.0E-01	1.0E-01	1.0E-01	1.0E-01	1.0E-01 U50450.1	1.0E-01 AW9523	1.0E-01 W86490	1.0E-01,	1.0E-01 AF27487	1.0E-01 AA48187	1.0E-01
Expression	2.75	3.91	1.39	1.31	1.58	3.21	3.21	2.81	1.65	1.36	3,92	1.97	3.15	2.74		2.63	1.85	1.11	1.19	1.03	96'0	96.0	2.53	96.0	1.19	2.35	57.6	1.21	14.15	8.0	0.7
ORF SEQ ID NO:		36903	36911	31399	87078	37117		37230					30977			20086	26794	27952	28913	29100	29200	29201	28326		30032	30217			31675	31997	
Exan SEQ ID NO:	23622	23650		18480	23802	23836		23938	24269	24529		25160	25012	13932		13998	14119	15210	16259	16461	16569	16569	16885	17253	17398	17594	18044	18580	18717	19017	11
Probe SEQ ID NO:	10840	10974	10983	11002	11134	11169	11169	11277	11674	11990	12098	12341	12750	1179		1249	1371	2493	3503	3708	3817	3817	3835	4518	4884	4866	5238	5789	5834	6243	6256

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					:		
Probe SEQ ID NO:	Exam SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
		·					The second secon
_			,	į	,		yndyndei'r Sogree pigoenta Ndzhip Framo sapiens Clyna agne iwa Chijolo o' similar 10 cantains Alu
47,90	┙		1.51	1.00.0	1.0E-01 R238Z1.1	ES! HOMAN	informive monitorit,
7635	!		267	1.0E-01	1.0E-01 Y12488.1	N	M.musculus with gene
7709	20373	33486	99.0		1.0E-01 AJ011400.1	LN.	Bos taurus mRNA for b17.2 subunit of NADH:ubiquinone addoreductase complex (complex I)
7708		33487	0.65	1.0E-01	1.0E-01 AJ011400.1	¥	Bos taurus mRNA for b17.2 subunit of NADH:ubiquinone addoreductase complex (complex I)
7682	20520	22856	200		4 OE 04 A A BRADOM 4	ECT LIBAN	ak32g01.s1 Source_tests_NHT Homo sapiens cDNA clone INAGE:1407896 3' similar to gb:M34182 CAMP- DEPENDENT PROTIEM KINASE CAMAA.CATA! YTIC SI ISHINT GLIMANY
8088	1		0.6			LN-	Homo seciene fibroblest growth fector 13 (FGF13) mRNA
	ı						MORPOT YT NC! CRAP Life Homo serviens CDNA clone IMAGE-2675689 3' similar to chix17206 40S
8390	21083		96.0	1.0E-01	1.0E-01 AW189797.1	EST HUMAN	RIBOSOMAL PROTEIN S4 (HUMAN); contains TAR1.t3 TAR1 repetitive element;
88	L		2		27	N IN	Rattus novegicus synaptic SAPAP-interacting protein Synamon mRNA, complete ods
8886	22057	35228	0.51		1.0E-01 R44983.1	EST_HUMAN	yg33h04.s1 Soares Infant brain 1NIB Homo saplens cDNA clone IMAGE:345493'
70 1 0	22069		1.8		1.0E-01 M76729.1	Į.	Human pro-elphe-1 (V) collegen mRNA, complete cds
9450	22000		3.02		1.0E-01 AE001501.1	¥	Helicobacter pylori, strain J99 section 62 of 132 of the complete genome
948	L	35245	0.75		1.0E-01 W01955.1	EST HUMAN	208010.s1 Scenes fetal_heart_NbH119W Home sapiens cDNA clane IMAGE:327282.3
9721	22372	35571	1.67	1.0E-01	1.0E-01 BF240154.1	EST HUMAN	601905861F1 NIH_MGC_54 Hamo sapiens cDNA clane IMAGE:4133487 5
9835	22486	35687	8.12		1.0E-01 AB046799.1	ᅜ	Homo sepiens mRNA for KIAA1579 protein, pertial cds
9835		35688	8.12		1.0E-01 AB046799.1	TN	Homo sepiens mRNA for KIAA1579 protein, pertial cds
10043	72691		26.0	1.0E-01	1.0E-01 AW957425.1	EST_HUMAN	EST369615 MAGE resequences, MAGE Homo seplens cDNA
	<u> </u>						yb29e06.s1 Stratagene fetal spiesn (#637205) Homo sapiens cDNA clone IMAGE:72562 3' similar to
199	_1		0.51	1.05-01	1.0E-01 151952.1	ESI HUMAN	Contrains All reporting exerting it
10220		36089	0.80	1.05-01	1.0E-01 BE792750.1	EST HUMAN	601884004F1 NIH, MGC, / Home septems cluna cone IMAGE:3838086 5
10554			1.95	1.0E-01	1.0E-01 AU150127.1	EST HUMAN	AU169127 THYRO1 Hamo suplems cDNA clone THYRO1000895 31
10958	┙	36884	235		1.0E-01 BF242946.1	EST HUMAN	801877703F1 NH_MGC_65 Hamo septems cDNA clone IMAGE:4106069 5
10958		36885	2.35		1.0E-01 BF242946.1	EST_HUMAN	601877703F1 NIH_MGC_55 Hamo suplens cDNA clane IMAGE:4106089 51
11378	23983	37283	6.22	1.0E-01	1.0E-01 BE790543.1	EST_HUMAN	601582558F1 NIH_MGC_7 Hamo septens aDNA clane IMAGE:3936734 5'
11510	24110		1.52	1.0E-01	1.0E-01 AP000400.1	Į.	Eacherichie coli 0157:H7 genomic DNA, prophage (Sakal-VT1) inserted region, substrain:RIMD 0509952
11594	24193	37511	1.48	1.0E-01	1.0E-01 Z71448.1	<u>F</u>	A. thaliena mRNA for OLC-b chloride channel protein
11694	24193	37512	1.48	1.0E-01	1.0E-01 Z71448.1	Ę	A.theliana mRNA for CLC-b chloride channel protein
11832	24416	37756	1.89	1.0E-01	5.1	EST HUMAN	AV649035 GLC Homo sepiene dDNA clone GLCBPG01 31
11832	24416	37756	1.89	1.0E-01	1.0E-01 AV649035.1	EST_HUMAN	AV649035 GLC Homo septems aDNA clame GLCBPG01 3'
12083	24921		4.32	1.0E-01	1.0E-01 BE537719.1	EST_HUMAN	801085554F1 NIH_MGC_10 Hamo septens aDNA alone IMAGE:3481833 5'
12300	24725		1.71	1.0E-01	7862165 NT	NT	Homo sapiens KIAA0514 gene product (KIAA0514), mRNA

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Table 4
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Childre Lyonas Lybrassed in Drail	Moet Similar Top Hit Acession (Top) Hit Acession ID NO: Signal BLASTE No. Source Source	3273 36510 2.36 9.5E-02 BF035891.1 EST_HUMAN 601453642F1 NIH_MGC_68 Homo sepiens cDNA clone IMAGE:3867243 5	27275 2.82 9.4E-02 BF671063.1 EST_HUMAN	27310 0.99 9.4E-02 U55944.1	27311 0.99	29249 4.43	31976 0.63	2.46 9.4E-02 Z46963.1 NT Achretcher sp. cysD, cobQ, sodM, lysS, rubA, rubB, estB, coyR, ppk, mtgA, ORF2 and ORF3 genes	33258 2.44 9.4E-02 L78833.1 NT	1.78 9.4E-02 U31815.1 NT	1.92 9.4E-02 AF199036.1 NT Mycoplasma pulmonis hypothetical membrane protein P93 gene, complete cds	1.97 9.3E-02 4809280 NT	6.32 9.3E-02 6912525 NT	28865 1.85 9.3E-02 BF575511.1 EST_HUMAN	29502 3.51 9.3E-02 BE391943.1 EST_HUMAN		2.04 9.3E-02 AV732224.1 EST_HUMAN	1373 0.67 9.3E-02 AP001507.1 NT Bacillus hatodurans genomic DNA, section 1/14	33972 0.62 0.3E-02 AW566007.1 EST_HUMAN	35449 2.15 9.3E-02 BE962831.2 EST_HUMAN	35953 3.67 9.3E-02/Q15034 SWISSPROT	2739 36954 3.87 9.3E-02 Q15034 SWISSPROT HYPOTHETICAL PROTEIN KIAA0032	3.6 9.3E-02 AW206117.1 EST_HUMAN UI-H-Bit-afix-h-05-0-UI.s1 NCI_CGAP_Sub3 Homo septens dDNA done IMAGE:2723553 3'	2.51 9.3E-02 AJ249850.1 NT	209 8.43 9.3E-02 AW 488950.1 EST_HUMAN hd28h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IWAGE:2910887.3	Mus musculus major histocompatibility locus class II region; Fas-binding protein Daox (DAXX) gene, partial	2.1 9.3E-02 AF100956.1 NT	25868	1034 25669 8.37 9.2E-0.2 UG0315.1 NT Molluscum contagiosum virus subtype 1, complete genome	25670 8.37 9.2E-02[U60315.1 NT	1.68 9.2E-02 R54156.1 [EST_HUMAN	28587 3.28 9.2E-02 Q28631 SWISSPROT	0.85
									L																								
	be Exan	10578 23273	1825 14564	1857 14595	1857 14595	3860 16610	6225 18999	8498 21190	351 20106	11941 25255	12671 24965	2988 15754	3026 15792	3251 16013	4132 16874	4132 16874	4685 17419	5576 18373	8146 20840	9810 22263	10091 22739	10001 22739	10218 22868	12194 25181	12550 25209			222 13034	222 13034	13034		3175 15938	1000
	Probe SEQ ID NO:	Ę	Ľ	Ĕ	Ē	8	6	9	10851	Ĕ	126	X	ಶ	3	4	4	¥	ਨ	έδ	ď	ğ	ξ	<u>0</u>	12	125		 12)	. 7	,4	. 1	7	3	ć

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	Top Hit Descriptor	aicha (Picra), mRNA	Human herpeswirus 1 strain KOS-63, latency-essociated transcript, promoter region	ns cDNA clone IMAGE:2960176 5'	ye99009.r1 Strategere placenta (#837225) Homo sepiens cDNA clone (MAGE-69906 5' similar to similar to children to		(OVI) gene, complete ods	ets genome		config fragment No. 54	Homo sepiens MSH55 gene, pertial cds; and CLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b, CSK28, BAT4, G4, Apo M, BAT2, BAT2, AF-1, 1C7, LST-1, LTB, TNF, and LTA genee, complete ode	au74a05.y1 Schneider fetal brain 00004 Homo sapiens cDNA done JMA GE:2781968 5	77	complete cds	6.	piens cDNA clane FB19F10 3'end	urchine, embryos, Genomic, 5275 nf]	-8, and PRL1 genes	2038h12.s1 Stratagene muscle 537209 Homo septens cONA clone IMAGE:811783 3' similar to SW:TRT3_HUMAN P45378 TROPONIN T, FAST SKELETAL MUSCLE, ISOFORM BETA;	OC gene, complete cds	JC3B mucin, exams 1-11	FOLATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED ANTIGEN MOV18) (KB CELLS FBP)	h/S9010.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175842.3' similar to contains Alu recettifive element:	oprofein (env) gene pertial cds	oprotein (erry) gene, partial cds	Dictycetellum discoldeum spore cost structural protein SP65 (cotf.) gene, complete cds	gene
dingle Labil Flobes Lapressed in Digiti		Mus musculus pre T-cell antigen receptor alpha (Ptora), mRNA	Human herpeswirus 1 strain KOS-83, let	600944365F1 NIH_MGC_17 Hamo sepiens cDNA clone IMAGE:2960176 5		T	Mesocricetus euratus oviductin precursor (OVI) gene, complete ods	Podospora anserina mitochondrion, complete genome	O. cuniculus k12 keratin gene	Arabidopsis fhaliana DNA chromosome 4, config fragment No. 54	Homo sepiens MSH55 gene, partial ods; CSK28, BAT4, G4, Apo M, BAT3, BAT2	Ė	Г	Mus musculus thymopoletin zete mRNA, complete cds	Homo sepiens gamma adducin gene, excn 9	FB19F10 Fetal brain, Stratagene Homo sapiens cDNA clone FB19F10 3'end	Tg616=Cyl actin [Tripneustes grattila=sea urchins, embryos, Genomic, 5275 m]	A.thaliana RH1, TC1, G14587-5, G14587-8, and PRL1 genes		Rattus norvegicus cell cycle protein p66CDC gene, complete cds	Homo sapiens partial MUC3B gene for MUC3B mucin, exons 1-11	FOLATE RECEPTOR ALPHA PRECUI RECEPTOR, ADULT) (ADULT FOLATE ANTIGEN MOV18) (KB CELLS FBP)	hv39g10.x1 NCI_CGAP_Lu24 Homo sal	HIV-1 p8c095-06 from USA envelope alycoprotein (env) gene, perfiel ods	HIV-1 p8c085-06 from USA envelope glycoprotein (erry) gene, pertial cds	Dictyostalium discoldeum spore cost stra	Plasmodium falciparum P-type ATPase 3 gene
שולים בול	Top Hit Database Source	L'N	N	EST_HUMAN	EST HUMAN	N	Z	NT NT	NT	TN	Į Ę	EST HUMAN	F	Į.	Z	EST HUMAN	Z	FX	EST_HUMAN	Ę	IN	SWISSPROT	EST HUMAN	5	Ĭ	Į.	N
	Top Hit Acessian No.	6755215 NT	1	21			52.3	11486872 NT	X77665.1	9.1E-02 AL181554.2	9.1E-02 AF129756.1	9.1E-02 AW160658.1		_	-	1		1	91.1	9.1E-02 AF052895.1			27			9.0E-02 AF279135.1	2
	Most Similar (Top) Hit BLAST E Value	0.2€-02	9.2E-02 U92048.	9.2E-02	9.2E-02 T49920.	9.2E-02 X95256	0.2E-02 AF0266	9.2€-02	9.1E-02 X77885	9.1E-02	9.1E-02	9.1E-02	9.1E-02	9.1E-02 U39073.	9.1E-02 Y14379.	9.1E-02 T02984.	9.1E-02 S74050	9.1E-02 Y11187	9.15-02	9.1E-02	9.1E-02	9.0E-02 P16328	9.0E-02	9.0E-02	9.0E-02	9.0E-02	9.0E-02 X65740.
	Expression Signal	1.28	96.0	0.76	1.98	22	1.27	1.4	4.19	1.33	1.44	14.94	97.0	0.72	0.88	1.37	1.25	1.19	1.4	2.12	1.83	4.3	5.28	6.45	5.45	0.84	3.27
	ORF SEQ. ID NO:				33732	L		L	25438	29812	31352	33045	33349	33383	34659		36218	36244				26155	27064	28252	28253	28744	29989
	Exan SEQ ID NO:	16328	16954	17013	20002			25412	12825	17187	18438	19968	20244	20275	21514	72827	23001	62062	25348	24653	25204	13501	14377	L.		16091	17354
	Probe SEQ ID NO:	8573	4213	4274	7907	8078	11695	12736	414	4461	5843	7285	7575	7809	8822	10327	10354	10383	12110	12181	12637	727	1831	2808	2806	3331	4619

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	SEQ ID	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Verlue	Top Hit Acession No.	Top Hit Detebase Source	Top Hit Descriptor
5906	18691	31640	5.21	9.0E-02 W58037	W56037.1	EST_HUMAN	za88a12.r1 Soares_fetal_lung_NbHL19W Homo eapiens cONA clone IMAGE;297694 5' similar to PIR-S52171 S52171 small G protein - human ;
3,00				1			The3de3x1 NCI_CGAP_Co16 Homo sepiens cDNA clone IMAGE:3320645 3' similar to contains Alu
200	18291		 	9.0E-02	9.0E-02 BF002001.1	EST CHANN	INDUMINE CONTROL OF THE PROPERTY OF THE PROPER
8000	င်ဆင်္သေ	32619	0.72	9.0E-02 R62805.	K62800.1	ESI HUMAN	YELLOWS: STOCKED PROGRAM INCOME THAT A CHINA CHAIN CHAIN CHINA CE. LOGGOS
						!	Escherichia coli strain E2348/89 pathogenicity island, rOrf1 (rorf1), rOrf2 (rorf2), EscR (escR), EscS (escS), EscT (escT), EscU (escU), CesD (cesD), EscC (escC), EscJ (escJ), SepZ (espZ), EscV (escV), EscN
12486	24845		2.01	9.0E-02 AF02223	AF022238.1	NT	(escyl), SepQ (sepQ), I'r (ur), OrtU (ortU), >
1418	14106	64892	1.99	8.9E-02	8.9E-02 BF701583.1	EST_HUMAN	602128030F2 NIH_MGC_56 Homo septens cDNA clone IMAGE:4285951 5'
1418	14166	L	1.80	8.0E-02	8.0E-02 BF701503.1	EST_HUMAN	602/29030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
2386	15107		1.22	8.9E-02	8.9E-02 BE153572.1	EST_HUMAN	PMOHT0339-251199-003-401 HT0339 Homo sapiens cDNA
4175	16915		1.83	8.9E-02	8.9E-02 AF286055.1	Ę	Atrichum angustatum AtranFlo2 protein (AtranFlo2) gene, partial cds
22,60	18552	31474	3.22	8.9E-02	8.9E-02 AW462122.1	EST_HUMAN	UI-H-BI3-alo-f-08-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068294 3'
5780	18552	31475	3.22	8.9E-02 AW4521	AW452122.1	EST_HUMAN	UIH-BI3-alo-f-08-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068294 3'
5776	18567	31496	3.39	8.9E-02	11433478 NT	Ę	Homo sapiens similar to endoglycan (H. saplens) (LOC63107), mRNA
							FOLD BIFUNCTIONAL PROTEIN (INCLUDES: METHYLENETETRAHYDROFOLATE
7083	19782	32848	1.64	8.9E-02 P47259	P47259	SWISSPROT	DEHYDROGENASE; METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE]
7458	20132		206	8.9€-02	279021.1	NT	H. septens flow-sorted chromosome 6 Hindill fragment, SC6pA20F8
1	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,						NITRIC-OXIDE SYNTHASE, BRAIN (NOS, TYPE I) (NEURONAL NOS) (N-NOS) (NNOS)
948	7887	}	1.08	8.95-02 7.294/6	7294/0	SWISSPRO	(CONSTITUTIVE NOS) (NC-NOS) (BNOS)
8030	20725		0.72	8.9E-02	8.9E-02 BF701665.1	EST_HUMAN	802128111F2 NIH_MGC_56 Hamo sapiens cDNA clone IMAGE:4285827 5'
8030	20725	33820	0.72	8.9E-02	8.9E-02 BF701685.1	EST_HUMAN	802128111F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285827 51
8406	21188	34331	4.72	8.9E-02	8.9E-02 AA308319.1	EST_HUMAN	EST180187 Liver, hepatocellular carcinoma Homo saplens cONA 5' end
							qu55c05.x1 NCI_CGAP_Lym6 Homo septens cDNA clone IMAGE:1988680 3' shrillar to contains MER10.b1
9520	22173	35356	0.8	8.9E-02 A1285627	Al285627.1	EST_HUMAN	MER10 repetitive element;
					i		qu55c06.x1 NCI_CGAP_Lym6 Homo saplens cDNA clone IMAGE:1968680 3' similar to contains MER10.b1
9620	22123	35357	0.8	8.95-02	8.9E-02 AI286627.1	EST_HUMAN	MER10 repetitive element;
9632	22284	35477	0.78	8.9E-02 AA33935	AA339356.1	EST_HUMAN	EST44454 Fetal brain I Homo sapiens cDNA 5' end
11882	25173		1.40	8.9E-02 P30143	P30143	SWISSPROT	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)
11940	25207		1.48	8.0E-02 P19524	P19524	SWISSPROT	MYOSIN-2 ISOFORM
12085	24591		3.05	8.9E-02 BF69691	BF696918.1	EST_HUMAN	602/29682F1 NIH_MGC_56 Hamo sepiens cDNA clane IMAGE:4286180 5'
12284	24718		1.61	8.9E-02 U29895.	U29895.1	NT	Human 4-hydroxyphenybyruvate-dioxygenase gene, complete cds
1352	14100	26775	1.59	8.8E-02 Q27474	027474	SWISSPROT	PROBÁBLE DNA LIGASE (POLYDEOXYRIBONUCLEÓTIDE SYNTHASE (ATP))
3883	16633	29272	1.03	8.8E-02	8.8E-02 AA299128.1	EST_HUMAN	EST11595 Uterus Homo septens cDNA 5' end

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Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signer	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Databese Source	Top Hit Descriptor
4014	16760		3.55	8.8E-02	000268	SWISSPROT	TRANSCRIPTION INITIATION FACTOR TFIID 135 KDA SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130)
4214	16055		0.99	8.8E-02	4502804 NT	IN	Homo sapiens chromogranin A (parathyroid secretory protein 1) (CHGA) mRNA
4269	17009		1.27	8.8E-02	4580423 NT	NT	Homo sapiens paired box gene 6 (enirtida, keratitis) (PAX8), isoform b, mRNA
7444	20120		0.57	8.8E-02 D17520.	D17520.1	NT	Sheep mRNA for anglotensinogen, complete cds
8886	21577	34719	1.07	8.8€-02	8.8E-02 AA151872.1	EST_HUMAN	Z189805.81 Strategene colon (#937204) Homo septens cDNA clone IMAGE:568288 3'
11062	23732	37003	2.7	8.8E-02	8.8E-02 BE284455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Hamo sepiens cDNA clone IMAGE:3535648 5'
11062	23732	37004	2.7	8.8E-02	8.8E-02 BE264455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sepiens cDNA done IMAGE:3535648 5'
11228	73891	37178	6.92	8.8E-02	8.8E-02 ALO40129.1	EST_HUMAN	DKFZp434D1313_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D1313 5'
11805	24395	37729	1.49	8.8E-02 P97803	P97803	SWISSPROT	CYTOKINE INDUCIBLE SH2-CONTAINING PROTEIN 3 (PROTEIN EF-10)
12155		31098	2.66	8.8E-02	271561.1	INT	S.carevisiae chromosome XIV reading frame ORF YNI_285w
1642	14388	27077	1.15	8.7E-02	8.7E-02 A1167281.1	EST_HUMAN	ox65b01.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1681161 3'
3681	16434	22002	S.	8 7F-02	R 75-00 IIROROK 0	IN	Homo septions zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and bighycan (BGN) protein contribute calculation of these leaferm 3 (PMCA3) name, restlict orts.
				20.11.0	2,000,000		and the state of t
3661	16434	29078	3.86	8.7E-02	8.7E-02 U82695.2	Į.	Homo sepiens zho finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and pleame membrane calcium ATPase (soform 3 (PMCA3) gene, partial cds
4658	17302	30027	1.10	8.7E-02	8.7E-02 AF178638.1	N	Mas musculus JNK interacting protein-3a (Jip3) mRNA, complete cds
5231	18037	30863	5.88	8.7E-02	8.7E-02 AA286875.1	EST HUMAN	zs55g08.s1 NC _CGAP_GCB1 Homo sepiens cONA clone IMAGE:701438 3'
5231	18037	30684	5.88	8.7E-02	8.7E-02 AA286875.1	EST_HUMAN	2255g08.s1 NCI_CGAP_GCB1 Homo septems cDNA clone IMAGE:701438 3'
6745	19578	32812	0.77	8.7E-02	8.7E-02 AJZ71885.2	LN	Mus musculus partial Kong1 gene for potasstum channel protein, exons 10-14
6745	19578	32613		8.7E-02		NT	Mus musculus partial Konq1 gene for potassium channel protein, excns 10-14
6943	19425	32440	0.71	8.7E-02		LN	Oncorhynchus mykiss TAT-binding protein 1 mRNA, pertial cds
7761	20457		0.45	8.7E-02		EST_HUMAN	zt20e03.s1 Sceres overy lumor NbHOT Homo septems aDNA dane IMAGE:7138923'
8413	21106	34246		8.7E-02		NT	Pseudomonas aeruginosa PA01, section 348 of 529 of the complete genome
8413	21106	34246		8.7E-02	7.1	NT	Pseudomonas aeruginosa PA01, aection 348 of 529 of the complete genome
10810	23304		2.48	8.7E-02	8.7E-02 L04758.1	IN	Oryctolagus cuniculus cytochrome P-450 (CYP4A4) gene, 5' end
11282	23943	37237	2.55	8.7E-02	8.7E-02 AJ007763.1	N.	Gluconobacter oxydans tRNA-lie and tRNA-Ala genes
12145	24633		2.1	8.7E-02	8.7E-02 X17116.1	LN	Human DNA for immunoglobulin alpha heavy chain from a case of alpha heavy chain disease
12340	24750		1.75	8.7E-02	8679057 NT	NT	Mus musculus nidogen 2 (Nid2), mRNA
1230	13979		7.02	8.6E-02		NT	Homo sapiens Xq pseudoautosomal region; segment 2/2
240	14968			8.0E-02	8.0E-02 BE408687.1	EST HUMAN	601304018F1 NIH_MGC_21 Hamo sapiens aDNA dane IMAGE:3638643 5
3183	15946	28596	4.57	8.6E-02	8.6E-02 L05468.1	Ę	Trichamanas vaginalis beta-tubulin (blub1) gene, complete ads

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Г		T	Τ	Τ	Τ	Τ		Γ		Γ	Γ	Γ	Γ		Γ		Γ	Γ	Γ	Γ	Γ	Γ	Γ		Γ		Γ	Γ	Γ		[Γ	Γ	Γ	П
	Top Hit Descriptor	Homo septions chromosome 21 segment HS210006	FILOCOTE ANTIGEN COST PRECURSOR	LEUCOCYTE ANTIGEN CD97 PRECURSOR	LEUCOCYTE ANTIGEN COST PRECURSOR	Mus musculus zinc transporter (ZnT-3) gene, complete cds	T.infletum transposon Resiless DNA	801438678F1 NIH_MGC_72 Hamo septems cDNA clone IMAGE:3924523 5'	Bos taurus connective tissue growth factor precursor (CTGF) gene, complete cds	AV743341 CB Hamo septens cDNA clane CBLANF07 5	RC2-PT0004-031299-011-d05 PT0004 Homo sepiens oDNA	Beet necrotic yellow vein virus RNA-2	801115055F1 NIH_MGC_16 Hamo sapiens cDNA clane IMAGE:3355596 5'	Chlamydophila pneumoniae AR39, section 73 of 94 of the complete genome	Mus musculus epidermal growth factor receptor (Egifr) gene, exons 5 through 28, and complete cds,	elternatively spiloed	Xylella fastidiosa, section 152 of 229 of the complete genome	A1484F Heart Homo sapiens cDNA clone A1484	Homo septens chromosome 21 segment HS21C079	wd86f08.xf NCL_CGAP_Lu24 Homo explens cDNA clone IMAGE:2338503 3'	Homo sepiens hypothetical protein FLJ10080 (FLJ10080), mRNA	Homo saplens hypothetical protein FLJ10080 (FLJ10080), mRNA	Homo expiens extracellular glycoprobah lacritin precursor, gene, complete cds	Homo sepiens chromosome 21 segment HS21C002	EST366723 MAGE resequences, MAGC Homo sepiens cDNA	Molluscum contegiosum virus authype 1, complete genome	Human gane for dihydrotpoamide succinyltransferasa, complete cds (excn 1-15)	Human gene for dihydrolipoamide succhnyfransferase, complete cds (exon 1-15)	PMS-BT0347-170200-001-b08 BT0347 Homo sapiens cDNA	Synechocystis ap. PCC8803 complete genome, 17/27, 2137259-2287259	Synechocystla sp. PCC8803 complete genome, 17/27, 2137259-2287259	801855548F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075619 5'	Dictyceelium discoldeum cyclio nucleotide phosphodiesterase gene, complete cds	Thermoplasma acidophilum complete genome; segment 5/5	EST378191 MAGE resequences, MAGI Homo sapiens cDNA
	Top Hit Detebose Source	 	TORGSSIMS	SWISSPROT	SWISSPROT	Ę	Z	EST_HUMAN	LN.	EST_HUMAN	EST_HUMAN	M	EST_HUMAN	Ę		Ę	¥	EST_HUMAN	¥	EST_HUMAN	Ę	Z	Ę	F	EST_HUMAN	F	M	¥	EST_HUMAN	Ę	ĮΝ	EST_HUMAN	ĹΝ	ĹΝ	EST_HUMAN
	Top Hit Accession No.	VI 163206.2	748080	248QB0	2489R0	176009.1	760803.1	8.2E-02 BE897030.1	8.2E-02 AF308555.1	1V743341.1	W875128.1	04197.1	3E254318.1	VE002246.2		8.2E-02 AF275366.1	8.1E-02 AE004008.1	11532.1	VL 163279.2	A/692681.1	11420074 NT	11426974 NT	8.1E-02 AY006150.1	8.1E-02 AL163202.2	8.0E-02 AW954653.1	U60315.1	128635.1)26535.1	3E067219.1	390915.1	390915.1	8.0E-02 BF246744.1	123449.1	8.0E-02 AL445067.1	W966118.1
	Moet Similar (Top) Hit BLAST E Vatue	8.7E-02 AL16320	R OF A D DARDEN	8 2F-02 248080	8 2F-02 P48960	8.2E-02	8.2E-02 Z60803.1	8.2E-02	8.2€-02/	8.2E-02 AV74334	8.2E-02 AW8751	8.2E-02 X04197.	8.2E-02 BE25431	8.2E-02 AE00224		8.2E-02	8.1E-02/	8.1E-02 T11532.	8.1E-02 AL 16327	8.1E-02 A169268	8.1E-02	8.1E-02	8.1E-02/	8.1E-02	8.0E-02	8.0E-02	8.0E-02 D28635.	8.0E-02 D28535.	8.0E-02 BE06721	8.0E-02 D90915.	8.0E-02 D90915.	8.0E-02	8.0E-02 M23449.	8.0E-02	8.0E-02 AW9661
	Expression Signal	107	4 07	497	4.97	244	230	1.49	3.09	0.57	2.95	5.36	2.24	₹.03		3.65	0.79	1.19	99.0	1.25	0.61	0.61	1.64	2.08	5.03	0.79	9.85	9.85	3.27	1.09	1.09	4.2	86'0.	1.45	1.01
	ORF SEQ ID NO:	28371	20617	29618	29619	30354		30687	32707		34509	35332	35512	31102			31378	32040			34067	34068	 	37395	25447	26344	27134	27135	27343	27835	27836		26486	28315	29182
	SEQ ID NO:	16737	16007	16902	16992	17743	17780	18058	19661	20298	21362	22152	22315	24648		25138	18463	19059	19786	20154	20832	20832	22463	24083	15534	13682	15576	15578	14633	15096	15096	15191	13827	15667	16549
	Probe SEQ ID NO:	3989	50.5	4251	4251	5022	5070	5252	6925	7632	8670	661/6	29963	12164		12554	2888	6286	1607	7482	8238	8238	9812	11482	20	915	1694	1684	1896	2374	2374	2473	2823	2901	3797

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Moet Similar (Top) Hit Top Hit Accession Detablese BLASTE No. Source	1.43 8.0E-02/A1434202.1 [EST_HUMAN 1131g02.x1 NCI_CGAP_Gae4 Homo sapiens cDNA clone IMAGE:2132114.3'	6.33 8.0E-02\X72794.1 NT M.musculus gene for geletimese B	0.87 8.0E-02 AW207037.1 EST_HUMAN UI-H-BIT-efd-f-10-0-UI.s1 NCI_CGAP_Sub3 Home eaplens cDNA clone IMAGE:2721547.3'	ŢŅ	8.0E-02 AF275948.1 NT	3.79 8.0E-02 AL114933.1 NT Botrytis cheres strain T4 cDNA library under conditions of nitrogen deprivation	1.12 8.0E-02 X74208.1 NT H.sepiers AGT gene, intron 4	1.12 8.0E-02 X74208.1 NT (H.sepierrs AGT gene, intron 4	0.55 8.0E-02 AL163209.2 NT Homo septens chromosome 21 segment HS21C009	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M88, and ADP-ribosylation factor related 2.27 8.0E-02 AF217798.1 NT protein 1 (ARFRP1) genes, complete cds	8.0E-02 AJ005375.1	8.0E-02	7.9E-02 BE250008.1 EST HUMAN	MANUEL TOTAL	(.25) / 3E-02 Albezuze, lest HUMAN (30'S KIBUSUMAL PROTEIN US (POINTY),	7.8E-02/AF030894.2 NT		7.9E-02 6881044 NT	4.1 EST_HUMAN		<u>L</u>	6.1 EST HUMAN	2.79 7.9E-02 U27832.1 NT Seccheromyces cerevisies suppressor of MIF2 Smith (SMT4) gene, complete cds	4.21 7.9E-02/A1061644.1 EST HUMAN CE08011;		4.21 7.9E-02 Al081644.1 EST HUMAN CE08611;	1.77 7.8E-02 AT03276.1 EST_HUMAN repotitive element;	1.77 7.8E-02 AI793275.1 EST_HUMAN repetitive element;
Moet Similar (Top) Hit BLAST E Value			L								8.0E-02	8.0E-02							L	7.9E-02			L	7.9E-02		7.9E-02		
Expression Signal	1.43	6.33	0.87	3.15	1.82	3.79	1.12	1.12	0.55	2.27	6.39	221	3.52		87.)				ļ	1.31	1.02	1.16	270	124		4.21	1.77	
ORF SEQ ID NO:	30083		30443	31518	31516	33854	36127	35128		36623			27634		28332			29218			30204		33764	35773		35774	28604	28905
SEQ ID NO:	17457	17496	17826	18591	18691	20722	21968	21956	22706	2383	L	L	1		15/44	 	16583	16583	17379	17492	17581		20828		_	22575	13940	13940
Probe SEQ ID NO:	4725	4704	5108	5801	7080	8027	9280	9289	10058	10692	12195	12748	2171	8	29/8	3777	3832	3832	4845	4760	4851	2007	7931	200		7200	1188	1188

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similer (Top) Hit BLAST E Vahue	Top Hit Acession No.	Top Hit Detebase Source	Top HR Descriptor
906	21753	34914	1.12	7.4E-02	7.4E-02 AW 629805.1	EST HUMAN	IN67411.71 NCI COAP GU1 Homo septens cDNA done IMAGE:2967861 5 similar to SW:SCA2_HUMAN 015127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2
9339		33525	0.52	7.4E-02	7.4E-02 AI672939.1	EST HUMAN	we74d02x1 Source Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346819 3
9339	20410	33526	0.52	7.4E-02	7.4E-02 AI672939.1	EST_HUMAN	we74d02.x1 Soares_Dieckgrassis_colon_NHCD Homo sapiens cDNA clone IMAGE:23488193'
9714	22365	35563	1.03	7.4E-02 U62283.	U62233.1	Z	Human LIM-kinase1 and alternatively spirod LIM-kinase1 (LIMK1) gene, complete cds
9841			0.52	7.4E-02 BF51287	BF512878.1	EST_HUMAN	UI-H-BW1-emg-g-08-0-UI.s1 NCI_CGAP_Sub7 Homo sepiens cDNA clone IMAGE:3089898 31
10839	23619	36869	1.26	7.4E-02	7.4E-02 AA059167.1	EST_HUMAN	2784601.r1 Sources retine N254HR Homo septens aDNA clane IMAGE:381720 5
12126	24618		1.53	7.4E-02	11525893 NT	F	Homo sepiens histone descatylese 5 (NY-CO-9), mRNA
12381			2.21	7.4E-02 AW3794	AW379431.1	EST_HUMAN	CM4-HT0243-081199-037-d11 HT0243 Homo sepiens cDNA
456	13242	25881	1.5	7.3E-02 BE96496	BE964961.2	EST_HUMAN	601658738R1 NIH MGC_69 Hamo sepiens oDNA olone IMAGE:3886209 3'
450	13242	25882	1.5	7.3€-02	7.3E-02 BE964961.2	EST_HUMAN	601658738R1 NIH MGC_69 Hamo sapiens cDNA clone IMAGE:3886209 3'
889	L.		3.9	7.3E-02	7.3E-02 AE001789.1	F	Thermotoga maritima section 101 of 136 of the complete genome
1484	15570	28900	3.62	7.3E-02	7.3E-02 AW900281.1	EST_HUMAN	CMC-NN1004-130300-284-g08 NN1004 Homo sapiens cDNA
1837	15580		12.41	7.3E-02		Z	Homo sepiens chromosome 21 segment HS21C102
						П	#24802.e1 Soares fettal liver_spleen_1NFLS_S1 Homo sapiens cDNA done IMAGE:451178 3' similar to
83			1.32	7.3E-02 AA77997	AA779977.1	П	gb:L02426 26S PROTEASE SUBUNIT 4 (HUMAN);
388 3	_		2.58	7.3E-02 P05143	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
7368		33129	2.58	7.3E-02 P05143	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8008	_		1.15	7.3E-02	2107	٦	Homo sepiens KIAA0424 protein (KIAA0424), mRNA
9110	21798		1.14	7.3E-02	7.3E-02 AB011090.1	Ā	Homo sepiens mRNA for KIAA0518 protein, pertial cds
7777	70707	20,00	-	20			2/24/202.s1 Scares fetal liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to
2/10/		35150	2007	1.3E-02 MA/ /WW/	F.//00///	7.1 EST HUMAN	go:Luzazo zos Proj Easie subloni 4 (Human);
<u> </u>	24472		9.07	7.35-02	11560138	Т	Kattus norvegious caspase recruitment domain protein 9 (LOC64171), mRNA
117	12037	25577	*	7.25-02	7.2F_02 AF000882.4	5	Metrationacterium mermoautotrophicum from bases 10.281.55 to 10.38934 (section 88 of 148) of the complete (section 88 of 148) of the compl
					T		Mathemathematical thematical from beans 40204 Et to 4030024 (a.m. time 00 at 440) at the contract of the contr
117	12837	25578	7-	7.25-02	7.2E-02 AE000882.1	Ż	merante de la company de la company de la company de la company (sector) de la company de company d
1458	14205		2.72	7.2E-02 AL18330	2		Homo sepiens chromosome 21 segment HS21C101
1458	14205	26891	2.72	7.2E-02 AL16330	1.2	Ę	Homo sepiens chromosome 21 segment HS2ICt01
							Human immunodeficiency white type 1 isolate 28 reverse transcriptuse (pol) gene, internal fragment, partial
2552			2.83	7.2E-02 U14794.			cds
3865	_ 1		0.05	7.2E-02 AW 2983;			UHH-BW0-ejf-e-05-0-UI.s1 NCI_CGAP_Sub6 Hamo sapiens cDNA clone IMAGE:2732049 31
4312		29676	4.65	7.2E-02	7.2E-02 BF572307.1	T HUMAN	602077757F1 NIH_MGC_62 Hamo sapiens aDNA clane IMAGE:4251950 5
4044	17378	30010	7.0	7.2E-02	11466563 NT		Rhodomones seline mitochondrion, complete genome

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Probe SEQ ID NO:	Exam SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Acessian No.	Top Hit Database Source	Top Hit Descriptor
5205	18013	30635	2.88		7.2E-02 U67531.1	LN	Methanococcus jannaschil section 73 of 160 of the complete genome
5206	18014	30636	10.1		P11120	SWISSPROT	CALMODULIN
7068	19759	32824	1.58		7.2E-02 BF216086.1	EST_HUMAN	601883558F1 NIH MGC 57 Homo septens cDNA clone IMAGE:4085710 5
							Streptococcus pneumoniae putative response regulator (zmpR), putative histidine kinase (zmpS), and putative
7085		32840	0.64		AF22112	ΝŢ	zinc metalicprotease (zmpB) genes, complete cds
7109	19797		1.5		5834897 NT	LN.	Strongykocentrotus purpuratus mitochondrion, complete genome
2808	20781	33910	8.0		P06143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
2808	20781	33911	0.8	7.2E-02 P05143	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
2968	21653		0.61		7.2E-02 Y17217.1	N.	Lactococcus lactis capE gene
7276			0.49		7.2E-02 X16349.1	Ę	Human gene for eac hormone-binding globulin (SHBG)
9511	22164	35346	2.32		7.2E-02 AV712452.1	EST HUMAN	AV712452 DCA Homo sepiens cDNA clone DCAAUG01 5'
							Homo sepiens plasma membrane calcium ATPase Isoform 1 (ATP2B1) gene, alternative spilice products,
9659		35509	3.8		7.2E-02 L14561.1	저	pertial cds
9814	22405	29958	0.83		7.2E-02 BF125399.1	EST_HUMAN	601783523F1 NIH_MGC_20 Homo septiens oDNA done IMAGE:4028438 5'
		ŀ					hq24f11.x1 NCI_CGAP_Adr1 Homo septens cDNA cione IMAGE:3120333 3' similar to TR:092340 Q92340
9903	22552	ļ	2.53		7.2E-02 AW873187.1	EST_HUMAN	ATYPICAL PKC SPECIFIC BINDING PROTEIN;
10092	_1	35955	0.62		7.2E-02 AA768204.1	EST HUMAN	oe62c07.s1 NCL_CGAP_GCB1 Homo sepiens cDNA clone IMAGE:1316844.3'
10250	27808	38408	8		7 OF AD 1 (8780K 0	_ 5	Homo septems zinc finger probain 92 (ZFP92), expressed-Xq28STS probain (XQ28ORF), and bightoen (BGN) dense commisse oder and plasma membrane calclism ATP and bightoen (BGN)
10872		L	X X		1	COT CHIMAN	2007 AND AND AS AS HOME STATEMENT OF A STATEMENT OF
10395	L		3.68		315	EST HUMAN	601085194F1 NIH MGC 10 Homo septens cDNA clone MAGE:3451559 5:
10509	L	36381	0.48		7.2E-02 AA706897.1	EST HUMAN	2/28h05.s1 Soares_fetal_liver_splean_1NFLS_S1 Homo sepiens cDNA clone IMAGE:451641 3'
. 10830	L		3.3		7.2E-02 AF049874.1	Ϋ́	Rattus norvegicus bHLH transcription factor Mist1 (Mist1) gene, complete cds
11849	24433	37775	1.34	7.2E-02	7.2E-02 AY009090.1	Ę	Homo sapiens putative transmembrane protein dectin-1 mRNA, complete cds
12035	24560	31113	1.67	7.2E-02	7.2E-02 AA773896.1	EST HUMAN	af81a04,r1 Soarse_NhHMPu_S1 Homo sepiens cDNA clone MAGE:1048398 51
12069	24583		4.45		7.2E-02 AJ230796.1	EST_HUMAN	AJ230796 Homo septens library (Seranski P) Homo sapiens cDNA clone PS13D5 3'
12182			1.73		7.2E-02 U82828.1	Ŋ	Homo saplens atada telangiectasia (ATM) gene, complete cds
12196	25185		8.19		7.2E-02 AW900962.1	EST_HUMAN	CMA-NN1009-200300-118-c11 NN1009 Homo sapiens cDNA
12599	25362		3.62		7.2E-02 AF020439.1	NT	Homo sepiens ATP-citrate lyase gene, Intron 3
1897	14634	27344	204	7.1E-02	7.1E-02 L02290.1	Ę	Human immunodeficiency virus type 1 (D9) provinal structural capsid protein (gag) gene, partial ods
2290	15015	27751	5.07	7.1E-02	7.1E-02 BF208802.1	EST_HUMAN	601872281F1 NIH_MGC_63 Homo septens cDNA clone IMAGE:4082981 6
7807	20502	33622	0.77	7.1E-02	7.1E-02 Ai125264.1	EST_HUMAN	qd92a10.x1 Soares_testis_NHT Homo septens cDNA clone IMAGE:1736922.31

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Probe Exam SEQ ID SEQ ID NO: NO:			=		=====================================	
_	D ORF SEQ	Expression Signal		Top Hit Acession No.	Database	Tap Hit Descriptor
			Value			
11822 24483	83	6.41	7.1E-02 BE3047	64.1	EST_HUMAN	601143974F1 NIH_MGC_15 Hamo sapiens cDNA clone IMAGE:3051234 5'
515 13299	25931	4	7.0E-02 Q07092		SWISSPROT	COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR
1486 14233	33	1.27	7.0E-02 X98677	1	Ę	M.artellia Mtcut-1 gene
1756 14498	27199	1.08	7.0E-02		EST_HUMAN	z/86/04.s1 Strategene colon (#637204) Homo sepiene cDNA clone IMAGE:509599 3'
3027 15793		2.1	7.0€-02,	7.0E-02 AW138152.1	EST HUMAN	UI-H-BI1-ecy-c-07-0-UI.s1 NCI_CGAP_Sub3 Hamo sepiens cDNA clane IMAGE:2716020 3'
3878 16628		0.74	7.05-02		EST HUMAN	ari65a12.s1 Soures_bests_NHT Homo sepiens cDNA done 1375678.31 similar to gb:K03002.80S RIBOSOMAL PROTEIN 132 (HIMAAN):
1	L		7.0E-02		Т	CM0-UM0001-080300-270-e12 UM0001 Homo septens cDNA
4189 16930			7.0E-02/	Γ	Т	Canis familiaris inducible nitric adde synthase mRNA, complete cds
4877 17804	30227	7.24	7.0E-02		EST HUMAN	801816291F1 NIH_MGC_56 Hamo sepiens cDNA clone IMAGE:4050071 5'
5293 18098	38	0.57	7.0E-02 Y09143	2	E	Lumbricus rubellus mRNA for cyclophilin B
7300 19983	33059	1.29	7.0E-02 AV6892	85.1	EST_HUMAN	AV689285 GKC Homo septens cDNA done GKCCAE06 5'
7506 20177	77 33271	0.84	7.0E-02 Y19187.	-		Galtus galtus mRNA for partial aczonin, XL spliced variant (acz gene)
8996 21686	34838	1.26	7.0E-02	9828113 NT	Z	African swine fever virus, complete genome
9497 22150	50 35331	1.24	7.0E-02 K02801.	1	Ę	Rat lg germline epsilon H-chain gene C-region, 3' end
9852 22502	35702	0.51	7.0E-02 U27288	1	LN PA	Human myosin binding protein H (MyBP-H) gene, complete cds
11345 24035	35 37338	4.98	7.0E-02		_	eh99e05.s1 Soeres_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:1327184 3' similar to gb:L14837_TIGHT JUNCTION PROTEIN ZO-1 (HUMAN);
501 13285		4.3	6.9E-02		IN	Homo sepiens chromosome 21 segment HS210010
501 13285	35 25918	4.3	6.9E-02	6.9E-02 AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1310 14058	52	12	6.BE-02	4507968 NT		Homo septens regulator of Gz-adective protein signaling (ZGAP1) mRNA, and translated products
3773 16625		1.41	6.0E-02 Q06384		SWISSPROT	28S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 2/107)
3773 18525	25 29164	1.41	6.9E-02 Q06364		SWISSPROT	28S PROTEASOME REGULATORY SUBUNIT SS (NUCLEAR ANTIGEN 2/107)
					:	Enterococcus faecium cysteine aminopeptidase (pepC) gene, partial cds; phospho-beta-glucosidase BgilB (bgiB), beta-glucoside specific transport protein (bgiB), transcription antiferminator (bgiR), enterocin B
			6.9E-02			precursor (entB), enterooin B Immunity prote>
	45 30462		6.9E-02		T_HUMAN	601192383F1 NIH_MGC_7 Hamo septems cDNA done IMAGE:3538253 5
7516 20187	37	19.0	6.0E-02	.1	INT	Canine distamper virus strain A75/17, complete genome
7951 20646	94	1.12	6.DE-02	6.9E-02 U12022.1	NT	Human calmodulin (CALM1) gene, exons 2,3,4,5 and 6, and complete ods
			6.9E-02			601340661F1 NIH_MGC_53 Homo septens cDNA clone IMAGE:3683030 5'
		1	6.9E-02	35.1	EST_HUMAN	201340881F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3883030 5
	34860		6.9E-02 U22967.	1		Barbarie duck parvovirus REP protein (rep) and three capsid protein VP (vp) genes, complete cds
12065 24580	O.	1.82	6.9E-02 X74315	1		Xlaevis XFD2 mRNA for fork head protein

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1461 2451 2732 1.56 6.8E-02 A-1690503.1 NT Horno auginen minichare-bound amtogoglduse P (A)PEC-87050 (HAMAN): 2007 1.58 6.8E-02 A-1460750.1 EST HUMAN MOOTO-HOUSIAL MATTRX PROTEEN CHANANI CERTISOR (HAMAN): 2007 1.59 6.8E-02 A-166750.1 EST HUMAN MOOTO-HOUSIAL MATTRX PROTEEN CHANANI CERTISOR (HAMAN): 2007 1.50 6.8E-02 A-151600 1.50 1.50 6.8E-02 A-151600 1.5		Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signel 1.69	Most Similer (Top) Hit BLAST E Value 6.9E-02 P44621	Top Hit Acession No. P44621	Top Hit Defaberee Source SWISSPROT	Top Hit Descriptor PROTEIN TRANSPORT PROTEIN HOFC HOMOLOG
14613 Z7321 1.58 6.8E-02 AA466759.1 EST HUMAN 14637 Z7322 1.56 6.8E-02 AA781969.1 EST HUMAN 14637 Z7346 3.77 6.8E-02 AA781969.1 EST HUMAN 15862 Z8504 1.19 6.8E-02 AA781969.1 EST HUMAN 15862 Z8505 1.19 6.8E-02 AA781969.1 EST HUMAN 16862 Z8505 1.19 6.8E-02 AA781969.1 EST HUMAN 17251 0.86 6.8E-02 BE141076.1 EST HUMAN 16260 32809 8.73 6.8E-02 BE141076.1 EST HUMAN 16260 32809 8.73 6.8E-02 BE141076.1 EST HUMAN 20260 32809 8.73 6.8E-02 BE141076.1 EST HUMAN 20260 33280 8.73 6.8E-02 BE141076.1 INT 2080 6.8E-02 BE141076.1 INT INT 2080 6.8E-02 BE141076.1 INT INT 2080 6.8E-02 BE141076.1 INT INT 2080 34017	님	24817		1.46		3.1	TN	Homo sapiens membrane-bound eminopeptidase P (XNPEP2) gene, complete cds
14613 Z7322 1.66 6.8E-02 AA460750.1 EST HUMAN 14637 Z7346 3.77 6.8E-02 AFT56873.1 IIIAMAN 15862 Z2504 1.19 6.8E-02 AA781906.1 EST HUMAN 15862 Z2505 1.19 6.8E-02 BE141000.1 EST HUMAN 17251 0.86 0.8E-02 BE141000.1 EST HUMAN 17251 0.86 6.8E-02 BE141000.1 EST HUMAN 16860 32836 0.68 6.8E-02 BE141000.1 EST HUMAN 16960 32836 0.63 6.8E-02 BE141000.1 EST HUMAN 20262 33356 0.63 0.8E-02 AL78628.1 INT 20880 34018 6.01 6.8E-02 AL78628.1 INT 20880 1.65 6.8E-02 AL78604.1 EST HUMAN 20840 1.68 <td></td> <td>14613</td> <td>27321</td> <td>1.56</td> <td>6.8E-02</td> <td>AA496759.1</td> <td>EST HUMAN</td> <td>ae30f02.r1 Geseler Wilms tumor Homo seplens cDNA clone IMAGE:897339 5' similier to gb:M22382 MITOCHONDRIAL MATRIX PROTEIN P1 PRECLRSOR (HUMAN);</td>		14613	27321	1.56	6.8E-02	AA496759.1	EST HUMAN	ae30f02.r1 Geseler Wilms tumor Homo seplens cDNA clone IMAGE:897339 5' similier to gb:M22382 MITOCHONDRIAL MATRIX PROTEIN P1 PRECLRSOR (HUMAN);
14637 27346 3.77 6.8E-02 A7158873.1 NT 15862 28503 1.19 6.8E-02 A7781980.1 EST_HUMAN 15862 28504 1.19 6.8E-02 A7781980.1 EST_HUMAN 17251 0.86 6.8E-02 BE141076.1 EST_HUMAN 17251 0.86 6.8E-02 BE141076.1 EST_HUMAN 17251 0.86 6.8E-02 BE161890.1 EST_HUMAN 17251 0.86 6.8E-02 BE161890.1 EST_HUMAN 18260 3.2838 0.68 6.8E-02 A716838.2 NT 20180 3.4017 6.01 6.8E-02 A116358.1 NT 20880 3.4018 6.01 6.8E-02 A116358.1 NT 24637 0.69 6.8E-02 A11638.1 NT 24637 0.69 6.8E-02 A116538.1 ST_HUMAN 24638 1.65 6.8E-02 A116538.1 ST_HUMAN 24630 2.73 6.8E-02 A116538.1 ST_HUMAN 24630 2.73 6.7E-02 A126055.1 NT 20446 3.3668 </td <td>75</td> <td>14613</td> <td>27322</td> <td>•</td> <td>6.8E-02</td> <td>AA496759.1</td> <td>EST_HUMAN</td> <td>8630f02.rl Gessler Wilms tumor Homo saplens dDNA done IMAGE:897339 5 similar to gb:M22382 MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);</td>	75	14613	27322	•	6.8E-02	AA496759.1	EST_HUMAN	8630f02.rl Gessler Wilms tumor Homo saplens dDNA done IMAGE:897339 5 similar to gb:M22382 MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
15862 28503 1.19 6.8E-02 AA781986.1 EST HUMAN 15862 28504 1.19 6.8E-02 AA781986.1 EST HUMAN 15862 28505 1.19 6.8E-02 BE141076.1 EST HUMAN 17251 0.86 6.8E-02 BE141076.1 EST HUMAN 17251 0.86 6.8E-02 BE141076.1 EST HUMAN 18291 0.08 6.8E-02 BE141076.1 EST HUMAN 18291 0.08 6.8E-02 BE141076.1 EST HUMAN 18490 3.203 6.8E-02 AL248287.1 NT 20262 3.3588 0.63 6.8E-02 AL248287.1 NT 20880 3.4018 6.01 6.8E-02 AL248287.1 NT 24637 2.3 6.8E-02 AL248287.1 NT 24637 3.06 8.8E-02 AL248287.1 NT 14623 2.73 6.8E-02 AL248287.1 NT 24637 3.06 8.8E-02 AL248287.1 NT 24638 1.65 6.7E-02 AV997588.1 ST HUMAN 24630 28097 4.62<	8	14637	27346		8.8E-02		NT	Homo sepiens putative hepatic transcription factor (WBSCR14) gene, complete cds
15862 28504 1.19 6.8E-02 AA781906.1 EST HUMAN 15682 28505 1.19 6.8E-02 AA781906.1 EST HUMAN 17251 0.86 6.8E-02 BE141076.1 EST HUMAN 16201 0.86 6.8E-02 BE141076.1 EST HUMAN 16201 0.86 0.8E-02 BE141076.1 EST HUMAN 16909 3.2836 0.63 8.8E-02 U10858.1 NT 20252 3.3358 0.63 8.8E-02 U10858.1 NT 2089 3.4017 5.01 6.8E-02 AJ248287.1 NT 2088 3.4017 5.01 6.8E-02 AJ248287.1 NT 24837 2.35 6.8E-02 AJ248287.1 NT 24858 1.65 6.8E-02 AA768014.1 EST HUMAN 24858 1.65 6.8E-02 AA768014.1 EST HUMAN 14623 2.7333 2.7 6.7E-02 AF116836.1 NT 20445 3.3568	6	15862	28503		6.8E-02	AA781886.1	EST HUMAN	a75a06.st Scares, testis_NHT Homo septens cDNA clone 1376626 3'
15862 25505 1.19 6.8E-02 AA781996.1 EST HUMAN 17251 0.86 6.8E-02 BE141076.1 EST HUMAN 19221 0.86 6.8E-02 BE141076.1 EST HUMAN 19450 3.2839 8.73 6.8E-02 BE061860.1 EST HUMAN 19600 3.2839 8.73 6.8E-02 AL163268.2 NT 2080 3.4018 6.01 6.8E-02 AL163268.1 NT 2080 3.4018 6.01 6.8E-02 AL248287.1 NT 2080 1.65 6.8E-02 AL248287.1 NT 2080 2.7E-02 AL248287.1 NT<	6	15862	28504		6.8E-02	AA781996.1	EST HUMAN	al/5a06.s1 Somes_testis_NHT Homo septens cDNA done 1378628.31
17251 0.86 6.8E-02 BE141076.1 EST_HUMAN 19201 0.8 6.8E-02 BE141076.1 EST_HUMAN 19460 32839 8.73 6.8E-02 BE061880.1 INT 20252 3358 0.63 8.8E-02 AL163268.2 INT 2089 34017 6.01 6.8E-02 AL163268.1 INT 2089 34017 6.01 6.8E-02 AL248287.1 INT 2089 34017 6.01 6.8E-02 AL248287.1 INT 24637 2.3 6.8E-02 AL248287.1 INT 24637 2.3 6.8E-02 AL248287.1 INT 24637 3.06 6.8E-02 AL248287.1 INT 24630 3.06 6.8E-02 AL248287.1 INT 24630 3.06 6.8E-02 AL248287.1 INT 24630 3.06 6.8E-02 AL248287.1 INT 24620 3.06 6.8E-02 AL248287.1 INT 24620 3.06 6.8E-02 AL24828.1 INT 24420 3.35587 0.56 0.7E-02 AV47578 <td>6</td> <td>15862</td> <td>28505</td> <td></td> <td>6.8E-02</td> <td>5.1</td> <td>EST HUMAN</td> <td>a75a06.s1 Soarse_tests_NHT Homo sapiens cONA clone 1376628 3</td>	6	15862	28505		6.8E-02	5.1	EST HUMAN	a75a06.s1 Soarse_tests_NHT Homo sapiens cONA clone 1376628 3
19201 0.6 8.8E-02 P20702 SWISSPROT 19460 3.2839 8.73 6.8E-02 BE061860.1 EST HUMAN 18600 3.2839 8.73 6.8E-02 AL163268.2 NT 20282 3.4017 6.01 6.8E-02 AL248287.1 NT 20890 3.4017 6.01 6.8E-02 AL248287.1 NT 20890 3.4018 5.01 6.8E-02 AL248287.1 NT 24837 2.8 6.8E-02 AL248287.1 NT 24839 1.65 6.8E-02 AL248287.1 NT 24837 2.8 6.8E-02 AL248287.1 NT 24839 1.65 6.8E-02 AL248287.1 NT 24830 1.65 6.8E-02 AL248287.1 NT 14026 2.73 6.8E-02 AL248287.1 NT 24630 3.06 8.8E-02 AL2630.1 SWISSPROT 24630 3.568 6.7E-02 AL76836.1 NT 24646 3.3568 0.56 6.7E-02 AW137356.1 EST HUMAN 24150 3.3534 0.69	힐	17251		0.80	6.8E-02	5.1	EST HUMAN	MR0-HT0069-071099-001-005 HT0069 Hano sepiens cDNA
19460 6.8E-02 BE061860.1 EST HUMAN 19600 32839 8.73 6.8E-02 AL163268.2 NT 20282 33358 0.68 0.8E-02 L16658.1 NT 20890 34018 6.01 6.8E-02 L16628.1 NT 20890 34018 5.01 6.8E-02 L26287.1 NT 20890 34018 5.01 6.8E-02 L26287.1 NT 24637 2.86 6.8E-02 L26287.1 EST HUMAN 24637 3.06 6.8E-02 AV66014.1 EST HUMAN 24637 3.06 6.8E-02 AV766014.1 EST HUMAN 14628 27833 2.77 6.7E-02 AF16538.1 NT 14629 27833 2.77 6.7E-02 AF16538.1 NT 20446 33568 0.56 6.7E-02 AV32656.1 EST HUMAN 27153 34167 0.47 6.7E-02 AV4656.1 EST HUMAN 27153 35334 0.69 6.7E-02 AV46716.1 NT 4400 27641 3.31 6.6E-02 AV33550.1 EST HUMA	8	19291		0.6	8.8E-02		SWISSPROT	CELL-SURFACE RECEPTOR DAF-1 PRECURSOR
18606 32839 8.73 0.8E-02 AL163268.2 NT 20282 33358 0.683 8.8E-02 U16658.1 NT 20890 34017 6.01 6.8E-02 AL248287.1 NT 20890 34018 6.01 6.8E-02 AL248287.1 NT 24837 2.3 6.8E-02 AL248287.1 NT 24837 2.86 6.8E-02 AL248287.1 EST HUMAN 24920 3.06 6.8E-02 AV66014.1 EST HUMAN 24920 3.06 6.8E-02 AV766014.1 EST HUMAN 14028 27383 2.7 6.7E-02 AF16536.1 EST HUMAN 14029 27383 2.7 6.7E-02 AF16536.1 EST HUMAN 20446 33568 0.56 6.7E-02 AV16536.1 EST HUMAN 2054 33589 0.56 6.7E-02 AV4656.1 EST HUMAN 2053 34167 0.47 6.7E-02 AV4656.1 EST HUMAN 2054 35334 0.69 6.7E-02 AV45616.1 NT 1400 27641 3.31 6.6E-0		<u>8</u>		1.80	6.8E-02	-	EST HUMAN	RC1-BT0264-090300-017-d09 BT0254 Homo septems cDNA
20252 33358 0.63 8.8E-02 Integer. Int 20890 34017 6.01 6.8E-02 AJ248287.1 Int 20890 34018 5.01 6.8E-02 AJ248287.1 Int 20890 34018 5.01 6.8E-02 AJ248287.1 Int 24537 2.3 6.8E-02 AJ26014.1 EST HUMAN 24637 3.06 6.8E-02 AJ766014.1 EST HUMAN 24620 3.06 6.8E-02 AJ766014.1 EST HUMAN 24620 3.06 6.8E-02 AJ766014.1 EST HUMAN 14208 27733 2.7 6.7E-02 AF16538.1 Int 14459 22097 4.52 6.7E-02 AF16538.1 Int 20446 33568 0.56 6.7E-02 AV2605.1 Int 2050 34167 0.47 6.7E-02 AV406268.1 EST HUMAN 2053 35334 0.69 6.7E-02 AV406268.1 EST HUMAN 14006 27641 3.31 6.6E-02 AV33550.1 EST HUMAN 16212 2885 10.57 6	စ္က	28 88	32839	8.73	6.8E-02	7	L	Homo saplens chromosome 21 segment HS21C068
20890 34017 6.01 6.8E-02 AJ246287.1 NT 20890 34018 5.01 6.8E-02 AJ248287.1 NT 25379 2.3 6.8E-02 AJ248287.1 NT 24537 2.86 6.8E-02 AJ768014.1 EST HUMAN 24620 1.65 6.8E-02 AJ768014.1 EST HUMAN 24920 3.06 8.8E-02 AJ768014.1 EST HUMAN 14208 3.06 8.8E-02 AJ768014.1 EST HUMAN 14208 2.7333 2.77 6.7E-02 AF146538.1 NT 14402 2.7333 2.77 6.7E-02 AF146538.1 NT 20446 33568 0.56 6.7E-02 AV20285.1 NT 20445 33588 0.56 6.7E-02 AV002588.1 EST HUMAN 20150 34167 0.47 6.7E-02 AV002588.1 EST HUMAN 20150 35334 0.69 6.7E-02 AV137356.1 EST HUMAN 14006 27641 3.31 6.6E-02 AV33550.1 EST HUMAN 16212 28865 10.57 6.6E-02 AV33	뒮	20262	33358	0.63	6.8E-02		L	Dictyostellum discoldeum myosth heavy chain kinase A (MHCK A) mRNA, complete cds
20880 34018 5.01 6.8E-02 AJ248287.1 NT 25370 2.3 6.8E-02 IO3214.1 EST_HUMAN 24537 2.86 6.8E-02 IO3214.1 EST_HUMAN 24658 1.65 6.8E-02 AV875830.1 EST_HUMAN 24920 3.06 8.8E-02 AV875830.1 EST_HUMAN 14268 2.7333 2.77 6.7E-02 AF116638.1 NT 144623 2.7933 2.77 6.7E-02 AF116638.1 NT 16459 2.8007 4.52 6.7E-02 AF116638.1 NT 20446 3.3567 0.56 6.7E-02 AF16638.1 NT 20445 3.3568 0.56 6.7E-02 AV02695.1 NT 2050 3.477 0.47 6.7E-02 AV03696.1 EST_HUMAN 22153 35334 0.69 6.7E-02 AV137356.1 EST_HUMAN 14906 27641 3.31 6.6E-02 AV33550.1 EST_HUMAN 14212 28865 10.57 6.6E-02 AV3560.1 EST_HUMAN 16227 28867 2.50	စ္ဆ	20880	34017		6.8E-02	:1	TN	Pyrococcus abyeel complete genome; segment 5/8
25376 2.3 6.8E-02 T03214.1 EST_HUMAN 24637 2.86 6.8E-02 AA768014.1 EST_HUMAN 24628 1.65 6.8E-02 AA768014.1 EST_HUMAN 24920 3.06 8.8E-02 AW975839.1 EST_HUMAN 14268 27333 2.77 6.7E-02 AF116638.1 NT 14469 25007 4.52 6.7E-02 AF116638.1 NT 20446 33567 0.56 6.7E-02 AF12638.1 NT 20445 33588 0.56 6.7E-02 AW137788 SWISSPROT 20446 33588 0.56 6.7E-02 AW137788 SWISSPROT 20446 33588 0.56 6.7E-02 AW137359.1 EST_HUMAN 22153 35534 0.69 6.7E-02 AW137359.1 EST_HUMAN 14906 27641 3.31 6.6E-02 AW137359.1 EST_HUMAN 16212 28865 10.57 6.6E-02 AW138537 NT	ᇑ	88 R	34018		6.8E-02	.1	NT	Pyrococcus abyest complete genome; segment 5/8
24537 2.86 6.8E-02 AA768014.1 EST HUMAN 24688 1.65 6.8E-02 AW975839.1 EST HUMAN 24920 3.06 8.8E-02 AW975839.1 EST HUMAN 14268 2.7333 2.77 6.7E-02 AF116638.1 NT 14623 2.7333 2.27 6.7E-02 AF116638.1 NT 14624 2.2097 4.52 6.7E-02 AF116638.1 NT 20446 33567 0.56 6.7E-02 AF2265.1 NT 20446 33568 0.56 6.7E-02 AW08268.1 SWISSPROT 20130 34167 0.47 6.7E-02 AW08268.1 EST HUMAN 22153 35534 0.69 6.7E-02 AW137359.1 EST HUMAN 14006 27641 3.31 6.6E-02 AV33536.1 NT 14212 28855 10.57 6.6E-02 AV32601.1 NT 16227 28881 2.59 6.6E-02 AV32601.1 EST HUMAN 16227 28881 2.59 6.6E-02 AV32601.1 EST HUMAN 16227 28881	2	25379		2.3	6.8€-02			FB4A8 Fetal brain, Strategiene Homo septens cDNA clone FB4A8 3'end similar to LINE-1
24888 1.65 6.8E-02 AW975839.1 EST HUMAN 24920 3.06 8.8E-02 5010565 NT 14286 27333 2.27 8.7E-02 AF116638.1 NT 14628 279097 4.52 6.7E-02 AF116638.1 NT 16459 29097 4.52 6.7E-02 AF20285.1 EST HUMAN 20446 33567 0.56 6.7E-02 AW08268.1 NT 20445 33568 0.55 6.7E-02 AW08268.1 EST HUMAN 27159 34167 0.47 6.7E-02 AW137359.1 EST HUMAN 27159 35333 0.69 6.7E-02 AW137359.1 EST HUMAN 14006 27641 1.07 6.6E-02 AF246116.1 NT 14205 2781 3.31 6.6E-02 AF246116.1 NT 14212 28865 10.57 6.6E-02 AF246116.1 EST HUMAN 16227 28881 2.59 6.6E-02 AF246116.1 EST HUMAN 16227 28881 2.59 6.6E-02 AF246116.1 EST HUMAN 16227	티	24537		2.85	6.8E-02	4.1		and 7005,s1 Source_teats_NHT Homo septens cDNA done 13207053'
24920 3.06 8.8E-02 9910565 NT 14266 1.63 8.7E-02 AFT16638.1 NT 14628 27333 2.27 8.7E-02 AF12688.1 NT 14629 22097 4.52 6.7E-02 AF1278 SWISSPROT 20446 33567 0.56 6.7E-02 XR2605.1 NT 20445 33568 0.55 6.7E-02 XR2605.1 NT 21030 34167 0.47 6.7E-02 XW137359.1 EST_HUMAN 22153 35333 0.69 6.7E-02 AW137359.1 EST_HUMAN 14096 2771 1.07 6.6E-02 AF245116.1 NT 14006 2774 3.31 6.6E-02 AF245116.1 NT 16212 28855 10.57 6.6E-02 R64506.1 EST_HUMAN 16227 28881 2.59 6.6E-02 AF245116.1 NT 16227 28882 2.59 6.6E-02 R650000.1 EST_HUMAN	딝	24888		1.65	6.8E-02	9.1	HUMAN	EST387948 MAGE recognitiones, MAGN Homo septens cDNA
14268 1.63 6.7E-02 AF116538.1 NT 14623 27333 2.27 6.7E-02 AF116538.1 INT 14623 22007 4.52 6.7E-02 AI220285.1 EST_HUMAN 20446 33567 0.56 6.7E-02 X62605.1 NT 20445 33568 0.56 6.7E-02 X62605.1 NT 21030 34107 0.47 6.7E-02 XW082688.1 EST_HUMAN 22153 35333 0.69 6.7E-02 XW137359.1 EST_HUMAN 14096 25771 1.07 6.6E-02 AW137359.1 INT 14009 27641 3.31 6.6E-02 AV326241.1 NT 16212 2885 10.57 6.6E-02 AV326241.1 INT 16227 28881 2.59 6.6E-02 AV3267.1 INT 16227 28881 2.59 6.6E-02 AV3267.1 INT	5	24920		3.06	6.8E-02	9010585	NT.	Mus muscutus latent TOF beta binding protein (Tgfb.) mRNA
14623 27333 2.27 6.7E-02 Alz20285.1 EST_HUMAN 16459 25097 4.52 6.7E-02 P17278 SWISSPROT 20446 33567 0.56 6.7E-02 X6265.1 NT 20445 33568 0.56 6.7E-02 X6265.1 NT 21030 34167 0.47 6.7E-02 XW082688.1 EST_HUMAN 22153 35333 0.69 6.7E-02 AW137359.1 EST_HUMAN 14096 25771 1.07 6.6E-02 AV137359.1 NT 14202 27641 3.31 6.6E-02 AV137359.1 NT 14202 27741 1.07 6.6E-02 AV245116.1 NT 14202 27845 10.57 6.6E-02 AV326241.1 NT 16227 28881 2.59 6.6E-02 R64306.1 EST_HUMAN 16227 28881 2.59 6.6E-02 R64306.1 EST_HUMAN		14268		1.03	8.7E-02	1		Oncorthynchus myldae TAPT protein (OnmyTAP1) mRNA, OnmyTAP1*01 allele, complete cds
16459 28097 4.52 6.7E-02 P17278 SWISSPROT 20446 33567 0.56 6.7E-02 X6265.1 NT 20445 33568 0.56 6.7E-02 X6265.1 NT 21030 34107 0.47 6.7E-02 X6265.1 NT 22153 35333 0.69 6.7E-02 XW137359.1 EST HUMAN 22153 35334 0.69 6.7E-02 XW137359.1 EST HUMAN 14096 25771 1.07 6.6E-02 AF245116.1 NT 14202 27841 3.31 6.6E-02 AF245116.1 NT 16212 28881 2.59 6.6E-02 AF3651.1 EST HUMAN 16227 28881 2.59 6.6E-02 AF3651.1 NT 16227 28881 2.59 6.6E-02 AF3651.1 T108357.NT		14823	27333	227	6.7E-02	1		og79e04.x1 Soares NRL T GBC S1 Homo saplens cDNA clone IMAGE:1841406 3'
20446 33567 0.66 6.7E-02 X62605.1 INT 20445 33568 0.55 6.7E-02 X62605.1 INT 21030 34167 0.47 6.7E-02 XW082088.1 EST HUMAN 22153 35333 0.69 6.7E-02 XW137359.1 EST HUMAN 14096 25771 1.07 6.6E-02 AF245116.1 INT 14202 27841 3.31 6.6E-02 AF245116.1 INT 16212 28885 10.57 6.6E-02 R64306.1 EST HUMAN 16227 28881 2.59 6.6E-02 R04306.1 EST HUMAN 16227 28881 2.59 6.6E-02 R04306.1 EST HUMAN		16459	29097	4.52	6.7E-02			HOMEOBOX PROTEIN HOX-DA (CHOX-A)
20445 33568 0.55 6.7E-02 X62965.1 NT 21030 34167 0.47 6.7E-02 AW082688.1 EST HUMAN 22153 35333 0.69 6.7E-02 AW137359.1 EST HUMAN 14096 25771 1.07 6.6E-02 AF245116.1 NT 14600 27641 3.31 6.6E-02 AF245116.1 NT 16212 28885 10.57 6.6E-02 R64306.1 EST HUMAN 16227 28881 2.59 6.6E-02 R64306.1 EST HUMAN 16227 28881 2.59 6.6E-02 R64306.1 T108357 NT		8445 45	33587	0.55	6.7E-02			H. sepiens DNA for cOMP phosphodiscienase (exone 4-22)
21030 3416T 0.47 6.7E-02 AW082888.1 EST HUMAN 22153 35333 0.69 6.7E-02 AW137359.1 EST HUMAN 22153 35334 0.69 6.7E-02 AW137359.1 EST HUMAN 14096 25771 1.07 6.6E-02 AF245116.1 NT 14202 27841 3.31 6.6E-02 AF245116.1 NT 16212 28885 10.57 6.6E-02 R64306.1 EST HUMAN 16227 28881 2.59 6.6E-02 R64306.1 EST HUMAN 16227 28882 2.59 6.6E-02 R64306.1 7108357 NT		20445	33568	0.55	6.7E-02			H. saplens DNA for cOMP phosphodiesterase (exons 4-22)
22153 35333 0.69 6.7E-02 AW137359.1 EST HUMAN 22153 35334 0.69 6.7E-02 AW137359.1 EST HUMAN 14096 26771 1.07 6.6E-02 AF245116.1 NT 14009 27641 3.31 6.6E-02 AF245116.1 NT 16212 28865 10.57 6.6E-02 R64306.1 EST HUMAN 16227 28881 2.69 6.6E-02 R64306.1 7108357 NT 16227 28882 2.59 6.6E-02 7108357 NT		21030	34167	0.47	6.7E-02		Г	xb61c11.x1 Source_NFL_T_GBC_S1 Homo septems cDNA clone IMAGE:2580788 3'
22153 3534 0.69 6.7E-02 AW137359.1 EST HUMAN 14096 28771 1.07 6.6E-02 AF245116.1 NT 14009 27641 3.31 6.6E-02 AJ289241.1 NT 16212 28865 10.57 6.6E-02 R64308.1 EST HUMAN 16227 28881 2.59 6.6E-02 7108357 NT		22153	35333	0.69	6.7E-02			UI-H-BI1-ecr-g-01-Q-UI.s1 NCI_CGAP_Sub3 Homo sepiens cDNA clone MAGE:2715433 3'
14096 26771 1.07 6.6E-02 AF245116.1 NT 14009 27641 3.31 6.6E-02 AJ280241.1 NT 16212 28865 10.57 6.6E-02 R64306.1 EST HUMAN 16227 28881 2.59 6.6E-02 7108357 NT 16227 28882 2.50 6.6E-02 7108357 NT		22153	35334	0.69	6.7E-02		Г	UI-H-BI1-ect-g-01-0-UI.s1 NCI_CGAP_Sub3 Homo sepiens cDNA clone NAAGE:2715433 31
14009 27841 3.31 6.6E-02 AJ289241.1 NT 16212 28865 10.57 6.6E-02 R64306.1 EST_HUMAN 16227 28881 2.69 6.6E-02 7108357 NT 16227 28882 2.50 6.6E-02 7108357 NT		14096	26771	1.07	6.6E-02		Г	Drosconille melenogaeter cactin mRNA, complete cds
16212 28865 10.57 6.0E-02 R64306.1 EST_HUMAN 16227 28881 2.69 6.0E-02 7108357 NT 16227 28882 2.50 6.0E-02 7108357 NT		14909	27841	3.31	6.8E-02	.1		Mus musculus Capn12 gene for calpain 12, exons 1-21, three alternative transcipts
10227 28881 2.69 6.0E-02 7108357 NT 16227 28882 2.59 6.0E-02 7108357 NT		16212	28865	10.57	6.0E-02		T_HUMAN	y18b10.e1 Scenes placenta Nb2-IP Homo septens cDNA clone IMAGE:138579.3*
16227 28882 2.59 6.9E-02 7108357 NT	_	16227	28881	2.59	6.0E-02	7108357		Homo seplens mesothetin (MSLN), transcript variant 1, mRNA
	Ш	16227	28882	2.50	6.8E-02	7108357		Homo explene mesothein (MSLN), transcript variant 1, mRNA

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Acesskan No.	Top Hit Database Source	Top Hit Descriptor
							Rattus norvegicus differentation-associated Na-dependent inorganic phosphate cotransporter (DNPI) mRNA,
4304	l		1.02	6.2€-02	6.2E-02 AF271235.1	Ę	complete cds
4542			6.31	6.2E-02 Q62191	Q62191	SWISSPROT	52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO62)
8698	19615	32656	0.65	.052€+02 D49530.	D49530.1	뉟	Spirulina platenais DNA for adenylate cyclase, complete cds
7527	20198	33292	1.03	6.2E-02 U41453.	U41453.1	F	Rattus novegicus PKC binding protein and substrate mRNA, complete cds
8846			9.0		6.2E-02 M61101.1		Porche group C rotavirus (strain Cowden) outer membrane protein (VP7) mRNA, complete cds
9243	21922	35082	0.52		6.2E-02 AA778450.1	EST_HUMAN	#20s06.s1 Sosres_total_fetus_Nb2HF8_9w Homo sepiens cDNA clone (MAGE:1032178 3)
9380	22042	35214	1.05	6.2E-02	TN 8687700		Mus musculus stromal cell derived factor receptor 2 (Sdfr2), mRNA
11095		37039	1.56		6.2E-02 AF217490.1	Į.	Homo explems fragile 16D addo reductase (FOR) gene, exons 8, 9, and partial cds
11320	24011	37315	1.53		6.2E-02 AJ242735.1	NT	Metarhicium anisopliae mRNA for Chymotrypsin (chyf gene)
11865	24449	37791	1.74	6.2E-02	AF200359.1	Į.	Reftus noveptous UDP-ciucose divopordein:ciucosytransferase precuracy (Uoci) mRNA, completa cds
11989	25405	L	13.39	6.2E-02	6.2E-02 AE000750.1	Ę	Aquitiex section 82 of 109 of the complete genome
12394	24782	31037	2.5	6.25-02	6.2E-02 BF112039.1	EST HUMAN	737708.x1 Sources, NSF_PB_DW_OT_PA_S1 Homo septens aDNA clane, IMAGE:3523815.3' similar to TR.097456 Q97456 HYPOTHETICAL 30.3 KD PROTEIN. (1):
249	1	L	5.50	6.1E-02 D16471.	D16471.1	Z	Human mRNA, Xq terminal portion
3972	16721		2.29	6.1E-02 U73325.	U73325.1	Ę	Arabidopsis thaliana K+ inward rectifying channel protein (AtKC1) gene, complete cds
200	_			1			Homo sepiens SWISNF refered, metrix associated, actin dependent regulator of chromatin, subfamily a,
64.64	18603	90000	4 4	6.1E-02	450/0/0IN		MEMBER 3 (SMARKCAS) MRINA
1010		l	6,70	0.15-02	A50200.1		The september of the Delivery of the September of the Sep
800	┸		0.57	6.1E-02	6.1E-02 BE971853.1	Т	601651086R1 NIH MGC 81 Hamo saplens cDNA clone IMAGE:3834604 3
0000	2222	38580	0.07	0.1F-0Z	6.1E-02 BE9/1853.1	ESI HUMAN	0010031000KT NIM MGC 81 HOMO septens CLINA Cione IMAGE: 3534604 3
11862	1	37787	127	6 15-02		Т	Enterthink buttered mRNA for RNA authorages III ternest extrust medial colo
11945	1		221	6.1E-02 X70969.1			S aporticum mRNA for serine enzyme
12833			5.61	6.1E-02/	7.2		Homo sepiens chromosome 21 segment HS21C007
8	12922	25559	0.78	6.0E-02	6.0E-02 AA188730.1	EST_HUMAN	zp78004.rt Stratagone HeLa cell s3 937216 Homo saplens cDNA clone IMAGE:628310 5
96	12822	25560	0.76	6.0E-02	Γ	EST_HUMAN	2978004.11 Stratagene HeLa cell s3 937216 Homo sepiens cDNA cione IMAGE:626310 5
1230	13088	28855	1.54	6.0E-02 AE00177			Thermotoga maritima section 89 of 136 of the complete genome
2682	15391	28130	1.09	6.0E-02	6.0E-02 AW968848.1	EST HUMAN	EST380924 MAGE resequences, MAGJ Homo sepiens oDNA
2775	15480	٠	1.62	6.0E-02	6.0E-02 AB031289.1	ĬN	Mescossibides cort mitochondrial DNA, NADH dehydrogenese subunit 4, tRNA-Gh, tRNA-Phe, tRNA-Met, ATPese subunit 6, and NADH dehydrocenase subunit 2
2837	12822	25559	6.0	6.0E-02/		L HUMAN	\$78004.rf Stratagene HeLa cell \$3 \$37216 Homo sepiens cDNA clone IMAGE:626310 5
2837	12821	25560	6.0	6.0E-02/	6.0E-02 AA188730.1	Г	2078604.11 Strategene Hel.a cell s3 937216 Homo saplens cONA clone IMAGE: 628310 5
						1	

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SEQ ID NO: 3223 3223 3223 3223 3223 3223 3223 32
Probe SEQ ID NO: NO: 3223 3625 3627 5637 7689 7758 6691 7758 8321 8321 8321 8321 8321 8321 8321 832

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Ac assion No.	Top Hit Database Source	Тор Hit Descriptor
12515	25283		3.18	5.7E-02	5.7E-02 AF217490.1	MT	Homo sapiens fregile 16D axido reductase (FOR) gene, exons 8, 9, and partial cds
12650	25387		2.61	5.7E-02	5.7E-02 AF261280.1	Ŋ	Pan troglodytes apolipoprotein-E gene, complete cds
1518	14265	26951	1.57	5.8E-02	5.8E-02 AF094455.1	M	Hydrocotyle rotundifolia ribosomal protein L18 (rpl18) gene, intran; chloroplast gene for chloroplast product
S657	17330	2882	1.12		5.8E-02 AB013100.1	N	Lycopersicon seculentum LE-ACS8 mRNA for 1-aminocyclopropane-1-carboxylate synfhase, complete cds
4648	17382	30014	1.46	6.6E-02	6.6E-02 AA290599.1	EST HUMAN	2845c01.s1 NCI_CGAP_GCB1 Homo sapiene cDNA done IMAGE:7004163'
6562	19327	32334	6.57	5.0E-02	5.6E-02 AW172708.1	EST_HUMAN	xy02c10.x1 NCI_CGAP_Ut2 Homo sepiens cDNA clone IMAGE:2656050 3' similar to TR:094979 094979 KIAA0905 PROTEIN.;
6791	19535	32563	1.25	5.6E-02	5.6E-02 AAB66182.1	EST_HUMAN	od47f12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA done IMAGE:1371119 3' similar to contains Alu repetitive element contains element i.1 repotitive element contains
7051	19742	32804		5.6E-02	5.5E-02 BE008001.1	EST_HUMAN	QV0-BN0147-290400-214-907 BN0147 Homo sepiens cDNA
7063	19754	32819	0.60	5.8E-02	5.6E-02 Al983738.1	EST_HUMAN	w234705.x1 NCI_CGAP_Bm53 Homo sepiens cDNA done IMAGE:2559080 3' similar to gb:X06409 RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (HUMAN);
7725	20388	33502	99'0	5.6E-02	5.6E-02 Al183583.1	EST_HUMAN	qd64g11x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1734308 31
8701	21393	34539	2.88	5.6E-02	5.8E-02 BE542863.1	EST_HUMAN	801067158F1 NIH MGC_10 Homo sepiens CDNA clone IMAGE:3453279 5
8701	21393	34540	2.88	5.6E-02	6.6E-02 BE542663.1	EST_HUMAN	801087158F1 NIH MGC_10 Homo sepiens cDNA done IMAGE:3463279 6
9712	22363	35561	1.09	5.6E-02	5.6E-02 AA482864.1	EST HUMAN	nf48d07.s1 NCI_CGAP_AhrI Homo septens cDNA clone IMAGE:923245 similar to TR:G769859 G769859 LAMINA ASSOCIATED POLYPEPTIDE 1C.;
11556	24155		2.35	5.6E-02	5.6E-02 AF280225.1	Ā	Homo sepiens TESTIN 2 and TESTIN 3 genes, complete cds, attematively spliced
2080	15370	28108	8.8	5.5E-02	5.5E-02 X97869.1	TN	H.saplens gene encoding La autoentigen
3209	15972	28625	8.83	5.5E-02	6755501 NT	LN	Mus musculus SH3 domain protein 1B (Sh3d1B), mRNA
4191	16932	29561		5.5E-02		NT	Gallid herpesvirus mRNA fragment
5573	18370	31281	3.05	5.5E-02 Q01174	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
5935	18370	31281	3.58	5.5E-02 Q01174	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
7277	19961	33038		5.5E-02	6755902 NT	F	Mus muscutus tuffelin 1 (Tuff1), mRNA
8019	20714	33845		5.5E-02	5.5E-02 AF170911.1	L	Homo explens excitun-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds
8019	20714	33846	න 0	5.5E-02	5.5E-02 AF170911.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds
9665	22208	35392	9.0	5.5E-02	1	LN	Homo sapiens elF4E-transporter (4E-T), mRNA
9998	22208	35393	9.0	5.5E-02	10947034 NT	NT	Homo sapiens elF4E-transporter (4E-T), mRNA
9850	22302	35497	1.32	5.5E-02	5.5E-02 U69492.1	NT	Mus musculus second IL11 receptor alpha chain (IL11Ra2) gene, exons 1 and 2
100	20627	20871	7.38	5 AT 02	5 SE-09 100774 4	F.N	Citrobacter freundii DSM 30040 cyclopropane fatty acid synthese (cfa) gene, partial cds, dihydroxyacetone kinase (dhaK), glycerol dehydrogenase (dhaD), transcriptional activator (dhaR), 1,3-proparedid chandralese (dhaD), chand
2	1	1000	1	V.4-72	1.1		ייין באון אין אין אין אין אין אין אין אין אין אי

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SEQ ID SEQ ID NO: NO: 12797 25349 3019 15785	OBE SEO	Expression	Most Similar	Too Hit Accession	Top H#	
	Ö Ö	Signer	(Top) Hit BLAST E	No.	Database	Top Hit Descriptor
			_			
<u>.</u>	30604	1.49	5.5E-02	11421332 NT		Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
		16.0	5.4E-02	5.4E-02 AJ277468.1	INT	Oryza sativa rbbi3-1 gene for putative Bowmen Birk trypsin inhibitor
į		5.78		5.4E-02 BE073468.1	EST_HUMAN	RC5-BT0559-140200-012-CX3 BT0559 Homo sepiens cDNA
3891 16641	29281	0.76		5.4E-02 U85808.1	Ę	Hrudo medicinalis SNAP-25 homolog mRNA, complete cds
8024 20719		0.88		5.4E-02 Z99116.1	NT	Bacillus subtilis complete genome (section 13 of 21); from 2395281 to 2813730
8969 21859	34809	0.55		5.4E-02 AF280225.1	Ę	Homo sepiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
10537 23234	38467	1.62		5.4E-02 AU120889.1	EST_HUMAN	AU120889 HEMBB1 Homo sapiene cDNA clone HEMBB1001630 6'
10598 23292	38530	204	8.4F-02	5 4F-02 (120780 1	5	Neurospora crassa ubleuinol-cytochrome c oxidoreductasa subunit VIII (OCR8) mRNA combina oda
L	37078	1.32		7.0	T HUMAN	ROS-FN0112-190700-021-D06 FN0112 Homo sepiens cDNA
	37077	1.32		BF371289.1	7	RC8-FN0112-190700-021-D08 FN0112 Homo septems cDNA
1031 13791	26450	1.28		5.3E-02 AW391248.1	EST HUMAN	QV0-ST0213-021289-062-e09 ST0213 Homo septens cDNA
1031 13791	28451	1.28		5.3E-02 AW391248.1	EST_HUMAN	QV0-ST0213-021289-062-e09 ST0213 Homo septens cDNA
1495 14242	26929	14.72	5.3E-02 T94759.1	194759.1	EST HUMAN	ye3712.rl Strategene kung (#837210) Homo sepiens cDNA chore IMAGE:119951 5' similar to gb:K01506 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(1) ALPHA CHAIN (HUMAN);
2501 15218	27981	2.47	5.3E-02	5.3E-02 AJ276408.1	Г	Pseudomonas putida ttgS gene
2943 15709	28360	0.85			F	Drosophila melanogaster laminin B2 gene, complete cds
2943 15709	28361	98'0	5.3E-02 M58417.1		Ę	Drosophile melanogaster leminin B2 gene, complete cds
	28558	5.51	5.3E-02	5.3E-02 AJ276408.1		Pseudomonas putida ttgS gene
	30361	6.34	5.3E-02 M80463.		LN.	Mus musculus caudal type homeoboxi-1 (Cdx-1) gene, complete ods
	30670	1.98		7.1		Helicobacter pylori 20095 section, 5 of 134 of the complete genome
	30671	1.08	5.3E-02 AE00052	7.1	Į.	Helicobacter pylori 28895 section 5 of 134 of the complete genome
6785 19529	32556	5.01	5.3E-02	9895413 NT		Lymphocyatis disease virus 1, complete genome
	\$2733	11	5.3E-02 U32832.1			Haemophilus influenzae Rd section 147 of 163 of the complete genome
7280 19944		2.08	5.3E-02 S78221.1		<u>-</u>	nuclear protein TIF1 isoform [mice, mRNA, 4053 nt]
7777 20389	33514	0.65	5.3E-02 P38742		SWISSPROT	HYPOTHETICAL 130.0 KD PROTEIN IN SNP6-SPO11 INTERGENIC REGION
8304 20998		0.7	5.3E-02 U10098.1		Ę	Mus musculus 128/Sv cystafin C (cst3) gene, complete cds
9023 21713	34867	1.36	5.3E-02 XD3127.1		TN.	Podospora ansertna mitochondrial epallon-sen DNA
	35897	0.62	6.3E-02 AB02280	5.1		Homo sapiens hCMT to mRNA for mRNA (guanine-7-) methyltransferase, complete cds
10032 22680	35898	0.62	5.3E-02 AB02280	5.1		Homo sapiens hCMT1b mRNA for mRNA (guarrine-7-)metry/transferase, complete cds
10156 22804	:	0.63	6.3E-02 Y07907.1		אַל	D.rerlo mRNA for zp.23 POU gene, splice variant (neurula, 9-16 hpf and postsomitogenesis, 20-28 hpf)
10230 22878	38080	0.7	5.3E-02 X88432.1		IN.	B.rerio pouje] mRNA for transcription factor

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טווילופ בעטון רוטיסא בעעופאסט ווו בושווי	Signal BLASTE No. Signal Value Top Hit Accession Signal BLASTE No. Source Source	30964 1.43 5.3E-02 AF276815.1 NT Branchiostoma floridae homeodomain-containing protein Hox13 (Hox13) gene, expn 2 and partial cds	160.56 5.2E-02 5031908 NT Homo saplens meprin A, alpha (PABA peptide hydrolase) (MEP1A) mRNA	734		1.23	1.19 5.2E-02 6671757 NT	29609 3.02 5.2E-02 U07132.1 NT Human steroid hormone receptor Ner-I mRNA, complete cds	0.9 5.2E-02 AA297940.1 EST_HUMAN	31548 0.61 5.2E-02 U14731.1 NT Saccheromyces cerevisies Cdc54p (CDC54) gene, complete ods	w80e04.x1 NCI_CGAP_Lym12 Homo sapiens cDNA done IMAGE:2409150 3' similer to contains MER15.b1 0.96 5.2E-02 Al8300955.1 EST_HUMAN MER15 repetitive element:	TOGGOOMIC	2.19 5.2E-02 AL163204.2 INT	6.2E-02 D10927.1 NT	35473 1.87 5.2E-02 D10927.1 INT Turnip mosaic virus genomic RNA for Capsid protein, complete cds	1.83 5.2E-02 0.03030 SWISSPROT	5.1E-02 AL134071.1 EST_HUMAN	NT	49.38 5.1E-02 AL163246.2 NT	0.72 6.1E-02 AF280369.1 NT	1.44 5.1E-02 BF378625.1 EST_HUMAN	0.84 5.1E-02/M26434.1 NT	0.84 5.1E-02 M26434.1 NT	1.48 5.1E-02 AJ131986.1 NT	0.58 5.1E-02[P02533 SWISSPROT	0.58 5.1E-02 P02533 SWISSPROT	6.2 6.1E-02 AF012898.1 NT	35945 1.89 5.1E-02 P40603 SWISSPROT ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX)	2.44 5.1E-02 AF083930.1 NT	2.44	5.1E-02 AL139076.2 NT	2.56 5.1E-02 AF082467.1 NT Cucumis melo polygalacturonase precursor (MPG3) mRNA, complete cds
- - - - - -	ORF SEQ ID NO:		80								21			L			91															J
	Exan SEQ ID NO:	55030	3 15008	15877			1 16871	5 16986	3 17772	8 18617	18797	4000		22282	9 22282	L		9 16919		_ }		_ [22380	22730		3 23420		24797
	Probe SEQ ID NO:	12776	2283	3112	3112	3919	3921	4245	E909	5828	6016	7474	8085	9829	8628	12414	2364	4179	4960	8675	6760	8151	815	8245	8783	8783	9709	10082	10733	10733	11620	12421

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ORF SEQ Express ID NO: Signa S	M M M M M M M M M M M M M M M M M M M	Top Hit Accession		
24068 13256 25894 13256 25894 13334 26599 14719 27438 15731 26397 16002 26006 17502 28006 17502 2800 18990 31780 18980 33202 20114 33202 24074 37383 25246 25246 13028 25801 13168 25801 16334 28978 16334 28978 17519 30141 17519 30751 18091 30752			Database Source	Top Hit Descriptor
13256 25894 13734 26599 14719 27438 13731 26397 16002 16003		5.1E-02 AA534104.1	EST_HUMAN	nj73f02.s1 NCL CGAP_Pr10 Homo sepiens cDNA clone IMAGE:998139
13934 26599 14719 27438 13731 26397 16092 16092 16337 26006 17602 16425 26006 17602 20114 33202 20114 33202 20114 33202 20114 33202 20114 33202 20114 33202 25246 13028 25800 13158 25800 13158 25800 13168 25800 13168 25800 13169 3033 13169 3031 16334 28978 16334 28978 16334 28978 16334 28978 17519 30141 17619 30752		5.0E-02 AF098004.1		Mus musculus fatty acid amide hydrolase gene, exon 10
14719 27438 13731 26397 16092 26092 16337 26096 17502 31780 18980 31780 22748 35963 23167 37383 25246 25800 13158 25800 13158 25800 13168 25801 16043 28978 16334 28978 16334 28978 16334 28978 16334 30141 17519 30751			NT.	Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080
13731 28397 16992 16337 16425 28066 17602 18980 20114 33202 2014 33202 24074 37383 25246 13028 13168 25801 13168 25801 13168 25801 16334 28978 16334 28978 16334 28978 16334 28978 16539 30141	H 5.0E-02 P02810		SWISSPROT	SALIVARY ÁCIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1/PRP-3) (PRP-2/PRP-4) (PIF-FIPIE-S) (PRP-2/PRP-4) (PIF-FIPIE-S) (PROTEIN APROTEIN C) [CONTAINS: PEPTIDE P-C]
16092 16337 16425 28060 17602 18990 20114 33202 25246 13028 13028 13168 25800 13168 25800 13168 25801 16043 28978 16334 28978 16334 28978 16510	L		T	Oryctolegus cuniculus UDP-glucuronosyfransferase (UGT2B13) mRNA, complete cds
16237 16425 28080 17502 18819 31780 18980 20114 33202 22748 35963 22748 35963 24074 37383 25246 13028 25800 13158 25800 13168 25800 13168 28978 16334 28978 16334 28978 16334 28978 16334 30141	2 5.0E-02	7305610 NT		Mus musculus Unc-51 like kinase 2 (C. elegans) (Ulk2), mRNA
17502 18619 17502 18990 20114 33202 22748 33202 22748 33202 24074 33202 13028 13028 13028 13168 25800 13168 25800 13168 25800 13168 25801 16043 28978 16334 28978 16334 28978 16334 28978 16334	4 5.0E-02 U3Z782.		Ę	Heemophilus influerzae Rd section 97 of 163 of the complete genome
17502 18819 31780 18890 3202 20114 33202 22748 35963 224074 37383 25246 25800 13168 25800 13168 25801 16043 28978 16334 28978 16334 28978 16334 28978 16334 30141 17519 30142	S 5.0E-02 U12769.2		NT.	Antheraea pernyi period clock protein homolog mRNA, complete cds
18990 20114 33202 20114 33202 22748 35963 224074 37383 25246 13028 13168 25800 13168 25801 16043 28978 16334 28978 16334 28978 16334 28978 16334 28978 16334 28978 16334 28978 16334 28978 16334 16334 28978 16334 16334 16334 18091 30751	6 5.0E-02 P40232		SWISSPROT	CASEIN KINASE II BETA CHAIN (CK II)
20114 33202 122148 35963 23167 35963 2546 24074 37383 255246 13028 25800 13168 25801 16043 28978 16334 28978 16334 28978 16334 28978 16334 28978 16334 28978 16334 28978 16334 28978 16334 16334 28978 16334 16334 28978 16334		5.0E-02 AF096264.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
22748 33202 22748 35963 23167 37383 24074 37383 25246 25800 13168 25800 13168 25801 16043 28978 16334 28978 16334 28978 16334 28978 16334 28978 16334 28978 16334 28978		5.1	Nī	Mus muscalus Dmp-1 gene, exons 1-6
23167 23167 24074 37383 24074 37383 25246 13028 25800 13168 25801 16043 25801 16334 28978 16334 28978 16334 28978 16334 28978 16334 28978 16334 28978 16334 28978 16334 28978	8 5.0E-02 P35818		/ISSPROT	NEUROFILAMENT TRIPLET L'PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF.L.)
23167 24074 37383 25246 13028 25800 13168 25801 19043 25801 16311 28978 16334 28978 16334 28978 17519 30141 17519 30142 18091 30751		5.0E-02 AF305238.1	NT	Mus musculus Fas-Interacting sertne/threonine kinase 3 (Fist3) mRNA, complete cds
25246 13028 13168 25800 24 13168 25801 25801 26801 26801 26801 26801 26801 26801 26801 26901 26901 26901 30141 17619 30142 18091 30752		5.0E-02 BF213260.1	EST_HUMAN	601844753F1 NIH_MGC_65 Hamo sepiens aDNA done IMAGE:4070101 5
25246 13028 25800 2 13168 25801 2 16043 28692 2 16334 28978 0 16334 28978 0 17519 30141 1 17519 30142 1 18091 30752	.5 5.0E-02 U67800.	1	LN TN	Methanococcus jannaschil section 142 of 150 of the complete genome
13028 25800 13168 25801 18043 25801 16043 28978 16334 28978 17519 30141 17519 30142 18091 30751			SWISSPROT	NO-ON-TRANSIENT A PROTEIN
13168 25800 13168 25801 16043 28692 16334 28978 17519 30141 17519 30142 18091 30751				Chicken 28-kDa vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds
13168 25801 16043 28692 16334 28978 17519 30141 17519 30142 18091 30751		8.1		Homo sapiens ABCA1 (ABCA1) gene, complete cds
16043 28692 2 16311 28978 0 16334 28978 0 16334 28978 0 17510 30141 1 17618 30142 1 18091 30752		48.1	NT	Homo saplens ABCA1 (ABCA1) gene, complete ods
16311 28978 0 16334 28978 0 17519 30141 1 17519 30142 1 18091 30752	3 4.9E-02 P54258		ISSPROT	ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN)
16334 28978 0 16334 28978 0 17519 30141 1 17519 30142 1 18091 30751	-			zq48a12.s1 Stratagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632926 3' similar to
16334 28978 0 16334 28979 0 17519 30141 1 17519 30142 1 18091 30751		0.1		contains Alu repetitive element, contains element MSR1 repetitive element;
16334 28979 0 17519 30141 1 17619 30142 1 18091 30751	9 4.9E-02 AA40091	4.1	EST HUMAN	478e03.s1 Soares_tests_NHT Homo septens cDNA clone IMAGE:728428 3'
17519 30141 1 17519 30142 1 18091 30751 1	9 4.9E-02 AA40091	4.1	EST_HUMAN	2178a03.s1 Soares_testis_NHT Homo sapiens cDNA cione IMAGE:728428 3'
17519 30142 18091 30751 18091 30752			Г	xg58g10x1 NCL_CGAP_Ut4 Homo septems cDNA clone IMAGE:2632386 3/
18091 30751 18091 30752		4.9E-02 AW167821.1	EST_HUMAN	xg58g10.x1 NCI_CGAP_UM Homo sepiens cDNA clone IMAGE:2832386 3/
18091 30752			Г	Rat elastase II gene, excn 6
00107	9 4.9E-02 L00122.1		뒫	Rat elastase II gene, exon 6
2 19/33 32/83 0.91		4.9E-02 AE000980.1	LZ LZ	Archaeoglobus fulgidus section 127 of 172 of the complete genome
8513 21205 0.8		4.9E-02 AE002309.1	ᅜᆚ	Chlamydia muridarum, section 40 of 85 of the completa genome
21344		59.2	IN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
10191 22839 36054 0.48			ISSPROT	TRANSCRIPTION FACTOR E3
10494 23140 36366 0.46	6 4.9E-02 AL 16321	8.2	Г	Homo sapiens chromosome 21 segment HS21C018

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Single Exon Propes Expressed in Brain	Top Hit Descriptor	Homo saplens prepro placental TGF-beta gene, complete cds	Homo sepiens CS box-containing WD protein (LOC55884), mRNA	Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) games cymylafa yds	Human mRNA, Xq terminal portion	Human mRNA, Xq terminal portion	Arabidopsis fireliena AP2 domein containing protein RAP2.7 mRNA, perties cats	22/49b02.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:325611 3' similar to gb:M30038 LUPUS KU AUTOANTIGEN PROTEIN P88 (HUMAN):	Tetrahymena rostrata histone H3II and histone H4III Intercenic DNA	Sacrafa gene for skeletal muscle ryanothre receptor	Homo sapiens DKFZP434D222 protein (RENT2), mRNA	Homo sepiers DKFZP434D222 protein (RENT2), mRNA	MR2-ST0129-221099-012-b02 ST0129 Homo septens cDNA	Fugu rubribes rps24 gene	Fugu rubripes rps24 gene	y29709.r1 Source melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:291017 5' similar to contains Alu	Rat statin-related protein (s1) gene, complete CDS	B. teurus mRNA for RF-36-DNA-binding protein	H. seplens DNA for endogenous retrouted like element	Gallus gallus Wpkci-8 gene, complete cds	B. taurus mRNA for RF-36-DNA-binding protein	601892692F1 NIH_MGC_17 Homo sepiens cDNA clone MAGE:4138414 5	we/9c10x1 Soures_NFL_T_GBC_S1 Hamo eaplens aDNA clane IMAGE:2347314.3	Mus musculus ligand of numb-protein X (Lrx), mRNA	Bos taurus paired box protein (pex-8) gene, pertial cols	Bos taurus paired box protein (pex-8) gene, pertial cds	PM0-HT0339-261199-003-g05 HT0339 Homo septens cDNA	Escherichia celi K-12 MG1655 section 335 of 400 of the complete genome	am50d02.s1 Johnston fronted cortex Homo sepiens cDNA clone IMAGE:1538979 3' similar to TR:P90533 P90533 LIMA ;contains element LTR1 repetitive element :	AV727059 HTC Homo sapiens cDNA clone HTCBW C01 5'
JIB EXOII PIODE	Top Hit Detaberse Source	F		¥				EST HUMAN 9	Π				EST HUMAN IN				E L	Т	F	D EN		HUMAN	HUMAN			A L	EST_HUMAN PI	Г	EST_HUMAN P	EST_HUMAN A
Silk	Top Hit Acession No.	AF008303.1	B923880 NT	+	-	-	4.8E-02 AF003100.1	-			11693131	11693131 NT		4.8E-02,AJ001398.1		-	-			8.1	(15543.1	3F305237.1	1873042.1	6754585	173621.1		3.1	5.1		4.6E-02 AV727059.1
	Most Similar (Top) Hit BLAST E Vælue	4.9E-02	4.9E-02	4.9E-02 M18364.	4.8E-02 D16471.	4.8E-02 D16471.	4.8E-02/	4.8E-02 W51983.	4.8E-02 X17144.	4.8E-02 Z54280.	4.8E-02	4.8E-02	4.8E-02 AW3884	4.8E-02	4.8E-02/	4.7E-02 W01153	4.7E-02 M82752.	4.7E-02 X15543.1	4.7E-02 X89211.1	4.7E-02 AB02867	4.7E-02 X16543.1	4.7E-02	4.7E-02	4.7E-02	4.7E-02 U73621.1	4.7E-02 U73621.	4.8E-02 BE16358	4.8E-02 AE00044	4.6E-02	4.6E-02
	Expression Signal	3.22	1.77	3.41	1.5	3.94	96.6	1.82	21	1.15	1.03	1.03	1.32	0.95	96.0	3.83	2.02	8.24	96.0	2.68	6.89	0.67	0.57	1.4	1.39	1.30	0.83	2.91	0.90	3.47
	ORF SEQ ID NO:	37285			25760	25760	25899	27735	28620		30478	30479	33864	34870	34871	32597	32503	33973	34690		34981	35382		36582	37463	37454	25712	26149		28782
	SEQ ID NO:		24752	24912	13123		13262	14987	15966	17358	17863	17863	20732	21717	21717	19595	19480	20843	21643		1	2220	22287	23345	24145	24145	13072	13496	14018	14086
	Probe SEQ ID NO:	11378	12345	12598	321	322	478	2271	3203	4623	5144	5144	8037	206	206	9731	6819	8140	8852	8875	9127	827	9835	10654	11545	11545	हू	727	1260	1338

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Probe SEQ ID	Exan SEQ ID	ORF SEQ	Expression	Most Similar (Top) Hit	Top Hit Acession		Top Hit Database Top Hit Descriptor
ö	Ö	<u> </u>		Value	ġ	Source	
2482	15209	27951	2.31	4.0E-02	4.6E-02 AW 236023.1	EST HUMAN	xn24f03.x1 NCI_CGAP_Kid11 Home septens cDNA done IMAGE:2894653 3' similar to SW:CRF1_HUMAN Q12849 G-RICH SEQUENCE FACTOR-1;
2811	13072				4.8E-02 BE153583.1	EST_HUMAN	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
3325	16774	28423	0.74		4.8E-02 BE153583.1	EST_HUMAN	PM0-HT0339-261199-003-g06 HT0339 Homo septems cDNA
3487	15774		67.0	i	4.6E-02 BE133583.1	EST_HUMAN	PM0-HT0339-251199-003-005 HT0339 Homo sepiens cDNA
4103	16846		1.35		4.8E-02 AF220365.1		Mus musculus nucleoler RNA helicase II/Gu (ddz21) gene, complete cds
5121	17839	30455	68'0	4.6E-02	4.6E-02 AA079157.1	EST_HUMAN	zn92c10.s1 Strategene overlen cencer (#937219) Homo septens cDNA clone IMAGE:545394 3' similer to gb:xxx3212 KERATIN, TYPE II CYTOSKELETAL 7 (HUMAN);
5847	18442	31355	74.1	4 ME-02	4 AE-02 AE0780A2 4	Ė	Hapfochromis burtoni gonadotropin-releasing hormone and GriRH-associated peptide precursor (Grirh2)
<u>۾</u>				4.6E-02		LN	C.reinhardtii etb2 (etbB) mRNA
9138	18914		3.51	4.6E-02	4.6E-02 X81624.1	NT L	C.reinhardtii atp2 (atp8) mRNA
8702	19617	32850	1.47	4.85-02	4 RF-10 A1149574 1	EST HIMAN	qo80b06x1 Sceres_placerita_sto6weeks_2NbHP8tc6W Home sapiens oDNA olone IMAGE:1713971.3' similar to contains 1.13 1.1 recedibles element:
8554				4.6E-02	4.6E-02 BE154006.1	EST HUMAN	PM0-HT0339-060400-009-G12 HT0339 Hamo septens cDNA
11370	23986			4.6E-02	4.6E-02 AAP13328.1	EST_HUMAN	ol27h09.s1 Sorres_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:1524737 3'
12325	24744		1.88	4.0E-02	4.0E-02 AV712871.1	T_HUMAN	AV712871 DCA Homo sepiens oDNA clone DCAAZF07 5
12705	24985		96°E	4.6E-02	4.6E-02 X57808.1	NT	Human germline Immunoglobulin lambda light chain gene
홟	13220		1.72	4.5E-02 P22448	P22448	SWISSPROT	RETINOIC ACID RECEPTOR BETA (RAR-BETA)
1196	13948		11.11	4.5E-02	4.5E-02 AF005730.1		Marburg virus strain M/S. Africa/Johanneaburg/1975/Ozolin VP35 gene, complete cds
1186	13948			4.5E-02	30.1		Marburg virus strain M/S.Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds
1797	14537				P32182	SWISSPROT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)
2 8 8	<u>488</u>				4.5E-02 AE003964.1	۲	Xylella fastidiosa, section 110 of 229 of the complete genome
3710	10463	29102	3.8	4.5E-02	4.5E-02 AL163278.2	NT	Homo sapiens chromosome 21 segment HS210078
6137	18915	31885	.	4.6E-02	AJ400877.1	F	Homo sepiens ASGL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
6415	19163			4.5E-02	4.5E-02 AL163280.2		Homo seplens chromosome 21 segment HS21C080
6779	19623	32650	10.0	4.6E-02	4.6E-02 1.28487.1	Ę	Methanosarcha fitisia carbon monodde dehydrogenese large subunit (cdhiA) gene; carbon monodde dehydrogenase small subunit (cdhiB) gene, complete ods
8778	19523	32561	10.0	4.5E-02	4.5E-02 L26487.1	F	Methenceardha fitisla carbon monodde dehydrogensee large subunit (cdhiA) gene; carbon monodde dehydrogensee small subunit (cdhiB) gene, complete cds
8292	20986	34125	8	4.6E-02	4.6E-02 AF036684.1	NT	Arabidopeis thallana CCAAT-box binding factor HAP3 homolog gene, complete cds
9849	22499		4.57	4.5E-02	4.5E-02 AA325216.1	T HUMAN	EST28167 Cerebellum II Homo sepiens cDNA 5' end similar to similar to neuro-D4 protein
10000	22648	35860	0.48	4.5E-02			A.europaeum mRNA for legumin-like protein

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Table 4
Single Exon Probes Expressed in Brain

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						gle exon Prot	Single Exon Probes Expressed in Brain
Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signei	Most Similar (Top) Hit BLAST E Value	Top Hit Acceston No.	Top Hit Detabase Source	Top Hit Descriptor
876	13645	26315	1.35	4.2E-02	4.2E-02 AW003645.1	EST HUMAN	wx34g01.x1 NCI_CGAP_Ptt1 Homo saplens oDNA clone IMAGE:2645684 3' similar to TR:Q63291 Q63291 L1 RETROPOSON, ORF2 MRNA ;contains L1.13 L1 L1 repetitive element;
1714	14457		1.02	4.2E-02	AL445066.1	٦	Thermoplasma acidophilium complete genome; segment 4/5
1771	14613	27213	1.01	4.2E-02	4.2E-02 P23091	SWISSPROT	TRANSFORMING PROTEIN MAF
3655	16408	29047	2.43	4.2E-02 P23091	P23091	SWISSPROT	TRANSFORMING PROTEIN MAF
4100	16843	129471	0.7	4.2E-02	51	EST HUMAN	801150833F1 NIH_MGC_19 Hamo sapiens cONA clone IMAGE:3503505 5
4284	17023	29648	1.83	4.2E-02	4.2E-02 U28874.1	Z	Saccharomycee cerevisiae general sporulation (GSG1) gene, complete eds
4284	17023	29649	1.83	4.2E-02	4.2E-02 U20074.1	Ę	Saccharomyces cerevisiae general aporulation (GSG1) gene, complete cds
4695	17429	30080	2.32	4.2E-02	4.2E-02 BF342995.1	EST_HUMAN	602017105F1 NCI_CGAP_Bm64 Hamo septens cDNA clane IMAGE:4152672 51
							Homo septens cytochrome P450 polypeptide 43 (CYP3A43) gene, pertial ods, cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete ods; and cytochrome P450
5530	18328	31231	0.08	4.2E-02	4.2E-02 AF280107.1	닐	polypeptide 5 (CYP3A5) gene, partial cds
							Homo septens cytochrome P450 potypoptide 43 (CYP3A43) gene, pertial ods; cytochrome P450 potypoptide 4 (CYP3A4) and ovtrohrome P450 potypoptide 54 (CYP3A4) septentials ods; and ovtrohrome P450 potypoptide 54 (CYP3A7) septentials ods; and ovtrohrome 54 (CYP3A7) septentials ods; and ovtrohrome 54 (CYP3A7) septentials ods; and ovtrohrome 54 (CYP3A7) septentials odds; and ovtrohrome 54 (CYP3A7) s
5530	18328	31232	99.0	4.2E-02	4.2E-02 AF280107.1	뉟	polypeptide 5 (CYP3A5) gene, pertial cds
9889	17962	30517	0.56	4.2E-02	4.2E-02 BE208285.1	EST_HUMAN	801124586F1 NIH_MGC_8 Homo septens cDNA clane IMAGE:2980319 5
7426	20103	33190	4.7	4.2E-02	4.2E-02 AF276752.1	F	Legionella pneumophila catalase-percedase (katA) gene, complete cds
8710	21402	34547	3,96	4.2E-02 P05095	P05095	SWISSPROT	ALPHA-ACTININ 3, NON MUSCULAR (F-ACTIN CROSS LINKING PROTEIN)
10064	22712	06658	1.22	4.2E-02/Q16850	Q16850	SWISSPROT	T-BRAIN-1 PROTEIN (T-BOX BRAIN PROTEIN 1) (TBR-1) (TES-56)
10969	23845	36898	282	4 2F-02	4 2F-02 AA978118 1	EST HUMAN	on33b11.st NCL_CGAP_Lu6 Homo eaplens oDNA clone IMAGE:1568461 3' similer to gb:M65290 INTERLEUKIN-12 BETA CHAIN PRECURSOR (HUMAN):
11278	23939		2.54	4.2E-02	4.2E-02 BE815822.1	EST HUMAN	PM3-BN0174-250500-009-d10 BN0174 Homo saplens cDNA
11278	23939	37232	2.64	4.2E-02	4.2E-02 BE815822.1	EST_HUMAN	PM3-BN0174-250500-009-d10 BN0174 Homo saplens cDNA
11489	24090	37402	1.08	4.2E-02	4.2E-02 AF178458.1	N	PRRS isolate PRRSV36 envelope glycoprotein gene, complete cds
12415	25335		3.43	4.2E-02	4.2E-02 AI983494.1	EST_HUMAN	w/48g10x1 NCI_CGAP_Pen1 Homo sepiens cDNA clone IMAGE:2510850 3'
497	13281		1.24	4.1E-02		N	Homo saplens HPS1 gene, Intron 5
2683	15392	28131	1.04	4.1E-02	4.1E-02 AE002330.2	LN	Chlamydia muridarum, section 60 of 85 of the complete genome
4439	17175		7.52	4.1E-02	4.1E-02 AW893484.1	EST_HUMAN.	QV1-NN0012-180400-164-f06 NN0012 Homo sapiens cDNA
9556	18353	31262	0.82	4.1E-02	4.1E-02 BE251894.1	EST_HUMAN	801107535F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343856 5
9999	18353	31263	0.82	4.1E-02	4.1E-02 BE261894.1	EST_HUMAN	601107535F1 NIH_MGC_16 Homo septems cDNA clone IMAGE:3343856 6
9783	19527		0.67	4.1E-02		된	A.thallana mRNA for pleama membrane intrinsic protein 1a
6869	19691	32742	1.25	4.1E-02	4.1E-02 AE002132.1	NT	Ureaplesma urealyticum saction 33 of 59 of the complete genome
7413	20090	33174	209	4.1E-02	7662347 NT	LZ	Homo sapiens KIAA0867 protein (KIAA0867), mRNA

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Probe SEQ ID NO:	Econ SEQ ID NO:	ORF SEQ ID NO:	Expression Signel	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Detebase Source	Top Hit Descriptor
7502	20173	33265	0.66		4.1E-02 L02110.1	ΙN	Mus musculus provinal retrovinal insertion in the oGMP-phosphodiesterase (rd beta PDE) gene, intron 1, with the provinal insert encompassing the env pseudogene (3' end) and 3' LTR
7685	20329	33438	3.12		4.1E-02 AF028198.1	IN	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosie-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete ods; and calclum channel alpha-1 subunity
8541	21233	34376	0.08	4.1E-02 P34687	P34687	SWISSPROT	CUTICLE COLLAGEN 34
9052	21741	34809	18.0	4.1E-02	4.1E-02 AA372398.1	EST_HUMAN	EST84291 Colon adenocarchroma IV Homo sepiens cDNA 5' end
12728			4.07	4.1E-02	4.1E-02 AJ271909.1	NT	Brassloa napus gin gene for pleadd giutamine synthetase, exons 1-12
3238		05982	3.26	4.0E-02	4.0E-02 AB040904.1	F	Homo sapiens mRNA for KIAA1471 protein, pertial cds
3780	16532		1.27	4.0E-02	4.0E-02 L11910.1	NT	Human retinoblestoma susceptibility gene exons 1-27, complete cds
6295	18100	30759	5.4	4.0E-02	4.0E-02 AF280107.1	NT	Homo septens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
6120	18898	31866	0.83	4.0E-02	4.0E-02 BF110434.1	EST_HUMAN	7n52n07x1 NCI_CGAP_Lu24 Homo sepiens oDNA clone IMAGE:3688380 3' similar to TR:075298 075298 R29124_1.;
7590	20258	33368	6.57	4.0E-02	4.0E-02 L23838.1	LN	Strongylocentrotus purpuratus homolog of human bone morphogenetic protein 1 (submp) mRNA, complete eds
7850	20314		0.86	4.0E-02	4.0E-02 AL161535.2	Ę	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 35
7666		33440	0.7	4.0E-02	1.1	Į.	Homo sapiens DNA for GPI-enchared molecule-like protein, complete cds
7898	20330	33441	0.7	4.0E-02	4.0E-02 AB000381.1	F	Homo sapiens DNA for GPI-enchored molecule-like protein, complete ods
8617	21309	34451	72	4.0E-02 P08640	P08640 .	SWISSPROT	GLUCOAMYLASE S1/82 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
9544	22197		0.78	4.0E-02	78.1	EST_HUMAN	602153884F1 NIH_MGC_83 Homo sepiens cDNA cione IMAGE:4284724 5
299	22220	35406	4.01	4.0E-02	4.0E-02 AJ000941.1	N	Methanobacterium thermosurcotophicum strain Merburg, Thiol:fumarate reductase subunit A
9884	22534		1.21	4.0E-02		NT	Human mRNA for KIAA0082 gene, pertial cds
11778	24369		1.54	4.0E-02		攴	Kluyveromyces lectis gene for Ca++ ATP ase
12063	25158	30808	3.31	4.0E-02	4.0E-02 AJ001058.1	N-	Ovis aries mRNA for acetyl-coA carboxylase
1098	13856	26516	2.75	3.9E-02		EST_HUMAN	UFH-BW1-arx-h-08-0-UJ.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:30841343
1323	14072	28745	2.45	3.9E-02 P41047		SWISSPROT	FAS ANTIGEN LIGAND
1964	14689	27402	2.4	3.0E-02	3.0E-02 AJ403386.1	NT	M.musculus DNA for desmin-bhdhng fregment DesD7
2708	16415		1.00	3.9E-02	4506862 NT	LX.	Homo sopiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15tD (SDHC) mRNA
4118	16880	29487	8870	3.9E-02	8924019 NT	Z	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
4118	16860	29488	0.83	3.9E-02	8924019NT	FX	Homo saplens hypothetical protein PRO1163 (PRO1163), mRNA

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Test gene for cholecystoknin type-A receptor (CCKAR), complete cds Ret gene for cholecystoknin type-A receptor (CCKAR), complete cds G01646924471 NIH_MCG_74 Home septems cDNA clone IMAGE-3048304 5 G01138192F1 NIH_MGC_74 Home septems cDNA clone IMAGE-3048830 5 G01140729F1 NIH_MGC_74 Home septems cDNA clone IMAGE-3048830 5 G01140729F1 NIH_MGC_75 Home septems cDNA clone IMAGE-31048830 5 Home septems 269 the config between AML1 and CBR1 on chromosome 21qc22 segment 1/3 ANTIGEN GOR Home septems 269 the config between AML1 and CBR1 on chromosome 21qc22 segment 1/3 ANTIGEN GOR Humen germine 1 -cell receptor beta chean TCRBV1781A11, TCRBV281, TCRBV381P, T		0. 14. 14. 14. 14. 14. 14. 14. 14. 14. 14	8LAST E Na Vakus 3.9E-02 D50008.1 3.9E-02 D50008.1 3.9E-02 BE90884 3.9E-02 BE723941 3.9E-02 BE723941 3.9E-02 BE88513 3.9E-02 AD49899 3.9E-02 AD49899 3.7E-02 AD498999 3.7E-02 AD498999 3.7E-02 AD498999 3.7E-02 AD498999 3.7E-02 AD498999	0.55 0.05 0.05 0.07 0.07 0.07 1.13	╸╸╸┩╌╿╌╿╌╿═┩═┦═┦═┦═┦═┈╸╸╸╸┦╸╸ ┦╴┦╴┦╴┦╴┦┈┦┈┦┈╿┈╿┈╴┦╴╿╴┃╴┃	260 D NO: 18207 18207 18207 18207 18439 20435 2045	9EQ 1D NO: NO: 5408 5644 5646 6957 7739 7739 11386 11945 12543 12543 12543 1367 1367 1367 1367 1367 1367 1367 3045
Mus musculus potassium large conductance pH-sensitive channel, subfamily M, alpha member 3 (Konma3), mRNA		3.7E-02 6680541 NT	3.7E-02	1.17	·	16203	3447
flus musculus potassium large conductance pH-sensitive channel, subfamily M, alpha member 3 (Komma3),			1	Ţ		000	-
01886233F1 NIH_MGC_19 Hamp suptens CDNA done IMAGE:4125684 5	٦	1	3.7E-02	2.00	28458	200	ş
CARCOCALLANIA	OWNER TO !	T	7				: 15
MECONCOLINI	TOGGGGIVIO	T	2 75 00	000	28457	15811	Ę
tomo espiens mRNA for KIAA0718 protein, partial ods	Ę		3.7E-02	0.92	28034	15296	82
#85e08.x1 NCI_CGAP_Kid11 Hamo sepiens cDNA clane IMAGE:2494502.3*	EST_HUMAN		3.7E-02	3.84	27698	14958	ខ្ល
werdial cds	F		3.75-02	0.91		1415	ត្ត
formo sapiens plesme membrane calclum ATPase Isoform 1 (ATP2B1) gene, attennative spilce products,							
AMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)	SWISSPROT		3.7E-02	40.4		13736	Ξt
domo sapiens PELOTA (PELOTA) gene, complete cds	Ŋ		3.8E-02	2.62		23245	₽Ť
iuman von Willebrand factor gene, exons 23 through 34	Z		3.8E-02	1.33		21254	ম্ব
domo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA	NT		3.8E-02	1.88		╛	<u>≅</u>
IOMEOBOX PROTEIN HOX-84 (HOX-2.6)	SWISSPROT		3.8E-02	1.32			श्र
lumen protein C gene, complete cds	Ę		3.8E-02	=	30840		ह्रो
JU124122 NT2RM2 Hamp sepiens oDNA done NT2RM2001898 5	EST HUMAN	12	3.8E-02	1.1	30228		9
formo septems pertital steerin-1 gene	M		3.8E-02	1.77		_1	\$
01510891F1 NIH_MGC_71 Hamo sapiens cDNA clone IMAGE:3912215 5	EST HUMAN	37.1	3.8E-02	1.16			5
Inger protein 92, mmxq28crf	M		3.9E-02	5.31		26223	8
Aus musculus chromosome X control X-United Ivrophocyte requisited 5 cena. Zinc finest protein 275. Zinc							
CRBV18S1P, TCRBV15S1, TCRBV11S1A1T, HVB raitc, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2,>	NT	1	3.95-02	1.83			3
luman germine T-odil receptor beta chain TCRBV1781A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P,							
elis catus G-CSF gene for grenuticoye colony-stimulating factor, complete ods	NT	3.1	3.9E-02	15.38			ভা
NATIGEN GOR	SWISSPROT		3.9E-02	2			8
Homo sepiens 859 kb config between AML1 and CBR1 on chromosome 21q22; segment 1/3	F	11.1	3.9E-02	0.79			g
Homo septens 969 kb contig between AML1 and CBR1 on chromosome 21q22, segment 1/3	IN	11.1	3.9E-02	0.79		i	ŝ
301906848F1 NIH_MGC_54 Hamo septens cDNA clane IMAGE:4134779 5	EST_HUMAN	3.1	3.9E-02	1.14			8
201140729F1 NIH_MGC_9 Hamo septens cDNA clane IMAGE:3049830 5'	EST_HUMAN	BE271437.1	3.9E-02	1.18	<u> </u>		57
302138132F1 NIH_MGC 83 Homo sepiens cDNA clone IMAGE:4274910 5	EST_HUMAN	BF675203.1	3.9E-02	0.85			8
X01649874F1 NIH_MGC_74 Homo sepiens aDNA dane IMAGE:3833842 5	EST_HUMAN	BE968841.1	3.0E-02	1.04			*
Rat gene for cholecystokinin type-A receptor (CCIXAR), complete cds	IN	D50608.1	3.9E-02	0.55			8
Rat gene for cholecystokinin type-A receptor (CCKAR), complete cds	12	D50608.1	3.8E-02	0.55			8
I OP TR Descriptor	Database Source	o N	BLAST E Value		Ö NÖ:	S S S S S S S S S S S S S S S S S S S	<u>. </u>
	Dohnor	• • •		Signal	1	CLOT	2
	Too I	Top Hit Acession	Most Similar (Top) ∺it	Expression Signal	ORF SEO	Exem	Probe

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טווקים באסוין ויסיסט בילאוסטססט וויסיסט	Top Hit Descriptor	Xylella fastidiosa, section 121 of 229 of the complets genome	al55c08.s1 Soares_parathyrold_tumor_NbHPA Homo saplens cDNA clone 1360912.3'	801762117F1 NIH_MGC_20 Homo sepiens cDNA clone IMAGE: 4024973 5	Homo sapiens solute carrier family 22 (organic cation transporter), member 1 (SLC22A1), mRNA	H. vulgare Ss1 gene for sucrose synthese	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10q26.3] of Homo sapiens	C.glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase	C.gluternicum gap, pgk and tol genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase	Homo saplens RU2AS (RU2) mRNA, complete ods	CM2-EN0013-110500-192-510 EN0013 Homo sapiens cDNA	CM2-EN0013-110500-192-b10 EN0013 Homp sepiens cDNA	Chromattum vinosum suifur globule protein CV2 precursor (sgp2) gene, complete cds	rw20e05.s1 NG_CGAP_GCB0 Homo sepiens cDNA done IMAGE:1241024 3' similar to gb:J00314_ma2 TUBULIN BETA-1 CHAIN (HUMAN);	MR0-HT0158-030200-003-b08 HT0158 Homo septens cDNA	Dictyostalium discoldeum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete ods	Dictyostellum discaldeum unknown spare germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete ods	602020463F1 NCI_CGAP_Bm67 Hamo saplens cDNA clone IMAGE:4156116 57	801820416F1 NIH_MGC_58 Homo sepiens aDNA done IMAGE:4052570 5	801820418F1 NIH_MGC_58 Homo sepiens aDNA dane IMAGE-4052570 5	qk48b09.x1 NCI_CGAP_Co8 Homo espiens cDNA clone IMAGE:1872185 3'	Drosophila melanogaster tiggrin mRNA, complete cds	Homo sapiens microsomal epoddde hydrolase (EPHX1) gene, complete cds	602085136F1 NIH_MGC_83 Homo sepiens cDNA clone IMAGE:4246377 5	602085136F1 NIH_MGC_83 Homo appiens a DNA dane IMAGE:4249377 5	Thermotoga maritima section 85 of 136 of the complete genome	CYSTATHIONINE BETALYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE)	Maize actin 1 gene (MAc1), complete cds
-	Top Hit Database Source	X Y	EST_HUMAN 84	EST_HUMAN 60			Ĭ S	N. P.	S B	Ĭ	EST HUMAN C	EST HUMAN C	Г	EST HUMAN TI	EST_HUMAN M		1 <u>0</u> <u>8</u>	T HUMAN	EST HUMAN 60	EST_HUMAN 80	EST_HUMAN qk		Ĭ	EST_HUMAN 80	EST_HUMAN 60		SWISSPROT C	T.V
2 -	Tap Hit Acession No.	75.1	3.7E-02 AA782516.1	3.7E-02 BF124974.1	11418392 NT	+	6.1		+-	27	718.1	3.0E-02 AW945516.1			3.6E-02 BE143078.1	τ.	1		3.6E-02 BF131609.1	3.6E-02 BF131609.1	6.1		3.5E-02 AF263417.1		3.5E-02 BF678085.1	3.5E-02 AE001773.1		
-	Most Similar (Top) Hit BLAST E Valtue	3.7E-02 AE0039	3.7E-02	3.7E-02	3.7E-02	3.6E-02 X73221.	3.6E-02 AL09680	3.6E-02 X59403.	3.0E-02 X59403	3.6E-02 AF1817;	3.6E-02/	3.0E-02/	3.6E-02	3.6E-02	3.6E-02	3.6E-02 U20608.	3.6E-02 U20608.	3.65-02	3.6E-02	3.6€-02	3.6E-02 /	3.5E-02 U09508	3.5E-02 /	3.5E-02	3.5E-02	3.5E-02/	3.5E-02 P53780	3.5E-02 J01238.
	Expression Signal	0.58	-	3.86	\$	1.38	0.88	0.58	0.58	0.04	27.9	5.47	2.5	2.78	1.03	1.72	1.72	0.83	1.4	1.4	1.46	1.08	1.39	1.55	1.55	1.83	127	1.77
-	ORF SEQ ID NO:	33368		37811	30813	29039	29046	30806	30823	30821	32382	32383	32725	32967	33298	35130	35131	35347	37080	37081		20314	26413	26901	26892	29559	29647	31873
	SEQ ID NO:	20260	22563	24506	25183	16399	16407	18144	18144	18212	19370	19370	19678	19891	20203	21958	21958	22165	23803	23803	24436	13644	13751	14303	14303	16929	17020	18905
	Probe SEQ ID NO:	7592	9814	11954	12803	3646	3654	5341	5341	5413	2099	6607	6985	7206	7533	9281	9201	9512	11135	11135	11862	875	886	1558	1558	4188	4281	8127

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Probe SEQ ID NO:	Exam SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession Na.	Top Hit Database Source	Top Hit Descriptor
7877	20272		82'0	3.5E-02 H29951	H29951.1	EST_HUMAN	yp44e05.1 Soares retina N2b5HR Homo saplens cDNA clone IMAGE:190256 5' similar to contains Alu repetitive element;
8521	21213	34357	2.7	3.5E-02	3.5E-02 BE958970.1	EST_HUMAN	601644701R2 NIH_MGC_56 Homo septens cDNA done IMAGE:3922737 31
8917	22506	35762	1.45		X76642.1	Z	Lilectis MC1363 grpE and dneK genes
9965			0.5		3.5E-02 BE561042.1	EST_HUMAN	601344661F1 NIH_MGC_8 Horno septens cDNA clone IMAGE:3677654 5
11477	24078	37388	1.82		3.5E-02 AW861641.1	EST_HUMAN	PM1-CT0328-291288-002-h03 CT0326 Homo sapiens cDNA
11477	24078	37389	1.82		3.5E-02 AW861641.1	EST_HUMAN	PM1-CT0328-291299-002-h03 CT0328 Homo sepiene cDNA
12598	25234		60'9		3.5E-02 BE276948.1	EST_HUMAN	601178765F1 NIH_MGC_20 Homo septems cDNA clone IMAGE:3543833 5
564	13346	25973	1.14		3.4E-02 AK024424.1	N N	Homo saplens mRNA for FLJ00013 protein, partial cds
564	13346	25974	1.14	3.4E-02 AK0244	AK024424.1	뉟	Homo sapiens mRNA for FLJ00013 protein, partial cds
595	13346	25873	6.47	3.4E-02	3.4E-02 AK024424.1	N	Homo saplens mRNA for FLJ00013 protein, partial cds
265	13348	25974	6.47	3.4E-02	3.4E-02 AK024424.1	N	Homo sapiens mRNA for FLJ00013 protein, pertial cds
1020	13780	26448	2 0.2		3 4F-02 AW274020 1	MAM H TEST	X28d07.X1 Sourse_NFI_T_GBC_S1 Homo septens cDNA clone IMAGE:2814253 3' similar to SW-7211 HI IMAN PRANT PI ITATIVE SI IRFACE 12 YOURD CHEN CALORET BREIGHT
1184			7.14	Ì	11345459 NT	LN	Homo seplens hypothetical protein FLJ13220 (FLJ13220), mRNA
\$	46440	<u> </u>	8			1 1 1 L	yo20e08.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:81250 5' similar to conteins
3			877	Ì	r.mer/ei	ESI HUMAN	MILTAZA TEPORTUVE SIGNIFIK
3424			4.1	3.4E-02 AL1632	AL163208.2	Z.	Hamo septens chranosame 21 segment HS210008
3757	16500		0.7	3.4E-02	3.4E-02 BE839514.1	EST_HUMAN	RC3-FN0165-060700-011-d10 FN0165 Hamo sepiens cDNA
3900	16650	29291	3.19		3.4E-02 AW 794952.1	EST_HUMAN	RC8-UM0015-210200-021-A10 UM0016 Homo sepiens cDNA
4559	17294	28822	2.41	3.4E-02 X59799.	X59799.1	NT	M.musculus S-entigen gene promoter region
2000	17723		3.59	3.4E-02 028457	028457	SWISSPROT	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)
5019			1.2		AJ012469.1	NT	Caenorhabditts elegans mRNA for DYS-1 protein, pertial
6754	17823	30558	4.73	3.4E-02 U24393	U24393.1	NT	Human İyayi caddase-like protein gene, exon 3
8159	20853		3.25	3.4E-02 AI86962	Al869629.1	EST_HUMAN	WB9d04.X1 NCI_CGAP_Bn25 Homo septens cDNA clone IMAGE:2433031 3'
							ru70f08.s1 NCI_CGAP_Alv1 Homo seplens cDNA clone IMAGE:1216071 similar to contains Alu repetitive
88	21338	34482	1.36	3.4E-02	3.4E-02 AA664896.1	EST HUMAN	element, contains element MER25 MER25 repetitive element;
							200411.e1 Strategene muscle 937209 Homo saplens cDNA clone IMAGE:628749 3' similar to
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8814	21506		5.97	3.4E-02	3.4E-02 AA194306.1	EST HUMAN	PPT GPV/SDITEES/TLKWEPPK/DGGSOVTN/MLKRETSTAVWTFVSATVARTAMK/AKI
8296	L		0.83	3.4E-02	3.4E-02 A1002719.1	EST HUMAN	0299h08.x1 Soares_perathyroid_tumor_NbHPA Homo sepiens cDNA clone IMAGE:1683519.3'
383	13161		9.61	3.3E-02	3.3E-02 AA398735.1	EST_HUMAN	275608.s1 Scense_testis_NHT Hamo septens aDNA clane IMAGE:728198 3'
1143	13898	26559	17.86		AB035867.1	Ę	Cricetulus grieeus CYP2A17 mRNA for cytochrone P450 2A17, complete ods

Page 149 of 536 Table 4

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| Top Hit Descriptor | | Hand saplens cytochrome P4502C18 (CYP2C18) gene, exons 2 and 3 | Hamo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete ads | Aquitet section 32 of 109 of the complete genome | 1/25c09.r1 Somes fetal liver spleen 1NFLS Homo sepiens cDNA clone IMAGE:127888 51 | Mus musculus tumor rejection antigen gp96 (Tra1), mRNA | Homo asplens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds | mus musculus tumor rejection entigen gp96 (Tra1), mRNA | RATES AND AND MISC. 57 Home subjens cDNA clone IMAGE:4073787 51 | W rosus Intri Nith_MGC_37 Home sapiens cDNA clone IMAGE:4073787 5 | Through a high course mayodopherin synthese sulphurylese (crixti) gene, perties cds | THE STATE OF THE CASE BIRZS Home septems cDNA done IMAGE:3562423 3' | milezabe XI NCI CGAP Brizzs Homo sepiens cDNA done IMAGE:3562423 3' editore NbHFB Homo sepiens cDNA clone IMAGE:877673 3' similar to db:X70944 cdet | MYDBLAST CELL SURFACE ANTIGEN 24.105 (HUMAN); ad08f09.s1 Soares NbHFB Homo sequence CNA clave IMACE-6772672 ci. 1
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 | 3.3E-02 A | 3.35-02.0 | 3.35-02 | 3 35-02 | 3 2F-02 A | 3.2E-02 A | 3.2E-02 A
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 | 3.2E-02 Z | 3.2E-02 Z7 | 3.2E-02 X | 3.2E-02/AF | 3.2E-02 AF
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 | 1.64 | 1.64 | 14.21 | 3.42 | 1.09
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 | 19892 | 79 | 453 | 17448 | 17821
 | 18247 |
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NO: | 1489 | 1635 | 1732 | 2027 | 2453 | 4156 | 4435 | 8338 | 8338 | 7408 | 8222 | 2228 | 9324 | B324
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Page 150 of 536 Table 4 Single Exon Probes Expressed in Brain

ORF SEQ Expression (Top) Hit Top Hit Accession Signal Value No. Source	31136 1.83 3.2E-02 X68709.1 NT	19189 32198 3.13 3.2E-02 M32437.1 NT Ratipolyomevirus left junction in cell line W98.14	19200 33.45 3.2E-02 T89367.1 EST HUMAN Alu repetitive element.contains LTR1 repetitive element.	32279 4.14 3.2E-02 AF173845.1 INT	33436 0.84 3.2E-02 11424049 NT	34030 4.84 3.2E-02 6680565 NT	0.73 3.2E-02 AF109718.1 NT	34978 1.21 3.2E-02 AIZ78971.1 EST_HUMAN	34979 1.21 3.2E-02 AIZ78971.1 EST_HUMAN	4.07 3.2E-02.AA719795.1 EST_HUMAN	36114 0.95 3.2E-02 U96762.1 NT	2.14 3.1E-02 4503419 NT	26702 1.72 3.1E-02 P18845 SWISSPROT	27332 1.09 3.1E-02 6871584 NT	1.34 3.1E-02 Z50097.1 NT	30508 1.13 3.1E-02 U78104.1 NT	2.12 3.1E-02 AA278478.1 EST_HUMAN	31268 0.74 3.1E-02 BF687742.1	31338 0.59 3.1E-02/AJ391284.1 NT	34677 0.46 3.1E-02 BE965092.2	35778 2.93 3.1E-02 AF034779.1 NT	37689 1.78 3.1E-02 6754241 NT	1.98 3.0E-02 AF187125.1 NT	28040 0.97 3.0E-02 AA402242.1 EST HUMAN	28038 2.78 3.0E-02 AF247644.1 NT	0.74 3.0E-02 AW820223.1 EST_HUMAN	1.42 3.0E-02 AA364003.1 EST_HUMAN	30318 6.83 3.0E-02/AF281074.1 NT	30319 6.83 3.0E-02 AF281074.1 NT	3.43 3.0E-02 AB046783.1 NT
OR CI		19189	19200	19278	20326	20803	21531		21813	22605		13986						18358	25072		22579 3		14366		16398 2	16480				18112
	\$ 44 8	6431	6432	6513	7662	8199	8839	9125	9125	79867	10258	1237	1282	1885	1987	5182	5278	5561	5628	8840	9931	11785	1619	2590	3646	3728	3323	<u>8</u>	<u>8</u>	5307

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Probe E SEQ ID SI NO:	SEQ ID OR NO:	ORF SEQ ID NO:	Expression Signel	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Defebese Source	Top Hit Descriptor
8252	20946		1.08	2.7E-02	2.7E-02 Al377036.1	EST HUMAN	to 28g/08.x1 Sources, total fetus, Nb2HFB_9w Homo sepiens cDNA clone IMAGE: 2065982 3' shrilar to conteins Aiu repetitive element;
	21206	34340	0.49	2.7E-02	2.7E-02 S43442.1	NT	transmembrane secretory component [human, leukocytes, Genomic, 657 nt, segment 4 of 11]
	13340	25968	1.12	2.6E-02	2.6E-02 AL163282.2	NT	Homo seplens chromosome 21 segment HS210082
	15088	27825	3.29	2.6E-02	1.1	EST_HUMAN	ab02b02.s1 Stratagene fetal retina 937202 Homo saciens cDNA clone IMAGE:838595 3
	15090	27827	4.49	2.8E-02	6754241	1	Mus musculus histidine rich calcium binding protein (Hrc.), mRNA
2368	15090	27828	4.40	2.6€-02	6754241 NT	Į.	Mus musculus histidine non calcium binding protein (Hrc.), mRNA
	15682		188	2 85-02	2 RE-02 AE10000R 1	15	Mus musculus MHC class III region RD gene, pertial ods; Bf, C2, G9A, NG22, G9, HSP70, HSP70, HSC70t,
1	17577	30200	2.25	2.6E-02		TN	Chicken doteshir-1 mRNA, complete cds
. 2009	17728	30332	1.56	2.8E-02	17	NT	Dehococous radiodurans R1 section 151 of 229 of the complete chromosome 1
5032	17752	30364	2.35	2.0E-02	2.6E-02 AW241154.1	EST HUMAN	x832b04.x1 NCI_CGAP_Sar4 Homo septens cDNA clone IMAGE:2570383 3' similar to SW:Y069_HUMAN_015041 HYPOTHETICAL PROTEIN KIAA0099:
6754	18546		0.7	2.6E-02		K	Arabidopais thaliana DNA chromosome 4, contio fragment No. 63
2800	18590		0.59	2.0E-02	2	N.	Arabidopsis thallana DNA chromosome 4, contip fragment No. 63
Ц	18903		7.34	2.6€-02	-	EST_HUMAN	092711.x1 NCI_CGAP_Kid3 Homo sepiens cDNA clone IMAGE:1782317.3"
	19101	32080	1.9	2.6E-02	2.6E-02 BE621748.1	EST_HUMAN	60149347371 NIH MGC_70 Hamo sepiens aDNA dane INAGE:3896578 3'
	19562	32583	6.0	2.6€-02	2.6E-02 Z99064.1	Г	Vaccinia wrus ORF1L, strain Wyeth
	19562	32694	6.0	2.6E-02	2.6E-02 Z09064.1	ĮN.	Varcinia virus ORF1L, strain Wyeth
	19471	32404	7.11	2.6E-02	6981271 NT	N P	Rettue norvegious Nerve growth factor receptor, fest (Ngfr), mRNA
	21096	34232	0.71	2.6E-02	2.6E-02 AA860946.1	T_HUMAN	ak 22104.s1 Source tests, NHT Hamp septens cDNA clane IMAGE:14067/193/
0075	22014	35182	1.15	2.6€-02	11432020 NT		Homo sepiens KIAA1070 protein (KIAA1070), mRNA
9614	22267	35453	0.75	2.6E-02	2.6E-02 AF114952.1	Ŋ	Secoheromyces deirenensis NRRL Y-12839(T) ATP synthese subunit 9 (ATP9) gene, mitochandrial gene encoding mitochandrial protein, complete ods
- 4 884 2 4	23267	35454	37.0	2 85 02	2 ME (72) 4 E4440 K2 4	ţ	Seccharamyces dairenensis NRRL Y-12639(T) ATP synthase subunit 9 (ATP9) gene, mitochandrial gene
L		38185	4.30	2.05-02	\int		Home sanishs chromosome 24 segment 14024 (A)03
11191		 	1.67	2.6E-02	8488		Homo sapiens radyin (RDX) mRNA
L	24040		2.33	2.6€.02,	2.6E-02 AA279351.1	T HUMAN	2884002.r1 NCI CGAP GCB1 Homo septens cDNA clone MAGE: 704162 5
		37465	22	2.05-02		Г	UI-HF-BN0-akj-a-10-0-UI.r1 NIH MGC_60 Hamo septens oDNA clane IMAGE:3077468 51
12170 2		30615	2.09	20E-02	-		602015501F1 NCI_CGAP_Brn64 Harro septens cDNA clane IMAGE:4150944 51
510		25935	1.75	2.5E-02	1		on 28108, y S NCI_CGAP_Lu S Hamo sepiens a DNA done IMAGE: 1557827 5
╝		25836	1.75	2.5E-02 AI793130.	1	EST_HUMAN	on 28106; y 5 N CL_CGAP_Luf Hamo sepiens a DNA dane IMA QE: 1557827 5
<u>8</u>	13563	26224	15.9	2.5E-02	7.	EST HUMAN	601680305R2 NIH_MGC_83 Homo septens cDNA clone IMAGE:3650665 3'

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Oligie Exoli Flores Expressed in Brain	Most Similar Top Hit Acession Top Hit Acession Signal BLAST E No. Source Sour	7.2 2.5E-02 BE974314.1 EST HUMAN 601680305R2 NIH MGC 83 Homo eaplens cDNA clone IMAGE:3950685 3	2.24 2.5E-02 U12571.1 NT	4.35 2.5E-02 X99097.1 NT	4.35 2.5E-02 X99697.1 NT	1 2.5E-02 BE701165.1 EST_HUMAN PM2-NN0128-080700-001-412 NN0128 Homo sapiens cDNA	1 2.5E-02 BE701165.1 EST_HUMAN	62.4	0.61 2.5E-02 AI732776.1 EST_HUMAN	EST HUMAN	2.5E-02 BE746888.1 EST HUMAN	1.04 2.5E-02 [.28029.1 NT	1.7 2.5E-02 BF528722.1 EST HUMAN	1.7 2.5E-02 BF526722.1	0.81 2.5E-02 Q91713 SWISSPROT	0.47 2.5E-02 AW025821.1 EST_HUMAN	MT	0.65 2.5E-02 AI147615.1 EST HUMAN	2.01 2.5E-02 Q10335 SWISSPROT	2.01 2.5E-02 Q10335 SWISSPROT	2.32 2.5E-02 A.2237836.1 NT	Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha	Chain (IAalpha) and major histocompatibility protein class II beta chain (IEbeta) genes, complete cds;	2.5E-02 AB007548.1 NT	2.5E-02 11420078 NT	11433220 NT	1.94 2.5E-02 BE973327.1 EST_HUMAN	1.7 2.4E-02 H65884.1 EST_HUMAN	1.92 2.4E-02 P01901 SWISSPROT	1.92 2.4E-02 P01901 SWISSPROT	1.66 2.4E-02]J06110.1 NT	1.58 2.4E-02 P01901 SWISSPROT	1.58 2.4E-02 P01901 SWISSPROT
						1 2.5E	1 2.5E						L																				
	Exam ORF SEQ SEQ ID ID NO: NO:	13619 26289	15471	15722 28371	15722 28372		17879 29400		18422 31335	18878	18863	19018 31992	20233 33336	20233 33337	21416 34560	21554 34699	22814			23401 36641	23456 36700		23478	24361	25311	25182			15584 27501				17220 29848
	Probe E SEQ ID SE NO:	849	2786 1		2956				5625 1	6100	6115 1		7563 2		8724 2						10773 2		10795	1					2037 1			4485 1	_

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Table 4
Single Exon Probes Expressed in Brain

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
12186	24857	31104	1.06	2.4E-02 U78167	U78167.1	Į.	Refits novegicus cAMP-regulated guernine nucleotide exchance factor (1/24/APJ-97FF)
12216	24678		1.34	2.4E-02	2.4E-02 AF163864.1	N	Hamo saplens SNCA Isoform (SNCA) gene, complete ade, alternatively spliced
12360	24764		3.88	2.4E-02	2.4E-02 AB008509.1	<u> </u>	Ceenorhabditis elegans mRNA for iron-euftur subunit of mitochondrial succinate dehydrogenase, complete ods.
1865	14603		4.28	2.3E-02 W05340	W05340.1	EST HUMAN	2884008.11 Scenes fetal lung Nibill 19W Homo seriens cONA chose IMACE COCCOA F
1880	14617		10.45	2.3E-02 U94166.	U94165.1	Ł	4 Homo eaplens marrimary tumor-associated protein INT6 (INT6) cene. even 4
2350	15072	27809	2.08	2.3E-02 Z74283.	274293.1	¥	S. cerevisies chromosome IV reading frame ORF VDI 245c
3670		29064	6.19	2.3E-02 Z20377.1	220377.1	EST HUMAN	HSAAACADH P, Human fostal Brain Whole tassue Homo seniens onna
3702	18455		0.8	2.3E-02	2.3E-02 23429.1	¥	Canis beta-calactosides-binding lectin (LGALS3) mRNA. 3'end
4129		29469	1.08	2.3E-02 [.24789.1	124789.1	Ę	Gellus gellus connedn 45,6 (0x45,8) gene, complete ods
4129		29500	1.06	2.3E-02 124789.1	24789.1	N	Gallus gallus connextn 45.5 (Ox45.6) gene, complete cds
4386		29755	80'0	2.3E-02/	2.3E-02 AW800107.1	EST HUMAN	CM4-NN0080-290400-160-b04 NN0080 Homo sepiens cDNA
415		29780	0.88	2.3E-02	2.3E-02 BE835225.1	EST HUMAN	CM3-MT0118-010900-318-g07 MT0118 Hamo sapiens cDNA
4415	17152	29781	0.88	2.3E-02	2.3E-02 BE935225.1	EST HUMAN	CM2-MT0118-010900-318-g07 MT0118 Homo saplens cDNA
4416		29782	1.14	2.3E-02 AW 6636K	AW 563603.1	EST HUMAN	xs25d08.x1 NCI_CGAP_Ut2 Homo saplens cDNA clone IMAGE:2770871 3
4418	17880	29783	1.14	2.3E-02 AW 5936	AW 593593.1	EST HUMAN	xs25d08x1 NCI_CGAP_Ut2 Home saciens cDNA clone IMAGE:2770671 31
553	17290	29819	2.56	2.3E-02 BF02648	BF026487.1	EST_HUMAN	601672279F1 NIH_MGC_20 Homo septens cDNA clone IMAGE:3955386 57
4555	17280	29020	2.56	2.3E-02 BF02648	3F026487.1	Γ	601672279F1 NIH_MGC_20 Homo septens cONA clane IMAGE:3955386 51
30	900	90.760					Caulobacter crescentus topolsomerase IV ParE subunit (parE) gene, complete cds, and propionyl-CoA
200		00/20	20.00	2.3E-02 U86303.1		Z	carboxylase beta chain (pocB) homolog gene, partiel cds
3 8	0078	7070	80.4	2.3E-02 AL16150	2		Arabidopets thatiana DNA chromosome 4, contig fragment No. 17
3 5		STOUS	0.00	23E-02 BE14147	5.1	T_HUMAN	MRR-H10080-011099-002-009 HT0090 Hamo sapiens cDNA
2 2	7 E	CACCO	977.0	23E-02 U63610.1			Human plectin (PLEC1) gene, exons 3-32, and complete cds
	200	34204	0.94	2.3E-02/			Homo seplens PDX1 gene for thoyl-containing component X, exons 1-11
88 879	21083	34205	9.0	2.3E-02/		LN	Homo sepiene PDX1 gene for Ipol-containing component X, exons 1-11
8597	21289	34530	0.08	235-02	2.3E-02 Al685380.1	EST HUMAN	war78h10.x1 Soares, NFL, T, GBC, S1 Homo septens, cDNA, clone, IMAQE, 2302147.3
8897	21289	34430	0.68	23E-02 AI085380	\l685380.1	EST HUMAN	wa78h10.x1 Soares NFL T GBC S1 Homo saplens cDNA clone IMAGE 2302147.3
88	21728	34880	96.0	2.3E-02 P41998		SWISSPROT	HYPOTHETICAL 65.6 KD PROTEIN B0280.5 IN CHROMOSOME III PRECURSOR
9759	22410	35617	0.77	2.3E-02 P50532		SWISSPROT	CHROMOSOME ASSEMBLY PROTEIN XCAP-C
888	22577	35776	1.33	23E-02	23E-02 AE000189.1	Į.	Escherichia coli K-12 MG1665 section 89 of 400 of the complete genome
8	22677	35777	1.33	2.3E-02 A	2.3E-02 AE000190.1	Ł	Escherichia coli K-12 MG1055 section 89 of 400 of the complete genome
10524	23170	36307	0.46	2.3E-02 AF282894	6.1	NT	Becilius Icheniformis isolate NSTN1 KerA gene, partial ods

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Single Exoli Flores Expliesed III Diali	ORF SEQ Expression (Top) Hit Acession Detabese ID NO: Signal No. Source Surve	38815 2.16 2.3E-0.2 P08840 SWISSPROT GLUCOHYDROLASE)	5.07 2.3E-02 BE278331.1 EST HUMAN	30997 2.19 2.3E-02 U30394.1 NT	2.42 2.3E-02 U11077.1 NT	1.62 2.3E-02 11426388 NT	26147 4.13 2.2E-02/AF018267.1 NT	1.38 2.2E-02 4567448 NT	27197 1.06 2.2E-02 P07313 SWISSPROT	27198 1.06 2.2E-02 P07313 SWISSPROT	27469 2.13 2.2E-02 Z82001.1 NT	1.49 2.2E-02 AA577785.1 EST HUMAN	4.01 2.2E-02 AF083094.1 NT	29221 1.28 2.2E-02 AW801317.1 EST HUMAN	29290 0.75 2.2E-02 Z74293.1 NT	30333 1.05 2.2E-02 Z73597.1 NT	32902 3.63 2.2E-02 AV690721.1 EST_HUMAN	34104 1.62 2.2E-02 AL161515.2 NT	34105 1.62 2.2E-02 AL 161515.2 INT	34546 0.82 2.2E-02 X79488.1 NT	35422 2.2E-02 AB026898.1 NT complete cds)	35423 2.22 2.2E-02 AB026908.1 NT	0.89	37115 1.88 2.2E-02 BE797601.1 EST HUMAN	37766 1.54 2.2E-02 11423632 NT	FST HIMAN	6.11 2.1E-02 AV761502.1 EST HUMAN	0.09 3.45 00 A English 1
		38815		30997			26147		27197	27198	27.469			20221	29290	30333	32902	34104	34105	34546	35422	 35423	-	37115	37766			+-
	Exan SEQ ID NO:	23373	25188	24892	25409		13484	14483	14497	14497	14743	18185	16390	16585	16649	17729	19833	20963	20963	21401	22239	 22230	22753	23834	24425	24737	13186	43222
	Probe SEQ ID NO:	10882	12058	12582	12616	12807	720	1741	1766	1755	2008	3428	3637	3834	3890	5006	7146	8269	8209	8709	9586	828	10105	11167	11841	12315	4	438

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Probe E SEQ ID SE NO:	Excen ORF SEQ NO: NO:	2 Expression Signal	Most Similer (Top) Hit BLAST E Velue	Top Hit Acession No.	Top Hit Detabase Source	Top Hit Descriptor
1240 1	13989 28656	10.32		2.1E-02 U72073.1	Ā	Bacilius subtilis cotKLM cluster, CotK (cotK), CotL (cotL), and spore cost protein CotM (cotM) genes, complete cds
1366	14113 26787	121	2.1E-02	2.1E-02 AF204305.1	L	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1366 1	14113 26788	1.21	2.1E-02	2.1E-02 AF204395.1	Ŋ.	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partiel cds
1775 1	14517 27218		2.1E-02 P02438		SWISSPROT	KERATIN, HIGHSULFUR MATRIX PROTEIN, B2A
. 1	14517 27219	1.08		P02438	SWISSPROT	KERATIN, HIGH-SULPUR MATRIX PROTEIN, B2A
1775 1	14517 27220	1.06		P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
L	14763 27492	1.2		2.1E-02 BE072546.1	EST HUMAN	PM2-BT0546-120100-001-f11 BT0546 Homo sepiens cDNA
	14763 27493	1.2		2.1E-02 BE072546.1	EST_HUMAN	PM2-BT0548-120100-001-111 BT0548 Homo sapiens cDNA
	15305 28041	1.32		2.1E-02 AA225095.1	EST_HUMAN	nc21g03.r1 NCI_CGAP_Pr1 Hamo espiens cDNA clone IMAGE:1008820
2819 1	13534 25193	3 4.48	2.1E-02	2.1E-02 N29266.1	EST_HUMAN	yx43h07.r1 Sogres materiocyte 2NbHM Homo sapiens cDNA clone IMAGE:284541 5'
3147 1	14763 27492	1.07	2.1E-02	2.1E-02 BE072548.1	EST_HUMAN	PM2-BT0548-120100-001-f11 BT0548 Homo sapiens cDNA
	14763 27493	1.07	2.1E-02	2.1E-02 BE072546.1	EST_HUMAN	PM2-BT0548-120100-001-f11 BT0548 Homo sapiens cDNA
3571 1	16326 28973	3	2.1E-02 AA46127	AA461271.1	EST_HUMAN	zd3b09.r1 Scares_bbal_fetus_Nb2HF8_8w Homo sapiens cDNA clone IMAGE:796121 5'
4110 1	16853 29480	0.81	2.1E-02	2.1E-02 Z74203.1	¥	S.cerevisiae chromosome IV reading frame ORF YDI.245c
	17014 29641	19.0	2.1E-02	2.1E-02 BF343655.1	EST_HUMAN	802015308F1 NCI_CGAP_Bm84 Homo explens cDNA dane IMAGE:4151161 5
		1.47	2.1E-02	2.1E-02 U44914.1	١	Borrella burgdorfert plesmid cp32-2, erpC and erpD genes, complete cds; and unknown genes
4421 1	17157 29788	1.53	2.1E-02	2.1E-02 AI788127.1	EST_HUMAN	wg81d11.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sepiens cDNA clone IMAGE-2371509 3'
	17197	0.69	2.1E-02	2.1E-02 Y19213.1	IN	Homo saplens putative pathHbA peeudogene for heir keretin, excris 2 to 7
	17396 30031	4.51	2.1E-02	2.1E-02 Y08501.1	F	A thallana mitochondrial genome, part A
		1.05		2.1E-02 AL163302.2	LN	Homo sepiens chromosoms 21 segment HS21C102
	17501 30124	4 0.76	2.1E-02	2.1E-02 A1823432.1	EST_HUMAN	wh54e05.x1 NCI_CGAP_Kid11 Homo sepiens oDNA done IMAGE:2384528 3'
	18350 31259	1.13	2.1E-02	2.1E-02 AW379529.1	EST_HUMAN	CM4-HT0244-111199-040-h05 HT0244 Homo septens cDNA
	19448 32466	8 0.88	2.1E-02	2.1E-02 BF086199.1	EST_HUMAN	QV3-GN0058-120900-329-412 GN0058 Homo saplens cDNA
8417 2	21110 34249	9.0	2.1E-02	9790238 NT	Ž	Mus musculus earting near 1 (Srad), mRNA
			-		\Box	em63e07.s1 Strategene achizo brain 311 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains
┙			2.1E-02/		EST HUMAN	Alu repetitive element contains element MER11 repetitive element;
	22184 35368		2.1E-02)		L	Homo seplens partial 5-HT4 receptor gene, exons 2 to 5
9531 2	2184 35369	2.61	2.1E-02	2.1E-02 AJ243213.1	IN	Homo sepiens pertial 5-HT4 receptor gene, exons 2 to 5
2 2	22533 35730	1.15	2.1E-02 L28324.1		NT	Straptococcus pneumoniae integrase, eacislonese, repressor protein, relexese, UmuC MucB homolog, and UmuD MucA homolog genes, complete ods; and unknown genes
9961	2609 35814	0.00	2.1E-02 AA984288	 	1	em83e07.s1 Strategene actizo brain S11 Homo sapiens cDNA clone INAGE:1629732.3' shrifar to contains. Alu repetitive element contains element MER:11 repetitive element:
10522 2	23168 36395		2.1E-02/	=	N-	Bacillus halodurans genomic DNA, section 13/14

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Problem Exam Chick Problemsion Top Htt Top Htt <t< th=""><th>-</th><th></th><th></th><th>10.10</th><th></th><th></th><th></th></t<>	-			10.10			
30595 1.9 2.0E-02 AA456538.1 EST_HUMAN 28096 1.82 2.0E-02 AA572764.1 EST_HUMAN 28096 2.15 1.8E-02 AA572764.1 EST_HUMAN 27496 2.6 1.8E-02 AA572764.1 EST_HUMAN 27497 2.68 1.8E-02 AA163303.2 NT 27496 2.8 1.8E-02 AA163303.2 NT 27497 2.68 1.8E-02 AA163303.2 NT 27497 2.68 1.8E-02 AA163303.2 NT 27295 0.9F 1.8E-02 AA163303.2 NT 28309 1.8B-02 AA713866.1 EST_HUMAN 289402 1.48 1.8E-02 AA713866.1 EST_HUMAN 28959 1.8B-02 AA713866.1 EST_HUMAN 28960 0.95 1.8E-02 AA713869.1 EST_HUMAN 28961 1.83 1.8E-02 AA713869.1 EST_HUMAN 28962 4.09 1.8E-02 AA713869.1 INT 28963 4.09 1.8E-02 AA713600.1 NT 289645 1.38 1.8E-02 AA713600.1 NT<	SEQ IC NO:		Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Detabese Source	Top Hit Descriptor
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22266 35452 0.6 1.8E-02 L10114.1 NT 22563 35768 1.05 1.8E-02 BF695832.1 EST_HUMAN 22800 36017 0.54 1.8E-02 D64001.1 NT 23372 36614 1.44 1.9E-02 AF008938.1 NT 25171 30603 2.82 1.8E-02 AF101065.1 NT 25147 1.36 1.8E-02 L1008.1 NT			1.03	1.9E-02	.1	Г	301898130F1 NIH_MGC_19 Hamo septens cDNA clone IMAGE:4125462.5
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22800 36017 0.54 1.9E-02 De4001.1 NT 23372 36814 1.44 1.0E-02 AF008038.1 NT 25171 30803 2.82 1.8E-02 AF101085.1 NT 25147 1.36 1.8E-02 L11088.1 NT	1		1.05	1.9€-02]€	1.1	Π	301852385F1 NIH MGC_66 Hamo septens aDNA alone IMAGE:4076253 5
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30903 2.82 1.9E-02/AF101065.1 NT 1.36 1.9E-02/L11068.1 NT	23372		1.44	1.0E-02			/lbrito cholerae V86 phage putative replication protein gene, complete cds
1.36 1.9E-02 L11068.1 NT	25171		282	1.9E-02	5.1		lirudo medicinalis intermediate filament glierin mRNA, complete cds
	山		1.36	1.9E-02			Sandida albicans lambda Ca3/B fragment

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	https://www.nci_cgap_co17 Homo sapiens cDNA clone IMAGE:3027274.3' similar to contains element MER29 receitive element:	601894329F1 NIH MGC 17 Home seniens of NA cione IMAGE 4130083 ST	H.frendsci mRNA for myelin basic protein (MBP)	Droeophile melanogaster cytoplasmic protein encore (enc.) mRNA, complete cds.	Pseudomonas aerucinosa PA01, section 105 of 529 of the complete nercons	te52a09.x1 Sogres NFL T GBC S1 Homo saniens cDNA clone IMAGE-2002098 3'	at/24/04.s1 Sogres testis NHT Homo sepiene CONA come MAGE: 40/90/35.3	QV4-DT0021-301299-071-b11 DT0021 Homo seniena cDNA	HYPOTHETICAL 7.9 KD PROTEIN IN FIXW SIRECION	Mus musculus carbonic anhydrase IV cene, complete cals	QV2-NV1073-220400-169-h09 NN1073 Homo seniens CDNA	Mus musculus microhibule essociated materia 2 (Mena) mRNA	601877026F1 NIH MGC 55 Homo septens cDNA close IMAGE 4105402 F	601877028F1 NIH MGC 55 Home eablens cDNA clone IMAGE 4105303 5	e(6209.s1 Source, testis, NHT Homo sapiens cDNA done IMAGE:1394921 3' semiliar to gb1.11672 ZINC	FINACE TROLEIN 91 (HOWAN)	Adentifie m RNA for managed if a seminar of the control of the con	Homo seciens mRNA for KIAAA330 profes reference	Homo saplens mRNA for KIAA0330 protein, partial cds	Pyrococous horikoshii OT3 genomic DNA, 1166001-1485000 nt. position (8/7)	Zee mays acidic ribosomal protein P2a-3 (rpp2a-3) mRNA, partial cds	801310828F1 NIH_MGC_44 Homo sepiens cDNA clane IMAGE:3832190 6	Inf34e03.x1 Source_NFL_T_GBC_S1 Hamo sapiens cDNA clone IMAGE:2933740 3' straffer to contains	L1.t1 L1 repetitive element;	hr34e03 x1 Soeree_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similer to contains	Home sariens chromosome 21 sament HS24/2004	Orchologie Cinicipie mBNA for with serming a service of	(microsophile INRA41) (Ode greenshee) Centerio 284 of an enterest 4 of 7)	Homo septens butative RebS GDP/GTP emberge factor homologies (RABEYS) with a	db22ar0t.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:16969823'
gie Exon Pro	Top Hit Databese Source	EST HUMAN	EST HUMAN		N	뉟	EST HUMAN	EST HUMAN	EST HUMAN	SWISSPROT	IN	EST HUMAN	Į.	EST HUMAN	EST HUMAN	TOO TOO	ES HOMAN	FN FN	E	Ł	¥	FN.	EST HUMAN		EST HUMAN	EST HIMAN	Į.	L	Z	2	EST_HUMAN
S	Top Hit Acession No.	AW771104.1		X17664.1	1.8E-02 AF243382.1	1.8E-02 AE004544.1	1.8E-02 AI805829.1	1.8E-02 AA861446.1	1.8E-02 AW936363.1	P14310	U37091.1	1.8E-02 AW905327.1	TN 8483 NT	1.8E-02 BF241924.1	BF241924.1	A A BOTE 42 4	2 2		Γ	7.2			1.7E-02 BE394869.1		83.1	23	42	5		7057495	1.7E-02 AI147615.1
	Most Similar (Top) Hit BLAST E Value	1.8E-02 AW771	1.8E-02	1.8E-02 X17664.	1.8E-02	1.8E-02	1.8E-02	1.8E-02	1.8E-02	1.8E-02 P14310	1.8E-02 U37091.	1.8E-02	1.8E-02	1.8€-02	1.8E-02 BF24192	1 PE 02 A BOTE	1.8F-02 ACC 13	1.8E-02 X96033	1.8E-02 AB0023	1.8E-02	1.8E-02	1.8E-02 U62749.	1.7E-02		1.7E-02 AW5731	1.7E-02 AW5731	1.7E-02 AL16320	1.7E-02 AB00481	1.7E-02 S74186.	1.7E-02	1.7E-02/
	Expression Signal	1.4	0.83	1.32	1.73	1.71	0.94	0.99	1.17	5.02	0.69	0.91	0.8	0.49	0.40	176	1.51	1.37	231	2.31	1.50	3.32	1.86	•	2.17	2.17	3.41	10.5	0.80	1.01	1.44
	ORF SEQ ID NO:	222	28086			28133			20764	32671	33857	34200	34242	35225	35226		35815	35087	36400	38410	37535	37545	26323	9000	27.230	27231			27752		28411
	Exan SEQ ID NO:	13137	13448	13892		15394	16968	16810	17133	19627	20724	21060	21103	22054	22054	22195	100	22774	23181	23181	24211	2222	13055	11801	1204	14524	14802	14837	15016	15356	15762
	Probe SEQ ID NO:	336	970	1137	1418	2885	3205	4065	4396	6712	8029	8367	8410	8392	8392	8542	88	19128	11414	11414	11613	1,628	88		3	1783	1864	2108	72291	2848	2880

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						,	
Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Moet Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3502	16258		4.67	1.7E-02	1.7E-02 AW827368.1	EST HUMAN	hm45a04x1 NCI_CGAP_RDF1 Homo sapiens cDNA clone IMAGE:3015534 3' similar to contains MER19.b1 MER19 repetitive element;
3614	16367		0.73	1.7E-02 P04929	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
4148	16890		1.23	1.7E-02	1.7E-02 AA669618.1	EST HUMAN	ac19f04.s1 Stratagene overy (#837217) Homo septems cDNA clone IMAGE:856927.3' similar to contains Alu repeditive element;contains element.
4178	16918		204	1.7E-02 R02506.	R02506.1	EST_HUMAN	ye88f08.r1 Sogres fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124647 61
4420	17158	29787	1.49	1.7E-02 Al30527	Al305279.1	EST_HUMAN	qm08g07.xt NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881278.3' similar to gb.X52359 ZINC FINGER PROTEIN 30 (HUMAN);
4491	172271	29856	1.78	1.7E-02 AW673	AW673183.1	EST HUMAN	H34e03.XI Soeres NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE-2033740 3' similar to contains L1.ft L1 repetitive element:
4686	17400	30034		1.7E-02 V00641		L	Messenger RNA for anglerfish (Lophius emericanus) somatostatin II
4763	17495		5.84	1.7E-02 AI01507	Al015076.1	EST HUMAN	ov51e02.s1 Soares testis, NHT Homo sapiens cDNA clone IMAGE:1640858.31
5007	17730	30334	0.60	1.7E-02	6681289 NT	7.	Rattus norvegicus N-erginine dibasic convertase 1 (Nrd1), mRNA
5096	17815		0.91	1.7E-02 AJ22904	AJ229041.1	LN	Home sapiens 959 to config between AML1 and CBR1 on chromosome 21q22, segment 1/3
Mas	18815	3411E	20.0	4 75.02	1 7E-02 & 1780247 4	EST LIMBAN	wg35f09.x1 Soeree_NSF_F8_9W_OT_PA_P_S1 Hamo septens cDNA clone IMAGE:2367113 3' similar to
28	19251		1.47	1.7E-02	1.7E-02 Al038280.1	EST HUMAN	overtime And a special programment, and the second of the
0920	19432	32448	1.27	1.7E-02 AF1909	AF190830.1	L	Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
7103	19791	32858	244	1.7E-02	8400716 NT	ŁN	Homo sepiens nebulin (NEB), mRNA
7267	19941	33016	1.08	1.7E-02 L07899.	L07899.1	Ę	Human apolipoprotein (a) gene, exen 1
7257	19941	33017	1.06	1.7E-02 L07899	1	LN	Human apolipoprotein (a) gene, exon 1
7642	20307		1.78	1.7E-02 AJ0107	21	Z	Homo sapiens hyperion gene, exons 1-50
9336	20407	33523	96.0	1.7E-02 U21864	ļ.	Į.	Cesnorhabditis elegans cCAF1 protein gene, complete cds
9636	22251	35437	1.3	1.7E-02 AL0405	AL040554.1	EST_HUMAN	DKFZp434l0314_r1 434 (synonym: hies3) Hamp sepiens cDNA clone DKFZp434l0314 5
11801	24391	37724	1.38	1.7E-02	5902007 NT	IN	Homo sepiens serum constituent protein (MSE55), mRNA
12631	26337	30716	2.39	1.7E-02 AW903	AW903482.1	EST_HUMAN	CM4-NN1030-040400-130-f06 NN1030 Homo sepiens cDNA
498	13282		3.19	1.6E-02 AL02193	29.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 13/162
1653	14300	27088	10.	1.8E-02 Y18880.	*-	IN	Trebonema malfootilum flaß2, flaß3 and fliD cenes for flacellin subunit proteins and CAP protein homotonus
2248	14974	27711	0.0	1.6E-02 Q64176		13SPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2246	14974	27712	0.0	1.6E-02 Q64176		SWISSPROT	LIVER CARBOXY ESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2570	15284	28022	1.05	1.6E-02 AJ00634	15.1	¥	Homo septions KVLQT1 gene
2649	15359	28102	1.48	1.0E-02		EST_HUMAN	ne81d06.s1 NCI_CGAP_Ew1 Homo septens cDNA clone IMAGE:910967
888	15408		0.96	1.6E-02	1.6E-02 AB014534.1	NT	Homo saplens mRNA for KIAA0634 protein, partial cds

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Prob EXEM Prof # SEC Expression Top HR Abouston Top HR Abouston Top HR Descriptor 8CD NCD SSUD BLASTE BLASTE PLASTE PLASTE <th></th> <th></th> <th></th> <th></th> <th>1</th> <th></th> <th></th> <th></th>					1			
15782 28431 0.71 1.0E-02 AF112282.1 NT 16581 28626 5.9 1.0E-02 AF10282.1 EST HUMAN 16581 28626 5.9 1.0E-02 AF105301.2 NT 17007 28640 0.97 1.0E-02 AF105301.2 NT 17007 28640 0.97 1.0E-02 AF00531.1 NT 18334 31241 1.25 1.0E-02 AB015281.1 NT 19404 32518 1.75 1.0E-02 AB015281.1 NT 19404 32518 1.75 1.0E-02 AB015731.1 NT 20776 33384 0.86 1.0E-02 AA572818.1 EST HUMAN 22586 36184 1.29 1.0E-02 AA572818.1 NT 22788 36184 1.29 1.0E-02 AA572818.1 EST HUMAN 22841 37124 2.54 1.0E-02 AA572818.1 EST HUMAN 22843 1.29 1.0E-02 AA572818.1 EST HUMAN 22844 1.29 1.0E-02 AA572818.1 EST HUMAN 23847 1.54 </td <td>Probe SEQ ID NO:</td> <td>SEQ ID NO:</td> <td>ORF SEQ ID NO:</td> <td>Expression Signal</td> <td>Most Similar (Top) Hit BLAST E Vælue</td> <td></td> <td>Top Hit Databese Source</td> <td>Top Hit Descriptor</td>	Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Vælue		Top Hit Databese Source	Top Hit Descriptor
16531 28626 5.9 1.6E-02 AV85065.2 1 EST HUMAN 16531 28216 1.32 1.6E-02 AL163301.2 NT 16806 2.49 1.6E-02 AR1165301.2 NT 17007 28840 0.97 1.6E-02 AR815281.1 NT 18334 31241 1.25 1.6E-02 AR815281.1 NT 19404 32517 1.76 1.6E-02 AR815281.1 NT 19404 32517 1.75 1.6E-02 AR827571.1 NT 20775 33347 0.76 1.6E-02 AL161608.2 NT 22586 36185 1.28 1.6E-02 AR727818.1 EST HUMAN 22588 36186 1.29 1.6E-02 AR72818.1 EST HUMAN 22588 36185 1.29 1.6E-02 AR72818.1 EST HUMAN 22588 3618 1.29 1.6E-02 AR72818.1 EST HUMAN 22588 3618 1.29 1.6E-02 AR72818.1 EST HUMAN 22588 3618 1.29 1.6E-02 AR72818.1 EST HUMAN 23	3016	!		0.71	1.6E-02	AF112282.1	L'A	Lassea sp. iedate IBd cytochrome addase III gene, partial cds; mitochandrial gene for mitochandrial product
16881 28215 1.32 1.6E-02 AL163301.2 NT 16886 2.49 1.6E-02 AL163301.2 NT 17007 22640 0.97 1.6E-02 AW875407.1 NT 18334 32516 1.25 1.6E-02 AR97551.1 NT 19494 32517 1.75 1.6E-02 AR907571.1 NT 19494 32517 1.75 1.6E-02 AR907571.1 NT 20772 33384 0.76 1.6E-02 AR907571.1 NT 20772 33847 0.76 1.6E-02 AL277662.1 NT 20772 33847 0.76 1.6E-02 AL277662.1 NT 20772 1.6E-02 AL277662.1 NT NT 20772 1.6E-02 AL277662.1 NT NT 20773 1.6E-02 AL272818.1 EST_HUMAN NT 22868 36185 1.25 1.6E-02 AA572818.1 EST_HUMAN 23841 37124 2.54 1.6E-02 AA572818.1 EST_HUMAN 23841 37125 2.54 1.6E-02 AA572818.1	3518			5.9	1.6E-02	AW850652.1	EST HUMAN	IL3-CT0219-160200-063-C07 CT0219 Homo septens cDNA
18896 2.40 1.8E-02 AF110520.1 NT 17007 220540 0.97 1.0E-02 AW875407.1 EST_HUMAN 18334 31241 1.25 1.0E-02 AB015281.1 NT 170494 32517 1.75 1.0E-02 AB027571.1 NT 20276 33384 0.88 1.0E-02 AB027571.1 NT 20276 33384 0.88 1.0E-02 AB027571.1 NT 20276 33587 0.76 1.0E-02 AB027571.1 NT 20276 33587 0.76 1.0E-02 AB027571.1 NT 202772 1.08 1.0E-02 AB027571.1 NT 20278 33587 0.76 1.0E-02 AA572818.1 EST_HUMAN 20278 35185 1.29 1.0E-02 AA572818.1 EST_HUMAN 20372 35185 1.29 1.0E-02 AA572818.1 EST_HUMAN 20372 35184 1.0E-02 AA572818.1 EST_HUMAN 20373 35124 2.54 1.0E-02 AA572818.1 EST_HUMAN 20384 37724 2.54 1.0E-02 AA572818.1 EST_HUMAN 103508 37407 1.54 1.0E-02 AA572818.1 EST_HUMAN 103508 37407 1.54 1.0E-02 AA572818.1 EST_HUMAN 103508 37407 1.54 1.0E-02 AA572818.1 EST_HUMAN 103508 1.0E-02 AA572818.1 EST_HUMAN 103508 1.0E-02 AA572818.1 EST_HUMAN 103508 1.0E-02 AA572818.1 EST_HUMAN 103508 1.0E-02 AA572818.1 EST_HUMAN 103508 1.0E-02 AA572818.1 EST_HUMAN 103508 1.0E-02 AA572818.1 EST_HUMAN 103508 1.0E-02 AA572818.1 EST_HUMAN 103508 1.0E-02 AA572818.1 EST_HUMAN 103508 1.0E-02 AA572818.1 EST_HUMAN 103508 1.0E-02 AA572818.1 EST_HUMAN 103508 1.0E-02 AA572818.1 EST_HUMAN 103508 1.0E-02 AA5728208 1.0E-02 AA5728208 1.0E-02 AA572820 1.0E-02 AA572	3830		28215	1.32	1.6E-02	AL163301.2	NT	Homo sepiens chromosome 21 segment HS21C101
17007 28940 0.97 1.0E-02 AW875407.1 NT 18334 31241 1.25 1.0E-02 AW875407.1 NT 18334 31241 1.25 1.0E-02 AW875407.1 NT 19494 32517 1.75 1.0E-02 AB015281.1 NT 19494 32517 1.75 1.0E-02 AB027571.1 NT 20276 33384 0.88 1.0E-02 AL277662.1 NT 20272 20272 3384 0.88 1.0E-02 AL277662.1 NT 20272 20272 1.08 1.0E-02 AL277662.1 NT 20272 20288 36184 1.29 1.0E-02 AL277662.1 NT 20272 2038 1.0E-02 AL277662.1 NT 20272 2038 1.0E-02 AL277662.1 NT 20272 2038 1.0E-02 AL277662.1 NT 20272 2038 1.0E-02 AL277662.1 NT 20288 27728 1.0E-02 AL277662.1 NT 20288 27728 1.0E-02 AL277662.1 NT 20288 27728 1.0E-02 AL277662.1 NT 20389 1.0E-02 AL277662.1 NT 20389 1.0E-02 AL277662.1 NT 20389 1.0E-02 AL277688.1 EST HUMAN 18508 27758 1.0E-02 AL277688.1 EST HUMAN 18601 27758 1.0E-02 AL277688.1 EST HUMAN 18601 27758 1.0E-02 AL277688.1 EST HUMAN 18602 22848 1.0E-02 AL2776821.1 EST HUMAN 18602 228488 1.0E-02 AL27768228.1 EST HUMAN 18602 228488 1.0E-02 AL27768282 1.0E-02 AL27768282 1.0E-02 AL27768282 1.0E-02 AL27768282 1.0E-02 AL27768282 1.0E-02 AL27768282 1.0E-02 AL27768282 1.0E-02 AL27768282 1.0E-02 AL27768282 1.0E-02 AL27768282 1.0E-02 AL27768282 1.0E-02 AL27768282 1.0E-02 AL27768282 1.0E-02 AL27768282 1.0E-02 AL27768282 1.0E-02 AL27768282 1.	4454			970	A II	A EXAMESTS A	ţ	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH addoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapesin, RaiGDS-like, KE2, BING4, bets 1,3-galactosyl transferase, and DDS49.
18334 31241 1.25 1.0E-02 08071715 NT 19311 32316 2.05 1.0E-02 AB015281.1 NT 19494 32517 1.75 1.0E-02 AB027571.1 NT 20276 33384 0.88 1.0E-02 AL277662.1 NT 20772 1.68 1.6E-02 AL277662.1 NT 20772 1.88 1.6E-02 AL277662.1 NT 20772 1.88 1.6E-02 AL277662.1 NT 20772 1.88 1.6E-02 AA572818.1 BT HUMAN 2286 36186 1.29 1.6E-02 AA572818.1 BST HUMAN 2284 36186 1.29 1.6E-02 AA572818.1 BST HUMAN 22841 37126 2.38 1.6E-02 AA572818.1 BST HUMAN 23841 37126 2.54 1.6E-02 AA572818.1 BST HUMAN 14898 37407 1.54 1.6E-02	4267		29840	0.97	1.65-02	AW875407.1	EST HUMAN	CV2-PT0012-140100-030-007 PT0012 Homo sapiens cDNA
19311 32316 2.05 1.0E-02 AB015281.1 NT 19494 32517 1.75 1.0E-02 AB027571.1 NT 19494 32517 1.75 1.0E-02 AB027571.1 NT 20276 33847 0.76 1.0E-02 AL77662.1 NT 20772 1.88 1.6E-02 AL77662.1 NT 22868 36184 1.29 1.0E-02 AL77662.1 NT 22868 36184 1.29 1.0E-02 AA572818.1 RT 22888 36185 1.29 1.0E-02 AA572818.1 RST HUMAN 22841 37124 2.38 1.0E-02 AA572818.1 RST HUMAN 22841 37124 2.54 1.0E-02 AA572818.1 RST HUMAN 23841 37125 2.54 1.0E-02 AA572818.1 NT 24086 37407 1.54 1.0E-02 AA572818.1 RST HUMAN 14688 27568 1.56-02 AL161508.2 NT 14888 27568 4.24 1.0E-02 AA572818.1 RST HUMAN 16823 28467	5536		31241	1.25	1.6E-02		N L	Mus musculus CD5 antigen (Cd5), mRNA
19494 32517 1.76 1.6E-02 AB027571.1 NT 19494 32518 1.75 1.0E-02 AB027571.1 NT 20775 33384 0.86 1.6E-02 AL161608.2 NT 20772 1.68 1.6E-02 AC127062.1 NT 22588 2.72 1.6E-02 AC127062.1 NT 22686 36184 1.29 1.6E-02 AC17064.1 NT 22687 0.76 1.6E-02 AC17062.1 NT 22888 36185 1.29 1.6E-02 AC17064.1 NT 22888 36185 1.29 1.6E-02 AC17062.1 NT 22841 37124 2.54 1.6E-02 AC17062.2 NT 22841 37124 2.54 1.6E-02 AC101508.2 NT 22841 37125 2.54 1.6E-02 AC101508.2 NT 24086 37407 1.54 1.6E-02 AC101508.2 NT 14682 2758 1.5E-02 AC101508.2 NT 14883 2758 1.5E-02 AC10508.1 NT <td< td=""><td>6546</td><td></td><td>32316</td><td>2.05</td><td>1.6E-02</td><td>AB015281.1</td><td>L</td><td>Cerdida albicans CaGCR3 gene, complete cds</td></td<>	6546		32316	2.05	1.6E-02	AB015281.1	L	Cerdida albicans CaGCR3 gene, complete cds
19494 32518 1.75 1.6E-02 AB027571.1 NT 20775 3384 0.86 1.6E-02 AL161608.2 NT 20772 1.68 1.6E-02 AC177662.1 NT 20772 1.68 1.6E-02 AC17766.1 NT 22588 2.72 1.6E-02 AC1766.1 NT 22866 36184 1.29 1.6E-02 AC1761.1 NT 22841 37124 2.38 1.6E-02 AC1761.1 NT 22841 37124 2.54 1.6E-02 AC1761508.2 NT 23841 37124 2.54 1.6E-02 AC161508.2 NT 24086 37407 1.54 1.6E-02 AL161508.2 NT 24086 37407 1.54 1.6E-02 AL161508.2 NT 14801 2758 1.6E-02 AL161508.2 NT 14802 37407 1.54 1.6E-02 AL161508.2 NT 14803 2758 1.5E-02 AL161508.2 NT 14803 2758 4.24 1.6E-02 AL161508.2 NT 1	6832		32517	1.75	1.6E-02	AB027571.1	Ę	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cots
20776 33384 0.88 1.6E-02 AL101608.2 NT 20775 1.68 1.6E-02 AN577662.1 NT 20772 1.68 1.6E-02 AN572618.1 NT 22588 2.72 1.6E-02 AN572818.1 NT 22868 36184 1.29 1.6E-02 AN572818.1 EST_HUMAN 22841 37124 2.54 1.6E-02 AN572818.1 EST_HUMAN 23841 37124 2.54 1.6E-02 AN572818.1 EST_HUMAN 23841 37124 2.54 1.6E-02 AL161508.2 NT 24086 37407 1.54 1.6E-02 AL161508.2 NT 24086 37407 1.54 1.6E-02 AL161508.2 NT 14882 2758 1.6E-02 AL161508.2 NT 14888 2758 1.5E-02 AL161508.2 NT 14882 23.05 1.5E-02 AL161508.2 NT 14882 2246 1.6E-02 AL161508.2 NT 14882 2246 1.5E-02 AL161508.2 NT 14882 2246	6832		32518	1.75	1.6E-02	AB027571.1	Ä	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
20715 33847 0.76 1.6E-02 AJ277062.1 NT 20772 1.68 1.6E-02 X05151.1 NT 22588 2.72 1.6E-02 AF079764.1 NT 22898 36184 1.29 1.6E-02 AA572818.1 EST_HUMAN 22984 37124 2.38 1.6E-02 AA572818.1 EST_HUMAN 23841 37124 2.54 1.6E-02 AA572818.1 EST_HUMAN 23841 37124 2.54 1.6E-02 AA572818.1 EST_HUMAN 24086 37407 1.54 1.6E-02 AA572818.1 EST_HUMAN 13508 2.54 1.6E-02 AA572818.1 EST_HUMAN 14801 37407 1.54 1.6E-02 AL161508.2 NT 14808 27506 4.24 1.6E-02 AL161508.2 NT 14801 27506 4.24 1.6E-02 AL161508.2 NT 14802 23.05 1.5E-02 AL161508.2 NT 14803 27506 4.24 1.6E-02 AL161508.2 NT 1682 28467 1.6 1.6E-0	7610		33384	0.86	1.6E-02	AL161508.2		Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
20772 1.88 1.6E-02 AF079784.1 NT 22588 36184 1.29 1.6E-02 AF079784.1 NT 22886 36184 1.29 1.6E-02 AA572818.1 EST_HUMAN 25132 36748 2.38 1.6E-02 AA572818.1 EST_HUMAN 25841 37124 2.54 1.6E-02 AL161508.2 NT 23841 37125 2.64 1.6E-02 AL161508.2 NT 23841 37125 2.64 1.6E-02 AL161508.2 NT 23086 37407 1.54 1.6E-02 AL161508.2 NT 13508 27508 4.24 1.6E-02 AL161508.2 NT 14888 27508 4.24 1.6E-02 AL161504.2 NT 15823 28467 1.6E-02 AL008216.1 NT 15823 28468 1.6 1.6E-02 AL008216.1 NT 16842 29103 0.58 1.6E-02 AL008216.1 NT 16904 29103 0.58 1.6E-02 AL008216.1 NT 18904 1.6 1.6E-02 A	8020	20715		0.76	1.6E-02	AJ277662.1		Homo septens pertial TUB gene for tubby (mouse) hamdon and LMO1 gene for LIM domain only 1 protein
22588 2.72 1.0E-02 AF079764.1 NT 22986 36184 1.29 1.0E-02 AA572818.1 EST HUMAN 22986 36185 1.29 1.0E-02 AA572818.1 EST HUMAN 25841 37124 2.54 1.0E-02 AA572818.1 NT 23841 37124 2.54 1.0E-02 AL161508.2 NT 23841 37125 2.54 1.0E-02 AL161508.2 NT 24086 37407 1.54 1.0E-02 AL161508.2 NT 14508 27508 4.24 1.0E-02 AL161508.2 NT 14801 27508 4.24 1.0E-02 AL161508.2 NT 14801 27508 4.24 1.0E-02 AL161509.2 NT 14801 27635 1.09 1.0E-02 AL161509.2 NT 16823 28467 1.0 1.0E-02 AL008216.1 NT 16823 28468 1.0 1.0E-02 AL008216.1 NT 16804 28103 1.0 1.0 1.0 16904 1.0 1.0	8078			1.88	1.6E-02	X05151.1	FA	Human spoC-II gene for preprospolipoprotein C-II
22966 36184 1.29 1.6E-02 AA572818.1 EST HUMAN 22966 36185 1.20 1.6E-02 AA572818.1 EST HUMAN 25132 36748 2.38 1.6E-02 ZA4628.1 NT 23841 37124 2.54 1.6E-02 ZA161508.2 NT 23941 37125 2.64 1.6E-02 ZA161508.2 NT 24086 37407 1.54 1.6E-02 AL161508.2 NT 13508 23.05 1.5E-02 AL373558.1 EST HUMAN 14801 27598 4.24 1.6E-02 AL161508.2 NT 14801 27759 4.24 1.6E-02 AL161504.2 NT 14802 27635 1.69 1.6E-02 AL006216.1 NT 16823 28467 1.6 1.6E-02 AL006216.1 NT 16823 28468 1.6 1.6E-02 AL006216.1 NT 16824 1.6 1.6E-02 AL006216.1 NT 16904 29103 0.98 1.6E-02 AL006216.1 NT 18904 33060 1.6E	9940	22588		2.72	1.0E-02	AF079784.1	N	Drosophile melanogaster enhancer of polycomb (E(Pc)) mRNA, complete cds
22966 36185 1.29 1.6E-02 AA572818.1 EST HUMAN 25132 36748 2.38 1.6E-02 Z94828.1 NT 23841 37124 2.54 1.6E-02 AL161508.2 NT 23841 37125 2.64 1.6E-02 AL161508.2 NT 24086 37407 1.54 1.6E-02 AL161508.2 NT 13508 27598 4.24 1.5E-02 8623734 NT 14801 27636 4.24 1.5E-02 8623734 NT 14801 27636 4.24 1.5E-02 NT NT 16823 28467 1.6 1.5E-02 AJ006216.1 NT 16823 28467 1.6 1.5E-02 AJ006216.1 NT 16823 28467 1.6 1.5E-02 AJ006216.1 NT 16824 29103 0.96 1.5E-02 AJ006216.1 NT 18977 31955 1.5 1.5E-02 AJ006216.1 NT 18904 1.6 <	10319			1.29	1.0E-02	AA572818.1	EST_HUMAN	nf19g03.st NCI_CGAP_Pr1 Homo septens cDNA clone IMAGE:914280 semiler to SW:TELO_RABIT P29294 TELOKIN. [1];
25132 36748 2.38 1.0E-02 Z94628.1 NT 23841 37124 2.54 1.0E-02 AL161508.2 NT 23841 37125 2.64 1.0E-02 AL161508.2 NT 24086 37407 1.54 1.0E-02 AL161508.2 NT 13508 27.59 4.24 1.5E-02 8623734 NT 14801 27635 1.69 1.5E-02 N38521.1 EST_HUMAN 16823 28467 1.6 1.6E-02 AJ006216.1 NT 16823 28488 1.6 1.6E-02 AJ006216.1 NT 16823 28488 1.6 1.6E-02 AJ006216.1 NT 16844 28103 0.98 1.6E-02 AJ006216.1 NT 18977 31955 1.5 1.6E-02 AJ006216.1 SWISSPROT 19904 1.6 1.6E-02 AJ006216.1 SWISSPROT 19904 1.6 1.6E-02 AJ006216.1 SWISSPROT 19904 1.6 1.6E-02 AJ006711 SWISSPROT	10319		36185	1.20	1.6E-02	AA572818.1		mf19g03.s1 NCI_CGAP_Pr1 Homo septens cDNA clone IMAGE:914280 similar to SW:TELO_RABIT P29294 TELOKIN, [1];
23841 37124 2.54 1.0E-02 AL161508.2 NT 23841 37125 2.64 1.6E-02 AL161508.2 NT 24086 37407 1.54 1.6E-02 Al37358.1 EST_HUMAN 13508 27508 4.24 1.5E-02 Al37358.1 EST_HUMAN 14801 27636 4.24 1.5E-02 Al36521.1 EST_HUMAN 16823 28467 1.6 1.6E-02 AL101504.2 NT 16823 28468 1.6 1.6E-02 AL006216.1 NT 16823 28468 1.6 1.6E-02 AL006216.1 NT 16824 28103 0.96 1.6E-02 AL006216.1 NT 16804 28103 0.56 1.6E-02 AL006216.1 NT 18907 1.5 1.6E-02 AL006216.1 NT 1904 1.6 1.6E-02 AL006216.1 NT 1904 1.6 1.6E-02 AL006216.1 NT 18904 1.6 1.6E-02 AL006216.1 SWISSPROT 18904 1.6 1.6E-02 AL0062111 SWISSPROT	10826	25132	36748	238	1.6E-02	294828.1	Z.	G.gallus microsatelitis DNA (LEi0260 (*T16/iiE11))
23841 37125 2.64 1.6E-02 AL101508.2 NT 24086 37407 1.54 1.6E-02 AI373588.1 EST HUMAN 13508 23.05 1.5E-02 Be23734 NT 8623734 NT 14808 2758 4.24 1.5E-02 AL101504.2 NT 14801 27636 1.69 1.6E-02 AL101504.2 NT 16823 28467 1.6 1.5E-02 AL008216.1 NT 16823 28488 1.6 1.5E-02 AL008216.1 NT 16404 28103 0.98 1.5E-02 BF082942.1 EST_HUMAN 18907 31956 1.6 1.6E-02 AL008216.1 NT 18907 1.5 1.5E-02 AL008216.1 SWISSPROT 18904 1.6 1.6E-02 AL008211 SWISSPROT 19904 1.6 1.6E-02 AL008211 SWISSPROT 19904 1.6 1.6E-02 AL008211 SWISSPROT 19904 1.6 1.6 1.6 1.6	11174	23841	37124	2.54	1.6E-02			Arabidopeis thallana DNA chromosome 4, contig fragment No. 20
24086 37407 1.54 1.6E-02 AISTSSSS.1 EST HUMAN 13508 23.05 1.5E-02 ASST34 NT 8023734 NT 14888 27598 4.24 1.5E-02 ASSE21.1 EST HUMAN 14801 27636 1.69 1.5E-02 AL101594.2 NT 15823 28467 1.6 1.5E-02 AL008216.1 NT 16823 28488 1.6 1.5E-02 AL008216.1 NT 16464 28103 0.98 1.5E-02 BF082942.1 EST HUMAN 18977 31955 1.5E 1.6E-02 AU008211 SWISSPROT 18904 1.6 1.5E-02 AU00821 SWISSPROT	11174	23841	37125	2.54	1.6E-02			Arabidopala thallana DNA chromosome 4, contig fragment No. 20
13508 23.05 1.5E-02 8623734 NT 14868 27596 4.24 1.5E-02 N39521.1 EST_HUMAN 14901 27635 1.69 1.6E-02 AL161594.2 NT 16823 28467 1.6 1.5E-02 AL006216.1 NT 16823 28468 1.6 1.5E-02 AL006216.1 NT 16404 29103 0.98 1.5E-02 AL006218.1 NT 18977 31955 1.56 1.5E-02 BF092942.1 EST_HUMAN 19904 1.56 1.5E-02 Q09711 SWISSPROT 19884 33060 1.2 1.5E-02 (14487282) NT	11495	24096	37407	1.54	1.6E-02	Al373558.1	T_HUMAN	9290e10.x1 Soares_pregnant_uterus_NbHPU Homo sepiens cDNA clone IMAGE-2042442.3*
14888 27598 4.24 1.5E-02 N39521.1 EST HUMAN 14901 Z7635 1.69 1.6E-02 AL161594.2 NT 16823 28467 1.8 1.5E-02 AL006216.1 NT 16824 28468 1.6 1.5E-02 AL006216.1 NT 16464 28403 0.98 1.5E-02 AL006218.1 NT 18977 31955 1.56 1.5E-02 BF092942.1 EST HUMAN 18977 31955 1.56 1.5E-02 AL06711 SWISSPROT 1994 33060 1.5 1.5E-02 I14487282 NT 1984 33060 1.2 1.5E-02 I1418713 NT	3 8	13508		23.05	1.5E-02	8923734	ĻN	Homo sepiens transcription factor (HSA130894), mRNA
14801 27635 1.69 1.6E-02 AL161594.2 NT 15823 28467 1.6 1.5E-02 AL006216.1 NT 16824 28468 1.6 1.5E-02 AL006216.1 NT 16404 29103 0.98 1.5E-02 BF092942.1 EST JUWAN 18977 31956 1.56 1.5E-02 Q09711 SWISSPROT 19904 33060 1.2 1.5E-02 I14487282 NT 19884 33060 1.2 1.6E-02 I1418713 NT	2138	14868	27598	4.24	1.5E-02	N39521.1	T HUMAN	W27507.s1 Scarse fetal liver spleen 1NFLS Homo supiers cDNA clone IMAGE:243925 3'
15823 28467 1.6 1.5E-02 AJ008216.1 NT 16823 28468 1.6 1.5E-02 AJ008218.1 NT 16464 29103 0.98 1.5E-02 BF092942.1 EST_HUMAN 18977 31955 1.56 1.5E-02 G09711 SWISSPROT 19904 1.63 1.5E-02 T1487282 NT 19884 33060 1.2 1.5E-02 T1418713	2172	14901	27635	1.00	1.5E-02	4.2		Arabidopels thaliana DNA chromosome 4, contig fragment No. 90
16823 28468 1.6 1.5E-02 AJ008216.1 NT 16464 29103 0.98 1.5E-02 BF082942.1 EST HUMAN 18977 31955 1.56 1.5E-02 Q09711 SWISSPROT 19904 1.63 1.5E-02 11487282 NT 19884 33060 1.2 1.5E-02 1141873 NT	3057	15823	28467	1.6	1.5E-02			Homo septems CACNA1F gene, exons 1 to 48
16464 29103 0.98 1.5E-02 BF092942.1 EST_HUMAN 18977 31955 1.58 1.5E-02 009711 SWISSPROT 19904 1.63 1.5E-02 01487282 NT 11487282 NT 19984 33060 1.2 1.5E-02 11418713 NT	3067	16823	28468	1.6	1.5E-02			Homo sepiens CACNA1F gene, exons 1 to 48
18977 31955 1.56 1.6E-02 Q09711 SWISSPROT 19904 1.63 1.5E-02 11487282 NT 19984 33060 1.2 1.6E-02 11418713 NT	3711	16464	29103	96.0	1.5E-02		Г	WR4-TN0115-080800-201-b12 TN0115 Hamo sepiens cDNA
19904 1.63 1.5E-02 11487282 NT 19984 33060 1.2 1.6E-02 11418713 NT	6201	18077	31955	1.58	1.5E-02		/ISSPROT	HYPOTHETICAL CALCIUM-BINDING PROTEIN C18B11.04 IN CHROMOSOME 1
19884 33080 1.2 1.5E-02 11418713]NT	7219	19904		1.63	1.5E-02	11467282		Syanophora paradoxa cyanelle, complete genome
	7301	19984	33060	1.2	1.5E-02	11418713		formo septens KIAA 1009 protein (KIAA 1009), mRNA

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	Top Hit Descriptor Source	Homo sapiens chromosome 21 segment HS21C103	Homo sepiens vely-tRNA synthetese 2 (VARS2), mRNA	EST_HUMAN 602019135F1 NCI_CGAP_Bm67 Homo septens cDNA clone IMAGE:4154504 5	Homo eaplens kinase-related protein teoform 1 mRNA, complete cds	Seccharomyces cerevisiae chromosome VI plesmid GapC	EST_HUMAN yt64b10.r1 Soeres placents Nb2HP Homo septens cDNA clone IMAGE:133531.5	EST HUMAN (M54b10,r1 Sources placenta Nb2HP Homo septens cDNA clone IMAGE:133531 5'	Plasmodium falciperum (strain FCR3) variant-specific surface protein (var-2, var-3) genes, complete cds's	Botryas cinerea strain T4 cDNA Wherry under conditions of nitrogen deprivation	Arabidopais thallana DNA ohromosome 4, contig fragment No. 4	EST HUMAN IRC4-03/0049-140100-011-c11 CA0049 Homo senions cDNA	Г	EST_HUMAN repetitive element contains element MER28 MSR1 repetitive element;	Chlemydophila pneumoniae AR39, section 58 of 94 of the complete genome	Homo seplens NESH protein (LOC51225), mRNA	Haemophilius influenzae Rd section 115 of 163 of the complete genome	Xenopus leavis neurogenin related 1b (X-NGNR-1b) mRNA, complete cds	Homo sepiens headpin gene, complete cds	EST_HUMAN AV723785 HTB Homo sepiene CDNA done HTBAHH11 5	Bifidobactarium longum Na+/H+ antiporter (nhaß), cytosine deaminase, and alpha-galactosidase (agil.) genes, complete ods; and N-acety/glucosamine/xylose repressor protein (nag/CXx/R) gene, partial ods	EST HUMAN xb08409.xt NCL CGAP_GU1 Homo septens cDNA clone IMAGE:2575793 3'	Arabidopsis theliana DNA chromosome 4, config fragment No. 62	Arabidopsis thelians DNA chromosome 4, contig fragment No. 82	Mus musculus histocompetibility 2, complement component factor B (H2-Bf), mRNA	EST HUMAN EST374761 MAGE resequences, MAGG Homo septents aDNA		EST HUMAN 601687403F1 NIH_MGC_21 Homo septens oDNA done IMAGE:3842280 5'	EST_HUMAN 601567403F1 NIH_MGC_21 Home sapiens cDNA clone IMAGE:3842280 6'	Inf1co4.s1 NCI_CGAP_Br2 Homo sepiens cDNA clone IMAGE:1029990 3' similar to contains Alu repetitive EST_HUMAN element;
<u> </u>		ΓN	TN 6	EST	Ę	۲	EST	EST	둫	Ę	노	EST		EST	Ν	ONT	Ϋ́	Ł	١	EST	눌	EST	ż	F	노 8	EST	EST	EST	EST	EST
5	Top Hit Acession No.	1.5E-02 AL163303.2	11417739 NT	BF345554.1	AF096774.1	D44606.1	R32667.1	R32667.1	L40 6 09.1	1.5E-02 AL111238.1	1.5E-02 AL161492.2	1.5E-02 AW750834.1		AI763127.1	1.4E-02 AE002230.2	7705980 NT	U32800.1	J67779.1	1.4E-02 AF216854.1	1.4E-02 AV723786.1	1.4E-02 AF160869.2	1.4E-02 AW074212.1	4L161586.2	1.4E-02 AL161586.2	TN 8169699	4W962688.1	4W962688.1	1.4E-02 BE733142.1	1.4E-02 BE733142.1	1.4E-02 AA559030.1
-	Most Smilar (Top) Hit BLAST E Value	1.5E-02	1.5E-02	1.5E-02 BF34555	1.5E-02 AF09677	1.5E-02 D44606.	1.5E-02 R32867.	1.5E-02 R32887.	1.5E-02 L40609.	1.5E-02	1.5E-02	1.5E-02	!	1.5E-02 AI763127	1.4E-02	1.4E-02	1.4E-02 U32800.	1.4E-02 U67779.	1.4E-02	1.4E-02/	1.4E-02	1.4E-02/	1.4E-02 AL16158	1.4E-02	1.4E-02	1.4E-02 AWS628	1.4E-02 AW9628	1.4E-02	1.4E-02	1.4E-02
	Expression Signal	1.63	3.59	6.0	0.61	1.47	96'0	0.98	3.49	2.14	1.38	1.74		1.46	2.29	4.42	1.24	3.77	1.45	1.25	ื่น	1.07	6.33	6.33	8.63	7.7	77.7	7.21	7.21	5.47
	ORF SEQ ID NO:	33592	33902	34565		35251	35559	35560	37008	37109	37781					26513					28622	28805	28888	28880	29041	29817	20818	30174	30175	32079
	SEQ ID NO:	20469	20476	21421	21943	22079	22362	22362	23790	23830	24440	25214		8 8 8 8 8 8 8	13183	13854	13983	14025	14123	14263	15970	16152	16234	16234	16401	17191	17191	17552	17552	19091
	Probe SEQ ID NO:	7773	7781	8729	8986	9470	9711	9711	11121	11163	11856	12277		12787	408	1096	1234	1275	1375	1507	3207	3393	3478	3478	3648	4455	4455	4821	4821	6321

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Expression (Top) Hit Accession (Top Hit Accession Signal No. Source Source	EST_HUMAN	1.4E-02 AL022073.1 NT	0.75 1.4E-02 M81702.1 INT Candida boldinii methanol oxidase (AOD1) gene, complete cds	0.84 1.4E-02 AJZ72265.1 NT Homo seplens SPP2 gene for secreted phosphoprotein 24 precursor, excris 1-8	.1 EST_HUMAN		2.2 1.4E-02 X60459.1 NT Human IFNAR gene for interferon alpha/beta receptor	1.37 1.4E-02 AF324985.1 NT Arabidopsis theliana F21.18.2 mRNA, complete cds	426968	2 NT	2.23 1.3E-02 BF997081.1 [EST_HUMAN 602128475F1 NIH_MGC_56 Homo saplents cDNA clone IMAGE:4286203.57	2.23 1.3E-02 BF997081.1 EST_HUMAN 602120475F1 NIH_MGC_56 Home sapiens cDNA clone IMAGE:4286203 57	1.31 1.3E-02/AF169298.1 NT Mus musculus beta-sarooglycan gene, complete cds	Human garmitina T-osii receptor bela chein TCRBV17S1A11, TCRBV2S1, TCRBV2S4P, TCRBV2S4P, TCRBV2S4P, TCRBV19S1P, TCRBV19S1P, TCRBV14S1, TCRBV16S1, TCRBV15S1, TCRBV15S1, TCRBV15S1, TCRBV1SS1, TCRBV3S1, TCRBV3	1.3E-02/AL049999.2 INT finger protein 92, mmxq28orf	Z N	Homo sepiens bestic transcription factor 2 p44 (bt/2p44) gene, perties des, neuronal apoptoals inhibitory 1.3E-02 U80017.1 INT protein (natio) and survival motor neuron protein (smn) censes complete des	E	2 NT	2 NT	EST HUMAN	1.3E-02 AF156061.1 NT	1.91 1.3E-02 M63707.1 NT Mouse kidney androgen-regulated protein (KAP) gene, complete cds	1 NT	3.97 1.3E-02/AW288583.1 [EST_HUMAN xx34e03.xt Socree_NFL_T_GBC_S1 Homo septiens cDNA clone IMAGE:2815038.3"	.1 EST HUMAN
								1.37	2.36				1.31												İ	
ORF SEQ ID ID NO:	32080		34634		87 35141		37267	747	H3		171 28623		.01	30223	75 30532	75 30533	51 31816	83 31851	42 30635	42 30536	50 33244	73 34212		28 38040	93 36838	36839
D SEQ ID				53 21742			5 24528	11 24747	1 24913		l	15971	16701	17601	17975	17975	7 18851	5 18883	17942	17942	7 20150		7 22755	8 22828	3 23593	3 23593
Probe SEQ ID NO:	6321	8038	8796	9053	9300	10455	11985	12331	12601	1948	3208	3208	3951	4874	5168	5166	6072	6105	6865	6865	7477	8380	10107	10178	10913	10913

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Single Exon Probes Expressed in Brain	Top Hit Descriptor		# 1		Human herpesylrus 68, complete genome	name septens V1b vasopnessin receptor (VPR3) gene, complete cds 2785401_11 Soares milina N2h4HB User	L1 reportitive element:	HYPOTHETICAL 17.1 KD PROTEIN IN PURS ARFORDIN	qd68e12.x1 Soeres_testis_NHT Homo septens cDNA clone IMAGE:1734870.3' similar to contain 1 a fail a	repositive element;	Fromo septens chromosome 21 segment HS21 C013	AV/31/04 HTF Homo sepiens cDNA clone HTFBHG11 5	337 805 XI Sources NRL T GBC S1 Homo septems cDNA done IMAGE 265943231	3/3/609.X1 Sogres_NFL_T_GBC_S1 Homo saplens cONA clone IMAGE-2659432.3	ZNBBett3.r1 Stratagene overlan cencer (#637219) Homo sapiens c DNA cirne IMAGE Extenso at	V11508.s1 Source placenta Nb2HP Homo septens cONA clans IMAGE-138003.91	2b0807.35 Soares fetal king NbHL19W Home septens cDNA clone IMAGE:308532 3' similar to contains	SCHOOL METAL ENGINEERING	with structure of the Homo septems cDNA done INAGE:2438335 3'	Human heraditary hasmochromatosis region, histone 2A-ilike protein nama haraditary hamman	(HLA-H) gene, RoRet gene, and sodium phosphate transporter (NIPT3) gene, complete of	Cynops pyrrhogester CpUbiqT mRNA, pertial cds	AV731704 HTF Homo septems cDNA clans HTFBHG11 5	Rana rugosa mRNA for calretoulin, complete cds	nome septens when (WBSCR1) and when (WBSCR6) genes, complete cds, attenuatively spliced and	An annual Data	Muse Integrate DNA metryfransferase (Drintt) gene, excris 2, 3, 4, and 5	LICATION CONTROL DIACONTAIN NOZIP Homo explens cONA cione IMAGE:16069531	AV 32/38 H I F Hamo sapiens cDNA clone HTFBJC09 6	CMP-NACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2-3-SIAI Y1 TRANSFEDASE / PETA-	GALACTOSIDE ALPHA-2,3 SIALYLTRANSFERASE) (ALPHA 2,3-ST) (GAL-NACSS) (GAL-BETA-1,3	HOWEN CHALLING THE AND FERASE) (ST3GALA, 2) (SIATA-B)	Homo septents fringe protein mRNA, partial cds Homo septents fringe protein mRNA, partial cds
gle Exon Probe	Top Hit Database	-					EST_HUMAN L1			TSI HUMAN 100	Т	Т	NOMAIN.	Т	Т	EST_HUMAN y11		FOT LINAM	_				HOMAN				T HISMAN	7	EST HIMAN AV	7-	SWISSPROT CALL		
Sing	Top Hit Acession No.	:	-	0803000	2.4		90.1		_	1	1 2E-02 AV724704 4	Ţ	Ţ	1		1	•						_	N N N N N N N N N N N N N N N N N N N	F046556.1 NT	_			-				
	Most Similar (Top) Hit BLAST E	Value	1.3E-02 Z99117.	135-02	13E-02 AE4E929		126-02	1.2E-02 P38898	1.2F-02 A148382	1.2F.021	1 25-02/	1.2E-02/	1 25.00	125.02	1 2F (2) De200 F	7	1.2E-02 Ale68694	1.2E-02 AISB7378		1 2E_021 (64228 4	1 25-02	1 2F-02 AV721704	1 OF 02 79580 4		1.2E-02 AF045556.	1.2E-02 AF175412	1.2E-02 H02197.1	1.2E-02 AV732003	1.2E-02 BF218650		1.2E-02 Q11205	1.2E-02 AF193812.	1.2E-02 AF193612
	Expression Signal		<u>.</u>	2.41	28.18		348	1.88	2.02	1.81	17.	1.30	1.07	6.88	2.1		0.82	0.91		2.03	1.13	141	1.73		0.72	6.46	1.38	10.54	0.57		2.18	1.35	1.36
	ORF SEQ ID NO:					O. L.	20/02	500C7	26148	27637	27640	27901	27901		28601	-	28694	30045		30211		30358	31375	-	31767	32691	32952	32972	33222		33722	33917	339/18
	Exam SEQ ID NO:		1	24807	25145	42445		RASS	13405	14904	14907	15163	15163	15863	16042		18045	17409		17588	17704	17748	18461	-	18806	200	19878	19897	20130		20591	20786	20788
	Probe SEQ ID NO:	10001	3	12437	12607	245	9		721	2175	2178	2444	2842	960g	3281		3284	66/5		4859	4981	6025	2000		8238		7192	7212	7458	_	- 1	. 1	8082

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ORF SEQ Expression (Top) Hit Top Hit Accession ID NO: Signal BLASTE No. Source Source		35376 2.46	35408 1.35 1.2E-02 AJ246003.1 NT	31112 2.88 1.2E-02 015534 SWISSPROT	8.02 1.2E-02 C18119.1 EST_HUMAN	28682 1.49 1.1E-02 AA070384.1 EST_HUMAN	27143 1.36 1.1E-02\X75491.1 NT	27144 1.35 1.1E-02 X75491.1 NT	27495 4.92 1.1E-02 BF345283.1 EST_HUMAN	4.06 1.1E-02 N99623.1 EST_HUMAN	2892 11E-02 Aless508 1 FST HIMAN	0.86 1.1E-02 AW813798.1 EST HUMAN	30132 1.5 1.1E-02/AL048383.2 EST HUMAN	1.1E-02 U66480.1 NT (/met-), Ynal (ynac), Xian beta-1,4-xiosb 1.1E-02 U66480.1 NT (/met-), Ynal (ynac), Xian beta-1,4-xiosb	33261 2.51 1.1E-02 BE149611.1 EST_HUMAN	34372 0.91 1.1E-02 AW998160.1 EST_HUMAN	34556 0.67 1.1E-02 CO4803.1 EST_HUMAN	34639 6.45 1.1E-02 Q61982 SWISSPROT	35682 2.03 1.1E-02 AA082578.1 EST HUMAN	35854 3.55 1.1E-02 AA314095.1 EST HUMAN	· 36830 3.23 1.1E-02 11435505 NT	TOTAL TOCOGRAPT OF STREET	1.10	25448 0 48 4 0E 02 (MO48450 4 EST UTILIANI	28948 1.58 1.0E-02 AW388128.1 EST HILMAN	1.57 1.0F-0.2 AAROPTOR 1 FST HIMAN	28494 27 1.0E-02 BE83558.1 EST HUMAN	28869 1.49 1.0E-02 BE968989.1 EST_HUMAN	29250 0.79 1.0E-02 A1065086.1 EST_HUMAN	
1														31799	33261			34639					1	25448	28948		28494	28869	29250	
Exen D SEQ ID NO:	38 21480	39 22/92		34 24559		13905		14444		15847	3 16269	ı	17510	18837	20169	8 21230		0 21492		4 22842		78776	1.		1	L	L	7 16019	16611	
Probe SEQ ID NO:	8788	950	9570	12034	12615	1246	1701	1701	2031	2880	3513	4086	4778	6057	7497	8538	8721	8800	9829	9894	10900	41022	1267B		1613	2577	3087	3257	3861	

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There Explicated III Digiti	Top Hit Descriptor	MR1-ST0111-111199-011-h06 ST0111 Homo saniens cDNA	Cempylobacter leiuni NCTC1168 complete genome: segment 2/6	Mus musculus fusion 2 (human) (Fue2) mRNA	QV1-BT0677-040400-131-003 BT0677 Homo serolens cDNA	601475619F1 NIH MGC_68 Hamo sepiens cDNA clane IMAGE:3878405 5	S.cerevisies chromosome X reading frame ORF YJR(52w	Homo septens melenome-associated antigen (MAGE-C1) gene, controlete cds	2832611.rl Soeres retina N254HR Homo septens CDNA clone IMAGE:360748 61	802013941F1 NCI CGAP Bm84 Homo seciens cDNA done IMAGE 4149418 5	Oryctolegus cuniculus elF-2a kinase mRNA, complete ods	Homo supiens ABCG1 gene for ABC transporter (ATP-binding cassette, sub-family G (WHITE), member 1),	complete cds	Cryptosportdium pervum HC-10 gene, complete ods	Cryptosporklium pervum HC-10 gene, complete cds	Glycine max glutathione S-transforase GST 21 mRNA, partial cos	AV731712 HTF Homo septems cDNA clone HTFAZF10 5	FORKHEAD BOX PROTEIN D3 (HNF3/FH TRANSCRIPTION FACTOR GENESIS) (HEPATOCYTE NUCLEAR FACTOR 3 FORKHEAD HOMIOLOG 3/ HFH-3/	ab/3909.s1 Stratagene fetal retine 83/202 Home seniens cDNA close tMACE 883448 31	XX21b02X1 Soares NFL T GBC S1 Homo sablens clave IMA clone IMAGE-2813730 31	EST362626 MAGE resequences, MAGA Homo septens cDNA	EST362626 MAGE recequences, MAGA Homo sepiens cDNA	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR	q/34h/2.x/ Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1751955 3'	UI-H-BI3-eld-c-10-0-UI.s1 NCI_CGAP_Sub5 Homo sepiens cDNA cione IMAGE:2733691 31	Rathis normanifyie passonal nicolinia acceptations accessed a second (Alberta Normaniform)	UI-HBIG-ekb-c-10-0-11 s1 NC1 CGAD Subst Home entone china Acres 144 ACC 2020 202	hh89a05 of NCI CGAP GITH Home series of DNA close MAGE response in	Homo saciens chromosome 21 segment HS210078	y82g01.r1 Soares fetal liver splean 1NFLS Homo septens cDNA clone IMAGE:211824 5' similar to	RCI-CT0286-050400-018-c03 CT0286 Home services china	2d33f10.r1 Soares_fetal_heart_NbHH19W Home explene cONA clone IMAGE:342475 5
	Top Hit Detabase Source	EST HUMAN	NT	NT	EST HUMAN	EST HUMAN	\ \ \	۲	EST HUMAN	EST HUMAN	NT		Į.	LN.	LNT.	ĹΝ	EST HUMAN	SWISSPROT	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	SWISSPROT	EST_HUMAN	EST_HUMAN	5	EST HUMAN	EST HUMAN		COT LIBRARY	Т	17
	Top Hit Acession No.	AW 808692.1	AL139075.2	9789956 NT	8.0E-03 BE080509.1	BE788441.1	8.0E-03 Z49652.1		8.0E-03 AA016180.1	8.0E-03 BF342438.1	8.0E-03 M59035.1		161.1		7.0E-03 AF097183.1		7.0E-03 AV7317121		288.1	599.1	566.1			73.1	463.1	7.0E-03 AF196344.1		Ī	Γ		059.1	
	Most Similar (Top) Hit BLAST E Value	8.0E-03 AW80	8.0E-03 AL139	8.0E-03	8.0E-03	8.0E-03 BE788	8.0E-03	8.0E-03	8.0E-03	8.0E-03	8.0E-03		8.0E-03	7.0E-03 AF097	7.0E-03/	7.0E-03 /	7.0E-03/	7.0E-03 Q61060	7.0E-03	7.0E-03 AW303	7.0E-03	7.0E-03	7.0E-03 P04929	7.0E-03 A11502	7.0E-03 AW444	7.0E-03	7.0E-03/A	7.0E-031A	7.0E-03 A	7 01103	7.0E-03 AW861	7.0E-03 W68251.1
	Expression Signal	3.29	0.48	0.58	4.03	1.36	3.58	4.74	22.71	1.36	1.74		1.74	16.15	16.15	3.57	3.48	2.67	6.71	3.37	1.24	1.24	1.86	0.71	0.8	1.32	0.83	124	217	0.75	4.9	1.47
	ORF SEQ ID NO:	34646				36597		37632		37779				26098	20097	26387	28511	<u> </u>	78782	20024	27175	27178	27722	28951	20137	28,173	29137					31972
	Exen SEQ ID NO:	21500	L.	21569				_ 1	24402	24437	24401		200	25	13 <u>8</u> 8	13721	13852	14091	14122	14238	14477	14477	15589	16301	16502	10544	18502	17296	17857	18521	25083	18996
	Probe SEQ ID NO:	8088	8816	8878	9848	1000	10006	11715	11814	11853	11933	7,000	200	8/8	878	92 92	ğ	1343	1374	1491	1735	1735	752	38.46	3740	3792	4000	4560	4929	62.29	9021	6222

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+				,		
Probe E SEQ ID SE NO:	Exan SEQ ID NO:	SEQ Expression O: Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Detabase Source	Top Hit Descriptor
3377	16136 28	28794 1.18		6.0F-03 1.190880 1	<u> </u>	Fugu rubripes zinc finger protein, lectocin, fatty acid binding protein, sepiapterin reductase and vasotocin
L		:	ļ	6.0E-03 W37985.1	EST HUMAN	25/3a/1.r/ Source, perethyroid, tumor, NBHPA Homo sepiens cONA clone IMAGE:322/72 6
	16405 29	29044 3.68		8.0E-03 BF510988.1	EST HUMAN	UI-H-BI4-epm->-06-0-UI.s1 NCI_CGAP_Sub8 Homo sepiens cDNA clone MAGE:30877543'
		29079 1.08		6.0E-03 BE077356.1	EST_HUMAN	RC1-BT0606-280400-014-e07 BT0606 Homo septems cDNA
		25/147 1.22	2 6:0E-03	6754029 NT	LX.	Mus musculus glucosamine 8-phosphate deaminase (Gnpi), mRNA
	16852 29	29294 0.78		6.0E-03 AW847284.1	EST_HUMAN	RC0-CT0204-240999-021-b10 CT0204 Homo septens oDNA
3938 1	10688	1.28	L	6.0E-03 BE250108.1	EST HUMAN	800942804F1 NIH MGC 15 Hano septens cDNA clane IMAGE:2959513 5
		1.84		6.0E-03 AI016833.1	EST_HUMAN	0x33c11.x1 Soares_tests_NHT Homo saplens cDNA clone IMAGE:16391243'
	17381 30	30013 5.67	L	6.0E-03 AA324242.1	EST HUMAN	EST27116 Carebellum II Hamo sepiens cDNA 5' end similar to EST containing Alu repeat
5073 1				062209	SWISSPROT	SYNAPTONEMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN)
	25084 31			9627521 NT	N	Vericla virus, complete genome
		32876 1.16	6.0E-03 014994	014994	SWISSPROT	SYNAPSIN III
	17924 30	30559 0.57		6.0E-03 BE253748.1	EST_HUMAN	601112353F1 NIH_MGC_16 Hamo septens cDNA clane IMAGE:3353172 5
		32905 0.61		6.0E-03 AA299442.1	EST_HUMAN	EST11949 Uterus fumor I Homo septiens cDNA 5' end
		32906 0.81	L	8.0E-03 AA290442.1	EST HUMAN	EST11949 Uterus fumor I Homo eaplens cDNA 5' end
		33318 0.69		6.0E-03 AF128894.1	F	Homo saplens blomerase reverse transcriptase (TERT) gene, excris 7-16 and complete cds
7702 2	20365 33	33479 0.62	2 6.0E-03 P17964	P17964	SWISSPROT	RAS-RELATED PROTEIN RAP-28
7767	20453 33	33578 6.9		6.0E-03 AI033980.1	EST HUMAN	ow13e04.x1 Soares, perathyrold_tumor_NBHPA Homo sepiens cDNA clone INAGE:1646670 3' struiter to contains MER10.b1 MER10 repetitive element:
	20509 334	33685 2.17		6.0E-03 AW799337.1	EST_HUMAN	RC0-UM0051-210300-032-g02 UM0051 Homo saplens cDNA
	20840	1.58		6.0E-03 BF038198.1	EST_HUMAN	801454915F1 NIH_MGC_86 Hamp sepiens cDNA clone IMAGE:3858826 5'
9454 2	22004 35	35178 7.28		6.0E-03 D10548.1		Subscute scienceing penencephalitis (SSPE) virus mRNA for fusion protein
9943	22591	213		6.0E-03 A/432661.1	EST HUMAN	122022x1 NG_CGAP_KIG11 Homo septens CDNA clone IMAGE:2131202 3' similer to SW:R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN 113A ·
		35928 0.86	L	6.0E-03 AJ011849.1	N LX	Bacillus subtilis fenD gene
10194 2	22842	1.14		6.0E-03 AF084665 1	L	Homo septens cleadatc acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete cds.
10304		36166 0.59				M.fbermoformicicum complete plesmid pPV1 DNA
10645 2	23336 36	36575 1.75		7	EST HUMAN	EST374237 MAGE resequences, MAGG Homo septens cDNA
10713 2	23402	254		11545814 NT		Homo septens hypothetical zino finger protein FLJ14011 (FLJ14011), mRNA
10750 2	23435 364	36680 1.26		6.0E-03 AI420786.1	EST HUMAN	tegrat2xrt NCI_CGAP_Pr28 Homo septens cDNA clone IMAGE:2084070 3' similar to TR:000519 000519 FATTY ACID AMIDE HYDROLASE
					1	

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Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5963	18735	31694	2.97	5.0E-03	5.0E-03.000507	SWISSPROT	PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-Y (UBIQUITIN THIOLESTERASE FAF-Y) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF-Y) (DEUBIQUITIN-SPECIFIC PROTEIN RELATED, Y-LINKED) (UBIQUITIN-SPECIFIC PROTEASE 9, Y CHROMOSOME)
5968	18709		16.0	5.0E-03	5.0E-03 AE002234.2	LN	Chlamycohila presimoniae AR30 seeffon 82 of 64 of the complete seems
6499			7.58	5.0E-03	ľ	EST HUMAN	80094456471 NIH MGC 17 Homo septens cONA clone IMAGE: 2008443
6746		30678	7.45	5.0E-03		본	Mus musculus AMD1 gene for 3-adenosymethicning decarbondese, complete one
98	19422		0.64	5.0E-03		LN	Turstops truncatus mRNA for p40-phox, complete cds
7385	20065	33143	57.0	5.0E-03	5.0E-03 T05124.1	EST HIMAN	EST03012 Fetal brain, Stratagene (cet#636206) Homo sapiens cDNA clone HFBCR93 similar to EST
7498	20170		1.21	5.0E-03	5.0E-03 AW854327.1	EST HUMAN	RC3-CT0255-031099-011-077 CT0245 Home seniors ADNA
7867	20331	33442	7.5	5.0E-03	5.0E-03 AB016816.1	Į.	Homo seriens MASI 1 mRNA complete cde
8119	20813	33948	0.48	5.0E-03	5.0E-03 AW855907.1	EST HUMAN	ROS-CT0281-081199-0-11-406 CT0281 Homo services chas
8119	20813	33949	0.48	5.0E-03	5.0E-03 AW855907.1	EST HUMAN	ROS-C10281-081199-011-405 C10281 Homo embre chiva
8137	20831	33965	3.20	5.0E-03 P48982		SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
8500			5.63	5.0E-03	5.0E-03 M61132.1	L	Mouse complement receptor (CR2) mRNA, 3' and
8708	ŀ	34545	1.04	5.0E-03	5.0E-03 D90723.1	N	Escherichia coll genomic DNA, (19.1 - 19.4 min)
8838	ı	34676	0.71	5.0E-03 M25090.	1	N	Rabbit uteroglobin (UGL) gene, exm 1
2482		35315	0.45	5.0E-03 P33750		SWISSPROT	SOF1 PROTEIN
9739	- 1	35595	0.89	5.0E-03	5.0E-03 1.21710.1	NT	Plasmodium berghet 58 kDa phosohoprotein mRNA partial cols
9871	22521	35716	0.7	5.0E-03	5.0E-03 AW821888.1	EST HUMAN	RC0-ST0379-210100-032-c02 ST0379 Homo semiens cDNA
10057	22705	35923	0.45	5.0E-03	5.0E-03 AA533143.1	EST HUMAN	ny48h10.s1 NCI_CGAP_Pro Homo septems dDNA dame IMAGE:885587
10231	22878	36091	0.51	5.0E-03	7882557 NT		Homo sepiens PR00471 protein (PR00471), mRNA
10377	23023		0.48	5.0E-03.	1.1	EST_HUMAN	8g49c10.s1 Gessler Wilms turnor Homo saplens cDNA clone IMAGE:1128200 3'
1062	23314		4.90	5.0E-03	5.0E-03 T19586.1	EST_HUMAN	604F Heart Homo septens cDNA clone 694
10859	23539	36785	3.42	5 OF A3	5 OF-M3 AW170334 1	MAN ILLENAN	xn59g05x1 3oares_NHCeC_cervical_turnor Homo saplens cDNA clone IMAGE:2698040 3' similar to
40060	00000				Τ	T	An 50005X1 Scenes_NHCeC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to
3	2000	8/8	3.47	3.0E-03.	4.1		contains L1.t2 L1 repetitive element;
10971	23647	36900	1.89	5.0E-03 T49153.1		EST_HUMAN	yb08e04.r1 Stratagene placenta (#837225) Homo saplens cDNA clone INA GE-70000 sr
11021	23683	30956	1.47	5.0E-03	946753		Mus musculus hypothetical protein, MNCb-4780 (LOC58212), mRNA
33	23062	1	3.54	5.0E-03			1248c04.y1 NCI_CGAP_Bm62 Homo sepiens cDNA done IMAGE:2281622 5
12774	24366	37697	1.53	5.0E-03		토	Mus musculus genomic fragment, 279 Kb, chromosome 7
11774	24305	37698	1.83	5.0E-03	5.0E-03 AJ275505.1		Mus musculus genomic fragment, 279 Kb, chromosome 7

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טווקום באטור רוטמס באף פספט ווו ביומווו	Top Hit Databese Top Hit Descriptor Source	Gellus gallus giyceraldehyde-3-phosphate dehydrogenase mRNA, complete cds	Brugia meley V chromosome marker	Human pro-eighart type if collagen (COL2A1) gene exons 1-54, complete cds	2075a03.s1 Source overy tumor NbHOT Home expiens cDNA done MAGE:809648 3' similar to SW:DXA2 MOUSE P14886 PROBABLE DIPHENOL OXIDASE A2 COMPONENT:	HUMAN	HUMAN	SWISSPROT COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LO COLLAGEN)	EST_HUMAN UI-HE-BNO-Bic-h-04-0-UI. 11 NIH_MGC_60 Homo sepiens oDNA clane IMAGE:3078831 5	EST_HUMAN yg51604.s1 Soeres Infant brain 1NIB Homo sepiens cDNA done IMAGE:35988.3	Т	Γ	Π	Г	П	EST_HUMAN 2259801.11 NC_OGAP_GC81 Homo septens aDNA drone IMAGE:701736 5	EST_HUMAN AV708305 ADC Homo septens cDNA done ADCAKB06 51	Rattus norvegicus type 1 astrocyte and offactory-limbic associated protein AT1-48 inRNA, complete cds	EST HUMAN 1281s08.11 Strategene colon (#037204) Homo sapiens cDNA clone IMAGE:510908 6'	1	EST_HUMAN ROS-UM0014-170400-023-G01 UM0014 Homo sepiens cDNA		Homo septens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSF9), ribosomal probleh L18a (RPL18a), Ca2+/Calmodulin-dependent probleh kinase i (CAMKI), creatine transporter (CRTR), CDM protein (CDM, protein (CDM, protein (CDM), adrendes accordances problem.	Homo septems polygrutamine-containing C140RF4 gene	Homo sepiens polygitatemine-containing C140RF4 gene	Hamo sepiens chromosome 21 segment HS210084			EST_HUMAN 1/199704.x/ NCL_CGAP_Co18 Hamo septems aDNA clane IMAGE:2885279 31
5 -		눌	Ę	호	EST	EST	133 T	SIMS	EST	EST	EST	EST	EST	EST	EST.	EST	EST	눌	EST	띪	EST	Z	ż	ż	E	호	EST	EST	EST
5	Top Hit Acession No.	AF047874.1	5.0E-03 AF067253.1	L10347.1	5.0E-03 AA456597.1	5.0E-03 BF572332.1	AW449109.1		AW500196.1	R46482.1	4.0E-03 AAg3g339.1	R46482.1	AW749101.1	AA090777.1	4.0E-03 AW794740.1	4.0E-03 AA284374.1	4.0E-03 AV708305.1	J33472.1	AA000777.1	BE410556.1	4.0E-03 AW794740.1	J52111.2	J82111.2	4.0E-03 AJZ77365.1	4.0E-03 AJZ77385.1	AL 163284.2	4.0E-03 BE154134.1	4.0E-03 BE154134.1	4.0E-03 AW 188426.1
	Most Similar (Top) Hit BLAST E Value	5.0E-03 AF04787	5.0E-03	5.0E-03 L10347.1	5.0E-03	5.0E-03	5.0E-03 AW4491	5.0E-03 Q02388	4.0E-03 AW5001	4.0E-03 R46482.	4.0E-03	4.0E-03 R46482.	4.0E-03 AW7491	4.0E-03 AA09077	4.0E-03	4.0E-03	4.0E-03	4.0E-03 U33472	4.0E-03 AA00077	4.0E-03 BE41055	4.0E-03	.4.0E-03 U52111.2	4.0E-03 U62111.2	4.0E-03/	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03/
	Expression Signal	97.6	4.11	2.52	1.67	2.78	4.2	1.78	2.98	220	2.60	2.03	4.04	29.46	2.4	1.57	1.52	2.23	10.56	2.40	1.64	1.97	1.97	8	9	1.41	1.18	1.16	0.97
	ORF SEQ ID NO:						30980		25875	25755	25997	26298		26544	26563	26699		27178	27474		27742	28030	28031	28140	28141	28144	28634	28635	28831
	SEQ ID NO:	25367	24731	24792	24811	25183	24940	25253	13038	13117	13360	13626	13660	13884	13901	14030	14327	14479	14748	14972	15002	15283	15283	15405	15405	15409	15982	15982	16277
	Probe SEQ ID NO:	12176	12307	12409	12441	12467	12643	12662	226	313	289	857	891	1128	1148	1280	1581	1737	2011	2244	2276	2578	2579	2898	2888	2701	3219	3210	3521

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Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similer (Top) Hit BLAST E Value	Top Hit Acesslon No.	Top Hit Database Source	Top Hit Descriptor
3621	16277	28832	76.0	4.0E-03	4.0E-03 AW 188426.1	EST HUMAN	x98f04.x1 NCI CGAP Co18 Hamp sepiens cDNA dane IMAGE 2005279.3
3812	16385		0.73	4.0E-03 Q13806		SWISSPROT	OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OF F1)
3909	16659	28300		4.0E-03	4.0E-03 AF060868.1	Į.	Mus musculus tumor susceptibility protein 101 (ted 101) gene, complete cds
3977	16725		1.95	4.0E-03	4.0E-03 AJ011712.1	F	Homo saplens TNNT1 gene, exans 1-11 (and joined CDS)
5057	17778	SESSE	20'0	4.0E-03	4.0E-03 AW103719.1	EST HUMAN	xe83d03.x1 NCI_CGAP_Bm35 Homo sepiens cDNA clone IMAGE:2614469 3' similer to contains L1.t1 L1 L1 receitive element:
5114	17832		76.0	4.0E-03	8.1	EST HUMAN	ae/3a65.s1 Strategore schizo brain S11 Homo sepiens cDNA clone IMAGE:999776.3
5194	18002	30625	1.8	4.0E-03		1×	Drosophila melanogaster aron207 (aron207) mRNA, correlete cds
5314	18118	30774	23.91	4.0E-03		NT	Raftus nonegicus beta-caterin binding protein mRNA, complete ods
5705	18400	31421	2.48	4.0E-03 P04196	P04196	SWISSPROT	(HPRG)
2708	18502	31423	1.74	4.0E-03 P21849	P21849	SWISSPROT	MAJOR SURFACE-LABELED TROPHOZOITE ANTIGEN PRECURSOR
5782	18583	31510	0.88	4.0E-03 AL 13387	AL133871.1	EST HUMAN	DKFZp78111014_r1 761 (synonym: hamy2) Homo eaplene cDNA clone DKFZp78111014.5
5983			4.11	4.0E-03 U22180.	U22180.1	Ľ	Retitus norvegicus opein gene, complete cds
6140	18918	31888	0.95	4.0E-03 AW5805	72.1	EST HUMAN	hg40c07.x1 NCI_CGAP_GC0 Hamo sepiens cDNA clone IMAGE: 2948652 3
6217	18991	31967	1.6	4.0E-03		EST HUMAN	601076015F1 NIH_MGC_12 Hamo sepiens cDNA clane IMAGE:3481954 51
6572		32347	1.28	4.0E-03	4.0E-03 AA813222.1	EST HUMAN	aj32/11.s1 Scares teetts NHT Homo septens cDNA clone 1392045 3'
6877	19594	32632	1.01	4.0E-03 U76408.1		N	Lycopersicon eaculentum knotted 3 protein (TKn3) mRNA, complete cds
0200		32470	66.0	4.0E-03 AL 16327	32	M	Homo sepiens chromosome 21 segment HS21C078
0200	19452	32471	0.99	4.0E-03 AL 16327	8.2	N	Homo sepiens chromosome 21 segment HS21C078
2098	19787	32851	3.5	4.0E-03 Q02817		SWISSPROT	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)
7331	20013	33091	1.23	4.0E-03/	4.0E-03 AI681483.1	L	537g12x1 NCI CGAP Lu24 Homo serviens cDNA clone IMAGE:2271814.3
7333		33083	0.78	4.0E-03	4.0E-03 BE670170.1	П	7e31b02x1 NCI_CGAP_Lu24 Homo septens cDNA clone IMAGE:3284043 3'
7424	20101		0.74	4.0E-03 X92109.1		Γ	H.sapiens hogIX gene
7843	20538	33685	- C	4 OF 03 COTTOS		TOGOSSIMS	ADAM-TS 6 (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5)
242	20842	33787	5.45	4 0E-03 AE11104	-	Т	(ALAMITEA) (ALAMITEA) (AGALCANASE-2) (ALAMITE-2) (ALAMITE)
8103	20797	33928	208	4 0F-03	7882087	Į.	Progression in monoconson provincial process to the Control of the parties of the Control of the
į							te49b11.x1 Soares_NFL_T_GBC_S1 Home septens cDNA clone IMAGE:2090013.3' similar to contains Alu
4100	200	34448	86.98	4.0E-03 AI553983		T HUMAN	repolitive element
9/8/	21473		4.25	4.0E-03 AL 163209	2		Homo sepiens chromosome 21 segment HS21C009
8797	24 88 88	34635	297	4.0E-03 AL.163278	2	INT	Homo sepiens chromosome 21 segment HS210078
8827	2478	35670	0.67	4.0E-03 H30664.1		EST_HUMAN	yp42g12.r1 Scenes retina N2b5HR Hamo seplens cDNA clone IMAGE:190150 5
10275	22823	36135	1.3	4.0E-03 AL161550	[2		Arabidopsis thallana DNA chromosome 4, contig fragment No. 55
10468	23112		0.45	4.0E-03 AL163281	2	L L	Homo seplens chromosome 21 segment HS21C081

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Top Hit Descriptor	Homo seplens chromosome 21 segment HS21C006	Uresplasma urealyticum section 3 of 59 of the complete genome	PM4-BN0138-180600-002-b08 BN0138 Homo sapiens cONA	801118164F1 NIH_MGC_17 Hano sepiens cDNA dane IMAGE:3028085 5'	UI-HF-BN0-alp-g-04-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080622 5	7q74c00x1 NCI_CGAP_Lu24 Home saplens cDNA clone IMAGE: 3' similar to contains Alu repetitive element contains element MER31 repetitive element.	thr02c07.x1 NCI_CGAP_KId11 Homo sepiens cDNA done IMAGE:2953932.3' similar to contains element	LTR5 repetitive element;	Homo seplens Grb2-essociated binder 2 (KIAA0571), mRNA	Homo sapiens protein kinase CK2 catalytic suburit alpha gene, expn 1	Homo seplens protein khase CK2 catalytic subunit alpha gene, expn 1	nc73c05.s1 NCI_CGAP_Pr2 Home suplens cDNA clone IMACE:782984 similar to contains Alu repetitive element:	Hamo septens MHC class 1 region	S.cereale (cv. Halo) mRNA for triceschosphate isomerase	Mus musculus intestinal trefoil factor gene, pertial cds	Mus musculus intestinal trefol factor gene, partial cds	601237362F1 NIH_MGC_44 Hamo septens cDNA clone IMAGE:3809633 5	IL2-UN0076-240300-056-D03 UM0076 Homo sepiens cDNA	Mus musculus alpha-1(XVIII) collegen (COL18A1) gene, excn 1 and 2	Celegane samdo gene	AV762392 MDS Hamo saplens aDNA clane MDSBSG01 5"	IV762392 MDS Homo sepiens cDNA clone MDSBSG01 5	ar04f09.y5 Gessler Wilms tumor Homo septens cDNA clone IMAGE:1155699 5:	S.cereate (ov. Hato) mRNA for tricesphosphate isomerase	Rattus novegicus gdnf gene	ht68g08.x1 NCI_CGAP_Lu24 Homo sepiens cDNA done IMAGE:3151934.3'	xu8.Pf0.H3 conorm Homo eaplens oDNA 3'	ab18e0835 Stratagene lung (#637210) Homo saplens cDNA clone IMAGE:841142 3' similar to contains Alu	repolitive element,	601482715F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885483 5	Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA	Mus musculus mRNA for hypothetical protein (ORF2 ortholog)
Top Hit Detabase Source	¥	N.	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HIMAN	Π	EST_HUMAN		LN	Z	EST HUMAN	T				Г	EST_HUMAN			EST_HUMAN	Г		LN L	1	1	EST HUMAN	$\overline{}$	HUMAN	T_HUMAN		LN
Top Hit Acession No.		2.1	4.0E-03 BE815173.1	4.0E-03 BE288280.1	4.0E-03 AW504273.1	4 0F-03 BF224125.1		4.0E-03 AW614596.1	11436956 NT	3.0E-03 AF011920.1	3.0E-03 AF011920.1	3.0E-03 AA488110.1	: :				Γ	3.0E-03 AW802887.1			3.0E-03 AV782392.1	2.1	1		3.0E-03 AJ011432.1	2	T-		1	3.0E-03 BE787945.1	8922499 NT	-
Most Similar (Top) Hit BLAST E Value	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.0E-03	4.05-03		4.0E-03	4.0E-03	3.0E-03	3.0E-03	3.05-03	3.0E-63	3.0E-03 Z32521.1	3.0E-03 U46858.1	3.0E-03 U46858.1	3.0E-03	3.0E-03	3.0E-03 U34806.1	3.0E-03 Y12500.1	3.0E-03/	3.0E-03 AV762392	3.0E-03 AI 7922 78	3.0E-03 Z32521.1	3.0E-03 /	3.0E-03	3.0E-03 AI536141		3.0E-03 AI732754	3.0E-03	3.0E-03	3.0E-03 AJ249981
Expression Signal	4.09	1.82	1.78	2.38	227	3.41		2.08	217	2.38	5.37	3.35	1.38	8.44	1.09	1.09	3.31	2.52	1.72	5.97	6.97	6.97	1.35	1	5.63	0.73	4.97		238	7.94	3.96	1,98
ORF SEQ ID NO:	37017	37700							30956	25803	26299	27091			27753	27754	28488	28557	28819		28348	28349	20300		29737		29844		30138	30156	30508	31159
SEQ ID NO:	Ш		25385		24694	24841	L_	25283	25048	13160	13628	14403	L	15017	15018	L	15846			16177	16708	16708	16762	16872	17102	17164	17217		17514	17533	17892	18287
Probe SEQ 17 NO:	11074	11777	12147	12167	12246	12480		12521	12801	362	859	1857	2255	2282	2283	2283	3081	3140	3412	3420	3959	3958	4016	4130	4364	4428	4482		4782	4802	5184	2468

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Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similer (Top) Hit BLASTE Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5539	18337	31244	96.0	3.0E-03	3.0E-03 U35323.1	Ę	Mus musculus H2-M alpha chain (H2-Ma) gene, H2-M beta 2 chain (H2-Mb2) gene, H2-M beta 1 chain (H2-Mb1) cene, low molecular weight probain 2 i mn3 i mn3 mana complete alle
6458	19225		11.75	3.0E-03	3.0E-03 AA456701.1	EST HUMAN	88/3/10.1 Sogree NHHWPU SI Home serviens CDNA clare IMAGE 813/63 5
7104		32857	1.38	3.0E-03	3.0E-03 AJ011419.1	Į.	Kluweromyces merdanus bool3 gene for butthe cyloshe nameses
7422			3.64	3.0E-03	3.0E-03 AB021736.1	Į.N	Oryze sethe gene for bZIP protein, complete cds
7839	1	33661	0.82	3.0E-03	3.0E-03 BF333058.1	EST HUMAN	RC0-BT0812-250900-032-e07 BT0812 Homo sections cDNA
7830			0.82	3.0E-03	3.0E-03 BF333058.1	EST HUMAN	RC0-BT0812-250900-032-e07 BT0812 Homo serdens c/DNA
8056		33881	1.54	3.0E-03	3.0E-03 N92580.1	EST HUMAN	2027004.81 Source parathyroid tumor NbHPA Homo seniene cONA clone IMACE ANATRA 3
8214	20908		0.51	3.0E-03	3.0E-03 M63408.1	Ž	S.cerwikiae UGA35 gene, complete cds
8360		34194	1.32	3.0E-03 P51989	P51989	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2/A))
88		34213	1.47	3.0E-03	3.0E-03 AL163268.2	Ę	Homo sepiens chromosome 21 segment HS21C068
8485	21177		1.20	3.0E-03	3.0E-03 Q9QM81	SWISSPROT	NONSTRUCTURAL PROTEIN V
0688	21581	-	11.08	3 0E-03 AWR137	AW#13774.1	NAMI II TAT	hh80f10xt NCI_CGAP_GU1 Homo seplens dONA done IMAGE:2869131 3' similer to contains L1.t1 L1
8943		34778	4.01	3.0E-03	3.0E-03 AL 161589.2	LN.	Arabidopais fraillana DNA chromosome 4 confinitement No. 85
7968	21657	34808	0.44	3.0E-03	3.0E-03 Al016731.1	FST HIMAN	ov03d12.x1 NCI_CGAP_Kld3 Homo seplens dDNA clone IMAGE:1636247 3' similar to gb:X57138_ma1 HISTONE H2R 2 (HI MAN):
8977		34817	67.0	3.0E-03 BF33807	BF338078.1	Т	602035980F1 NCI CGAP Bm64 Homo emplene cDNA clone IMACE-4193039 R
6026	21978		0.83	3.0E-03 D90901.1	D90901.1	Т	Synechocystle sp. PCO8803 complete persons, 3/27, 271600, 4/2280
8347		33538	0.83	3.0E-03 BE15467	BE154670.1	EST HUMAN	PM3-HT0344-071299-003-d07 HT0344 Home seciens cDNA
8536	22189		0.54	3.0E-03 P03355	P03355	Т	POL POLYPROTEIN ICONTAINS: PROTEASE: REVERSE TRANSCRIPTASE - RIRONI 12 EASE IL 1
9000	22259		3.88	3.0E-03 P08672	P08672	П	CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
9795	22448	35051		3 0F-03 P11340	244340	SWISSBOT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE;
9886	22546	35740	120	3.0E-03 P51989	P51989	Т	HETEROGENEOUS NIIO EAR RIBONI IO EORDOTEN AS HOLLY ON A LUNDAD AND
10040	22688	36908	3.07	3.0E-03/	AL163303.2	T	Hamp sections of programmer HS2/CAAs
10762	23437		4.0	3.0E-03			Homo secions ATP/GTP-binden protein (HEAB) mRNA
11137	20099	33187	2.05	3.0E-03 AB02173	AB021736.1		Oryza sativa gene for bZIP protein complete cds
11353	24043	37346	1.60	3.0E-03 AP00922	AP009222.1		Pneumocyada cartrili kastrulika serine andozromese mRNA partial cyle
11424	23.19	36422	2.52	3.0E-03 /	3.0E-03 AF206285.1		Homo septens goldin-like protein (GLP) gene, complete cds
1462	24065	37372	272	3.0E-03 AF094481	AF094481.1		Homo septens trinucleotide repeat DNA binding protein p.20CGGBP (CGGBP) years complete ade
1462	24065	37373	272	3.0E-03 AF00448	AF084481.1	Į	Homo explans trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11543	24143	37452	1.58	3.0E-03 P11389	M1389	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN (CONTAINS: REVERSE TRANSCRIPTASE; ENDONNO EASE)
						1	

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Probe SEQ ID NO:	Ø	ORF SEQ ID NO:	Expression Signal	Most Similer (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Defeaberse Source	Top Hit Descriptor
11784			1.48	3.0E-03	3.0E-03 AW294812.1	EST HUMAN	UI-H-Bi2-ahi-d-08-0-UI.s1 NCI CGAP Sub4 Homo septens cDNA clone IMAGE: 2726842 3*
11927	25196		2.86	3.0E-03	3.0E-03 AI525056.1	EST_HUMAN	promma-5.E07.1 brumor Homo septems cDNA 67
11962		37256	1.88	3.0E-03	3.0E-03 AA993154.1	EST HUMAN	ot/7/b10.s1 Source_bnai_fetus_Nb2HFB_9w Homo sapiens cDNA clone IMAGE:1622779 3' similar to contains L1.53 MER28 receitive element:
12016	25321		2.28	3.05-03	3.0E-03 AB009668.1	Ę	Homo eaplens gene for CMP-N-acetyleauraminic acid hydroxylase martial cyle
12190		31066	2.71	3.0E-03	3.0E-03 AJ296282.1	TN	Returs noneglous mRNA for connecting (cade ciene)
502		25919	1.83	20E-03 Q04852	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
502	13286	25920	1.83	2.0E-03 Q04652	004652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
768	15552		12.31	20E-03 T70874.1	T70874.1	EST HUMAN	yd15h03.r1 Soeres fetal liver spleen 1NFLS Homo sepleme cDNA clone IMAGE-108244 F
1342		26768	2.07	20E-03 M20783.	M20783.1	N.	Human alpha-2-plasmin intibitor cene, exons 6 and 7
1345	14093	26768	1.4	2.0E-03	2.0E-03 AA681605.1	EST HUMAN	nu88f01.s1 NCI CGAP Alvi Hamo septens cDNA clane IMAGE-12/7563
1354	14102	28777	18.16	2.0E-03		N	Homo sapiens fumor-related protein DRC2 (DRC2) gene, complete cds
1473	14220	28908	£.1	2.0E-03 P48509	948509	SWISSPROT	PLATE ET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN)
1506	14252	28838	1.84	2.0E-03	4557836 NT	Ę	Homo sepiens procelegen-lysine, 2-conglutarate 5-dioxygenese (heine hydroxylase, Ehlere-Danlos syndrome toes (h) (Pt OD) mRNA
1508	14252	28839	2	2 OF 03	TA ACTRA	<u> </u>	Homo septiens procellagen-tysine, 2-cooglutarate 5-dicogenese (tysine hydroxylase, Ehlers-Danios syndrome
1586			6.31	2.0E-03 P29400		SWISSPROT	COLLAGEN AT PHA WIND CHAIN PRECITEND
1764	14506	27207	1.13	2.0E-03/	38.1	П	242a10,11 Sogres total fetus Nb2HF8 Sw Homo seciens cDNA close IMAGE-786114 F
1872	14610		1.01	2.0E-03	Γ	Т	CM2-HT0183-061089-018-dt3 HT0183 Homo seniens cDNA
1988		27445	1.57	2.0E-03	Γ	1	Mus musculus myelin expression factor-3-like profein gene, partial cds.
247	14975	27713	1.16	2.0E-03		LN	Homo sepiens chromosome 21 segment HS21C102
2658	15272	28007	4.01	2.0E-03 AF18797			8 Hamo saplens concentrative nucleoside transporter (CNT1) gene, excn 12
7208 7208	15272	28008	4.01	2.0E-03 /		NT	8 Homo saplens concentrative nucleoside transporter (CNT1) gene, excn 12
7287	15208		4.57	2.0E-03/			UI-H-BI1-edi-g-10-0-UI.s1 NCI_CGAP_Sub3 Homo septems cDNA clone IMAGE:2717010 3'
2	16160	28818	4.3	2.0E-03/	2.0E-03 AA450138.1	EST_HUMAN	2x42a10.r1 Sogres total fetus Nb2HF8 9w Homo eaplens cDNA clone IMAGE:789114.5
뒭	18174	28823	1.13	2.0E-03	2.0E-03 BF568955.1	EST_HUMAN	60218393011 NIH_MGC_42 Hamo septens cDNA clone IMAGE:4300070 3'
3657	18410	29048	6.62	2.0E-03 X87344.1		¥	H.sepiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RINGS, 9, 13 and 14 denses
4083	16835	29461	1.98	2.0E-03 P03374		Т	ENV POLYPROTEIN ICONTAINS: COAT PROTEIN CASS COAT PROTEIN CASS
4195	16936		11.03	2.0E-03 U68491.1		Z	Rattus noveglous 5-hydroxytryptamine7 receptor gene, partial cds
4383	17130		1.12	2.0E-03 /	.ú	Г	UI-H-BW 0-eing-03-0-UI.s1 NOI CGAP Subd Hamp septems aDNA clame IMAGE-2730413.3
4397	17134	29765	0.97	2.0E-03 A1064746	F.	EST_HUMAN	HA0507 Human febal liver cDNA library Homo septens cDNA
					1		

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Probe SEQ iD NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Velue	Top Hit Acession No.	Top Hit Detabese Source	Top Hit Descriptor
4509	17244	29877	22	2.0E-03	2.0E-03 L42612.1	<u>V</u>	Droecphila melanogaster shorteighted class 2 (shs) mRNA, complete cds
4509	17244		2.2	2.0E-03	2.0E-03 L42512.1	۲	Drosophile melanogaster shortsighted class 2 (shs) mRNA, complete cds
4863	17397		1.84	2.0E-03	2.0E-03 R87773.1	EST_HUMAN	yo45e02.s1 Soeres adult brain NZb4HB56Y Homo sapiens cDNA clone IMAGE:180890 3'
4956	17882	30290	2.67	2.05-03	2 OF AS AFORS 528 1	<u>L</u>	Homo sapiens X-Inked anhidrotito ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat motors.
5092	17811	30427	٦	2.0E-03	2.0E-03 BE798380.1	EST HUMAN	601883004F1 NIH MGC 7 Homo saplens cDNA clone IMAGE:3937660 5'
5399	18199	30803	1.38	2.0E-03	2.0E-03 BF241410.1	EST HUMAN	801878385F1 NIH MGC 55 Hamo septens cDNA clane IMAGE:4104892 67
5540	25070	31245	2.08	2.0E-03	2.0E-03 AB014593.1	LN.	Hamo sepiens mRNA for KIAA0683 protein, pertial cds
5823	18420	31333	1.86	2.0E-03 U63711	U63711.1	F	Xenopus laevis xetitin mRNA, complete cds
6018	18800	31760	3.58	2.0E-03 P23477	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6019	18800	31761	3.58	2.0E-03 P23477	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6253	19027	32001	2.17	2.0E-03 Q95203	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)
6253	19027	32002	2.17	2.0E-03 Q96203	096203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)
6255	19029	32004	7.5	2.0E-03	2.0E-03 BF308187.1	EST_HUMAN	601887434F1 NIH_MGC_17 Hamo sapiens cDNA clone IMAGE:4121408 5
							ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN
6201	19084	32046		2.0E-03	2.0E-03 Q9UKP4	SWISSPROT	MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
6292	19065	32047	96.0	2.0E-03 AV70907	AV709075.1	EST_HUMAN	AV709076 ADC Homo sepiers aDNA dane ADCAEF09 5'
8320	19090	32078	1.62	2.0E-03	2.0E-03 X94451.1	NT	L.esculentum mRNA for lysy-4RNA synthetase (LysRS)
920	18271		1.16	2.0E-03	2.0E-03 A1991089 1	EST HIMAN	Wu38h09.x1 Soarce_Diedigrastie_colon_NHCD Homo sapiens cDNA clone IMAGE-2522177 3' similer to SW:RL28 HUNAN P47814 60S RIBOSOMAL PROTEIN L28 :contains element MSR1 remetitive element:
1430	18306	32311	0.61	2.0E-03	2.0E-03 AA677831.1	EST HUMAN	213a11.s1 Sogres_fotal_liver_spleen_1NFLS_S1 Homo sepiens cDNA clone IMAGE:430652.3'
6862	17939	30675	1.62	2.0E-03	2.0E-03 AB038602.1	¥	Caenorhabditis elegans mRNA for galectin LEC-11, complete cds
6836	19674	32720	0.0	2.0E-03	5031864 NT	NT	Homo sepiens Itoma HMGIC fusion pertner (LHFP) mRNA
6639	19674	32721	9.0	2.0E-03	5031864 NT	ħ	Homo sapiens (poma HMGIC fuelon pertner (LHFP) mRNA
6981	19506	32531	3.56	2.0E-03	2.0E-03 BE067988.1	EST_HUMAN	CM4-BT0368-061299-054-d01 BT0366 Homo septens cDNA
7044	19735	32795	0.58	2.0E-03	2.0E-03 AI296863.1	EST_HUMAN	qm99d11.x1 NCI_CGAP_Lu5 Hamo sepiens dDNA clane IMAGE:1896885 3'
7183	19879	32953	9.0	2.0E-03 T88569.	T86569.1	EST_HUMAN	yd77g10,r1 Sceres fetal Ilver spleen 1NFLS Home sepiens cDNA clone IMAGE:114306 5
7617	20188	33281	1.18	2.0E-03 P07354	P07354	SWISSPROT	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
7950	20645	33709	1.86	2.05-03	2.0E-03 AW 592004.1	EST_HUMAN	h37b08x1 3cares_NFL_T_GBC_S1 Hano sapiens cDNA done IMAGE:2934035 3' similar to TR:Q60976 Q60976 JERKY;
8116	20810	33944	6.07	2.0E-03 N20287.	N20287.1	EST HUMAN	y42g08.s1 Source malancoyle 2NbHM Homo explans cDNA clone IMAGE:284442.3' similar to contains L1.b2.L1 repetitive element:

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					5	gie Exuli Flu	Single Exon Probes Expressed in Brain
Prabe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Deftabase Source	Top Hit Descriptor
8116	20810	33945	6.07	2.0E-03 N20287	N20287.1	EST HUMAN	19x42g06.s1 Soares melanocyte ZNbHM Homo sapiens cDNA clone IMAGE:284442 3' similar to contains 1.1.b2 L1 receditive element:
8162	20856		0.54	2.0E-03 Q92350	Q92350	SWISSPROT	HYPOTHETICAL 32.8 KD PROTEIN C609.05 IN CHROMOSOME
8184		34015	1.19	2.0E-03 P19137	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
8239			0.81	2.0E-03	6005855 NT	Z	Homo saplens Retina-derived POU-domain factor-1 (RPF-1), mRNA
8230	_	34070	0.81	2.0E-03	FN 5585009	Z	Homo saplens Retine-derived POU-domain factor-1 (RPF-1), mRNA
8264	20828	34097	0.88	2.0E-03 AU1366	-	EST_HUMAN	AU139679 PLACE1 Homo suplens cDNA clone PLACE1004839 5
8318	21011		0.01	2.0E-03 AJ40087	AJ400877.1	F	Home saplens ASCL3 gene, CEGP1 gene, C11 of 14 gene, C11 of 15 gene, C11 of 16 gene and C11 of 17 gene
8570	24262	34400	0.54	2.0E-03 AB0352	AB035256.1	Ę	Onchigatis Canicalis mRNA for estancific probabilities chain releases factor 3, positiol adv
908	18419		0.74	2.0E-03 AW79811	AW798111.1	EST HUMAN	MR2-UM0025-300300-102-02-UM0025-Homo sentens of NA
9084	18419	31332	0.74	20E-03/	AW 798111.1	EST HUMAN	MR2-UM0025-300300-102-002 MK0025 Horno september - DNA
8	21877			100			Homo saplens mannosidase, beta A, hysosomal (MANBA) gene, and ublquitin-conjugating enzyme E2D 3
828	┸		\$ 8	205-03/	2.0E-03 AFZ24669.1	Į.	(UBE-203) genes, complete cds
	1	Į	3 8.0	2.0E-03 H50832.	H50832.1	EST HUMAN	yp88809.s1 Scenes fetal liver epieen 1NFLS Homo saplens cDNA clone IMAGE:194296 3'
R d	22104	35277	0.80	2.0E-03 H50832.	H50832.1	EST_HUMAN	yp88e09.s1 Soares felal liver spleen 1NFLS Homo septens cDNA clone IMAGE:1942963'
							TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEM) (JI)
92,58			3.46	20E-03 P24821	24821	SWISSPROT	225) (TENASCIN-C) (TN-C)
888	_		1.38	2.0E-03 P48982		SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
86 86	ŀ	ł	1.38	2.0E-03 P48982		SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
823			0.53	20E-03/	2.0E-03 AF007732.1	LN	Homo sepiens caspase recruitment domain-containing protein (BCL10) gene, complete ods
88	\Box		0.53	2.0E-03	2.0E-03 AF097732.1	N.	Homo explens caspase recruitment domain-containing protein (BCL10) gene, complete ods
9815	_1	35668	0.81	20E-03	69.1	EST_HUMAN	QV3-0T0084-080400-144-601 OT0064 Hamo septems cDNA
8042	_ 1		5.75	2.0E-03 AA25137	8.1	EST_HUMAN	zs10a08.s1 NCI_CGAP_GCB1 Homo eaplens cDNA clone IMAGE:084754 3:
10508	_1	36377	0.45	2.0E-03 AW3611	76.1	EST HUMAN	RC1-C70251-141089-012-d01 CT0251 Homo septens cDNA
10506		36378	0.45	2.0E-03 AW3611	76.1	EST HUMAN	RC1-CT0251-141099-012-d01 CT0281 Home sections cDNA
10938	i		297	2.0E-03 M86524.	-	NT	Human dystrophin gene
11470		33281	2.58	2.0E-03 P07354		SWISSPROT	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (I D)
11531			2.14	2.0E-03 B	2.0E-03 BF330909.1	Г	RC3-BT0333-310800-115-004 BT0333 Homo serviens oDNA
11538	24138	37446	0.1	2.0E-03 Z11740.1		ᅜ	H. sapiens variable number tandem repeat (VNTR) locus DNA
11909	1		3.23	2.0E-03 A			1965h03.x1 NCI_CGAP_KId11 Homo septens cDNA clone IMAGE:2283989 3' similar to SW:VATG_MANSE Q25632 VACUOLAR ATP SYNTHASE SUBUNIT G.
11926	24487	37807	2.41	2.0E-03 A	2.0E-03 AF157516.2	Z	Homo septiens SEL1L (SEL1L) gene, partial ods

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Moet Similar (Top) Hit BLAST E Vatue	Top Hit Acession No.	Top Hit Detebese Source	Top Hit Descriptor
11949	24502	37810	2.41	2.0E-03	2.0E-03 Al084325.1	EST HUMAN	oy43g08.s1 Soares_parethyroid_tumor_NbHPA Homo sepiens cDNA done IMAGE:1088834.3' sknijer to TR:P97535 P97535 PS-PLA1 PRECURSOR.;
11972	17907		76.0	2.0E-03	2.0E-03 AJ245167.1	L	Camelus dromedantus cyho19 gene for immunoglobulin heavy chain variable region
12172	25361		2.89	2.0E-03	2.0E-03 AV697968.1	EST HUMAN	AV697966 GKC Homo seplens oDNA clone GKCGXD05 5"
12262	24707	31050	1.76		2.0E-03 Y00:508.1	Z	H. saplans M1 gane for muscarinic acetylcholine receptor
12433	25224		1.48		2.0E-03 AI375037.1	EST_HUMAN	te0802.x1 Source_total_fetue_Nb2HF8_ow Homo expiens cDNA clone IMAGE:2049061 3' similar to contains Alu repotitive element;
12542	24882		1.64	2.05-03	2.0E-03 AF129788.1		Homo sapiens MSH55 gene, pertial cds; and CLIC1, DDAH, G9b, G9c, G5b, G9d, G9c, G9f, BAT5, G5b, CSK2B, BAT4, G4, Abo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA prepare, complete ode
12713	25175		2.05		2.0E-03 AV697908.1	EST HUMAN	AV697966 GKC Homo seplens cDNA clone GKCGXD05 5
429	13215	25860	1.28	1.0E-03	1.0E-03 H96471.1	EST_HUMAN	y98c08.r1 Soares pheel gland N3HPG Homo saplens cDNA clone IMAGE:232334 5
810	13581	26248	2.31	1.0E-03	1.0E-03 AI720283.1	EST_HUMAN	8670b08.X1 Barsbeed colon HPLRB7 Homo explens cDNA clone IMAGE:2334039.3' similar to TR:Q13625 Q13825 AU-BINDING PROTEINENOYL-COA HYDRATASE.
810	13581	26249	231	1.0E-03	1.0E-03 A1720263.1	EST HUMAN	as70b08.X1 Barsteed colon HPLRB7 Homo sepiens cDNA done IMAGE:2334039.3' stmiler to TR:Q13625 Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE
1073	13831	28489	3.76	1.0E-03	1.0E-03 A1865788.1	Г	WASSACE.X1 NCI CGAP Pant Homo saplens cDNA clone IMAGE-2422258 37
1083	13851	28510	1.78	1.0E-03	N	Π	ws3e10.x1 NCI_CGAP_Met15 Hamo sapiens cDNA clane IMAGE:2551242.3
2021	14756	27486	3.38	1.0E-03 P47808	P47808	SWISSPROT	HIGH MOLECULAR WEIGHT FORM OF MYOSIN I (HMWMI)
2160	14880	27814	12.13	1.0E-03	1.0E-03 AJ131016.1	Z	Homo eapieris SCL gene locue
2979	15745	28393	1.37	1.0E-03	1.0E-03 AB033117.1	L	Homo sepiens mRNA for KLAA1291 protein, partial ods
3186	15949	28599	221	1.0E-03 P18916	P18916	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED CARBONIC ANHYDRASE) (SALIVARY CARBONIC ANHYDRASE)
3186	13949	28600	22	1.0E-03 P18915	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED CARBONIC ANHYDRASE) (SALIVARY CARBONIC ANHYDRASE)
3656	16409		1.65	1.05-03	1.0E-03 AB044400.1	Г	Homo saciens SVMT gene for synaptic vesicle monoamine transporter, exons 14, 15
4402	17139	29767	1.28	1.0Ё-03	1.0E-03 BE939162.1	EST_HUMAN	RC1-TN0128-190800-021-g01 TN0128 Homo sapiens cDNA
4441	17171	29803	4.05	1.0E-03	1.0E-03 BE246636.1	EST HUMAN	TCBAP1D4909 Pediento pre-B oell acute lymphoblastic leukemia Baylor-HGSC project≕TCBA Homo septens cDNA clone TCBAP4000
4815	17360	29986	0.84	1.0E-03		Т	Cenorhabditis elegans spliced leader RNA (SL3 siphe), (SL4), and (SL5) genes
4773	17505	30127	1.68	1.0E-03	1.0E-03 A1073485.1	EST HUMAN	ow5504.x1 Soares, leeds, NHT Homo sapiens cDNA clone IMAGE:1640262.3
4773	17505	30128	1.68	1.05-03	1.0E-03 AI073486.1		045004x1 Sogree_lestis_NHT Homo sepiens cDNA clone IMAGE:164026231
4774	17506		4.20	1.05-03	67.1	T	PMO-HT0339-200400-010-D02 HT0339 Hamo septens cDNA
5018	17739	30348	7.24	1.0E-03 046409		SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)

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Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Vaitue	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8978	21668		85.0	1.0E-03	U62111.2	Ľ	Homo septens X28 region neer ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ce2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), actranolautodystrophy protein >
9017		34858		1.0E-03	1.0E-03 M30471.1	NT	Human class III alcohd dehydrogenase (ADH5) chi subunit mRNA, complets cds
9017		34859	3.68	1.0E-03	1.0E-03 M30471.1	LN	Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds
9507	22160	35340	1.66	1.0E-03	1.0E-03 AF011400.1	NT.	Thermotoga neapolitana alpha-1,8-galactosidase (aglA) gene, complete cds
9607		35341	1.86	1.0E-03	1.0E-03 AF011400.1	LN-	Thermotoga neapolitana alpha-1,6-galactoeidase (agiA) gene, complete cds
97.20		35570	0.81	1.0E-03	1.0E-03 001129	SWISSPROT	BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN) (PG40) (DERMATAN SULFATE PROTEOGLYCAN-II) (DSPG)
10063	L	35929	0.65	1.0E-03	1.0E-03 AF003529.1	N F	Homo sepiens glypicen 3 (GPC3) gene, pertial cds and flanking repeat regions
10068	22716		0.75	1.0E-03	1.0E-03 AF097485.1	N E	Homo septems transducin beta-like 2 (TBL2) gene, complete cds
10214	23862	36075	1.72	1.0E-03	1.0E-03 A1024350,1	EST HUMAN	ov/3008.x1 Scenes_lesds_NHT Homo septens cDNA done IMAGE:1643175.3' similar to contains MER39.b1 MER39 MER39 repetitive element:
							age3ff2.a1 Stratagene hNT neuron (#937233) Homo sepiens cDNA clone IMAGE:1142063 3' straiter to
10503			0.46	1.0E-03	1.0E-03 AA706202.1	EST_HUMAN	contains Alu repetitive element;
10563			1.79	1.0E-03	1.0E-03 AW362393.1	EST_HUMAN	RC1-CT0279-181089-011-e09 CT0279 Homo sepiens cDNA
10563	23259	36496	1.79	1.0E-03	1.0E-03 AW362393.1	EST_HUMAN	RC1-CT0279-181099-011-409 CT0279 Homo eaplens cDNA
10051	23342		2.78	1.0E-03	1.0E-03 BE170859.1	EST_HUMAN	QV3-HT0543-220300-130-a03 HT0543 Homo sepiens cDNA
10726	23413		3.20	1.0E-03	1.0E-03 A1683847.1	EST HUMAN	tt73e12x1 NCI_CGAP_HSC3 Homo septens cDNA clone IMAGE:2246448 3' striller to TR:Q28195 Q28195 PVA1 GENE;
10808		36727	1.36	1.0€-03	1.0E-03 AW237482.1	EST_HUMAN	xm72d12.x1 NCI_CGAP_Kd11 Homo sepiens cDNA clone IMAGE:2889751 3'
11106			3.05	1.0E-03	1.0E-03 AV759949.1	Г	AV756849 MDS Hamo septens cDNA clane MDSD0F11 5
11905		37806	4.48	1.0E-03	1.0E-03 BE804488.1	EST_HUMAN	801433087F1 NIH_MGC_72 Hamo septens cDNA clans IMAGE:3918624 5
12124	24616		1.38	1.0E-03	1.0E-03 AV731520.1	EST_HUMAN	AV731520 HTF Homo sepiens cDNA clone HTFAJG05 5
12274	26342		9	10. 20.	4 OF 00 A19 178 FE 4	TOT LA BAAAL	tc05h11.x1 NCI_CGAP_Co16 Homo sepiens cONA clone IMAGE:2063013 3' similer to contains Alu
12478		30612	7.05	105-03	1.0E-03 RE780572 4	Т	604488978F1 NIH MGC 67 Homo sentens cDNA close MAACE-3872025 E
12821	25187		1.37	1.0E-03	Ē	7	ROp-CT0205-240999-021-d02 CT0205 Homo sapiens cDNA
5130	l		0.7	9.0E-04 P08548		SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
9699			1.28	9.0E-04 P06727		SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
6165			0.0	9.0E-04	9.0E-04 AJ006345.1	Ę	Homo sepiens KVLQT1 gene
8395		32165	96.0	9.0E-04 P02381		SWISSPROT	MITOCHONDRIAL RIBOSOMAL PROTEIN VAR1
9643	[1.42	9.0E-04	3.1		Glycyrhiza glabra GgbAS1 mRNA for bela-amyrin synfrase, complete ods
1471	14218		1.02	8.0E-04	8.0E-04 X96469.1	NT	X.laevis mRNA for C4SR protein

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	Top Hit Descriptor		LINE-I REVERSE TDANSCRIPTSE:	TOTAL TOTAL HOMOLOG	And Promise Fund Promein (Prin-) gene, complete cds	224c10.a1 Scenes fetal heart NMHH19W Homo explens con A close MA CE 277727.2.2	In85e08.x1 NCI_CGAP_UZ Home septems cDNA cirra IMAGE:3472646.31	Homo septens prior protein (P-P) gene, complete cds	Homo espiens chromosome 21 segment HS21C010	Homo seplens chromosome X open reading frame 6 (CXORF6) mRNA ng65g12.s1 NCI CGAP 1 to 2 Homo control of the con	repetitive element;	Wg36f09.x1 Soeres NSF Fe sw OT PA D S4 LL	Homo sapiens mRNA for FL 100035 protein north As	BONE MORPHOGENETIC PROTEIN 1 PRECTIDENT (1)	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)	Trans septers Bruton's tyroeine kinase (BTK), alpha-D-galactoeidase A (GLA), L44-ilke ribosomal routain	(VI) The Complete Com	V013c06 11 Shares Information and Home septems cDNA clone c-28e07 3'	Homo sepiens Refine Action Doctor	W15er11.x1 NCI CCAP KM12 London Textor-1 (RPF-1), mRNA	Homo sepiens epsitor-1 peeudopene (ICHEP1)	Homo sapiens epsilon-1 pseudopene (IGHFP1) neve Riffmula	Homo sepiens CCR8 chemoldine receptor (CAIKRRS) news	HYPOTHETICAL PROTEIN KIAA0032	VIDEOCUSE: INANSPORTER TYPE 5, SMALL INTESTINE (FRUCTOSE TRANSPORTER)	LOR1 reportitive element:	24 1 588 FEBRUARY: WALL IN	RC2-BN0120-250400-012-h11 BN0120 Home septems cDNA clone DKFZp586M2024	Lyborimus variegatus embryonic biastocoelar extracellular matrix protein precursor (ECMS) mRNA, complete cds	SD to contia between AMI 1 and CBS4	UHH-BIO-eab-6-09-0-UI.st NCI CGAP Suff Home China China	NUCLEOSIDE DIPHOSPHATE KINASE B AND BY ALES CON A CORB INA GE: 2708826 3'
Top Hit	Detaberse Source		SWISSPROT LINE-1 REV		FOT LIMINAL SALE	7	HOMAN					T_HUMAN			SWISSPROT BONE MORP	(L44L) and FT	EST HUMAN HSC29A072	T-	Τ	EST_HUMAN WITE 11.X1 NC	П	Homo sapiens		SWISSPROT HYPOTHETIC	Т			EST HUMAN RC2-BN0120-2	cds			SWISSPROT NUCLEOSIDE I
Top Hit Age	<u>9</u>				24.4	T		ļ	ALIOSZIU.Z INT	5		<u>.</u>	55.			U78027.1			8005855	5							7		F287478.1 NT		Ž.	
Most Similar (Top) Hit	BLASTE										7.01.04	2010. 2010.	7.05.04	7.0E-04 P13497	1.0E-04 P-13497	7.0E-04 U78027.	7.0E-04 Z40561.1	7.0E-04 R17336.	7.0E-04	6.0E-04 AI882525	6.0E-04 K01315.1	8 OF 041 145083	8 OF OA O45934	6.0E-04 P48408		6.0E-04 H92947.1	0.UE-04 AL048507	6.0E-04/BE005850	6.0E-04 AF287478	6.0E-04 AJ229042	8.0E-04 AW013847	0.0C-04 C01768
Expression	Signal	167	10.4	239	293	1.96	0.97	1.19	-	100	1000	7 2 0	200	2 2		228	408	234	85.0	3 5	2 6	2 8	0.61	3.33	- 4	0.0Z	200	077	0.71	20,00	247	180
ORF SEQ	Ö Q			900/08			27866	28164	28685	31748			35549	35550		27500	2000	+	2002	20440	2044	29531	33245		-	1	35837	-	3737g	37467	-	-
SEQ ID	Ö	16820	L	1	1	_1		[16035	18786	19188	19816	22364	22354		24185	36080	24064	18894	16812	16812	16902	20151	20461	20000	22530	22828		24070	24157	24233	25240
Probe SEQ ID	Ö	4159	4743	11002		11200	88	2718	3274	6005	6420	7128	9703	9703		1588	12845	13882	3941	4068	4068	4162	7478	7785	7914	9880	080	9000	┚			12082

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Single Exon Probes Expressed in Brain	ORF SEQ Expression (Top) Hit Acession Signal BLASTE No. Source Source	1.34 8.0E-04 Al817088 1 FST LITIMAN INTOMITION INTOMITION PROPERTY CONTRIBUTE	26051 6.81 5.0E-04 O10341 SWISSPROT	1.4 5.0E-04 AW851844.1 EST HUMAN	EST_HUMAN		30877 2.99 5.0E-04 AE2490K4 1 NT BACKET	TOTAL LAND	3.75 5.0E.04 M23804.1 NT		5.0E-04/AI188382.1 EST HUMAN	34033 0.96 5.0E-04/AA814519 1 EST HIBAAN MEDA MAN AMEDIA COST HOMO SADIENS CONA clare IMAGE:1339228 3'similar to contains element	5.1 EST HUMAN	T	1.44 5.0E-04 P29128 SWISSDBOT	5.0E-04 AWZ70938.1 FST HIMAN	Γ	2 EST HUMAN	Į.	5.04 5.0F-04 AA509643 4 FEET LIMAN	NT Heemochility Inflinence R4 earth et al. 1887	26267 1.79 4.0E-04 A1720263.1 EST HUMAN Q1825 AU-BNDNG PROTEINAN ON A CONTINUE OF THE CONTINUE	П	3.18 4.0E-04 AW753356.1 EST HIMAN	4.0E-04 AL163278.2
												_							30877		28076	26267	26268	26880	27538
	SEQ ID NO:	8 25058	_ [14237	16108	16457			19960	20551			21847	22025	1		22825	23577	18186	25184	13435	13597	13597	14198	14807
	Probe SEQ ID NO:	12816	88	148	3408	3704	5386	8532	7276	7856		8202	917	1728	9418	8098	10177	10897	11713	12020	828	827	827	1449	2075

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					,		ongo chora chicasad III Diani
Probe SEQ ID NO:	- <i>w</i>	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession Na	Top Hit Defebese Source	Top Hit Descriptor
2129			1	4.0E-04 AL04670	AL046704.1	EST_HUMAN	DKFZp434D059_r1 434 (synonym: https:// Homo sepiens cDNA clone DKFZp434D059 51
2833	1	28088		4.0E-04 098615	096615	SWISSPROT	SERICIN-2 (SILK GUM PROTEIN 2)
3162	15925	28672	0.95		4.0E-04 AF281074.1	TN	Homo sepiens neuroplin 2 (NRP2) gene, complete cds, alternatively spliced
4289	17028	29653	3.18	4.0E-04	4.0E-04 AA578331.1	EST_HUMAN	nh10e10.s1 NCI_CGAP_Co1 Homo septens cDNA done IMAGE:951930 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
4280	17028	29854	3.18	4.0E-04 AA6763	AA676331.1	EST HUMAN	inh10a10.s1 NCI_CGAP_Co1 Homo sepiens cDNA done IMAGE:951930 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN):
4500	17236	29968	1.78	١.	AA086324.1	EST HUMAN	zn61c08.s1 Strategene muscle 937209 Homo septems cDNA clone IMAGE:562670.3'
5028	17748	30360	3.1	4.0E-04	4.0E-04 BE560660.1	EST_HUMAN	001345895F1 NIH_MGC_B Homo saplens cDNA clone IMAGE:3678910 5'
7168	19855	32925	1.3	4.0E-04 P48442	548442	SWISSPROT	EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL CALCIUM-SENSING RECEPTOR)
7434	20111		0.76	4.0E-04	4.0E-04 AL161566.2	LN LN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 56
7618		33304	0.56	4.0E-04 AU1220	AU122079.1	EST_HUMAN	AU122079 MAMMA1 Homo sepiers cDNA done MAMMA1001620 5'
8434	21127	34284	1.07	4.0E-04	4.0E-04 BF240712.1	EST_HUMAN	801875985F1 NIH_MGC_55 Homo sapiens cDNA done IMAGE:4089700 5'
8442		34270	1.5	4.0E-04 N25507	N25507.1	EST_HUMAN	yx39e12.r1 Sceres malanocyte ZNbHM Homo sapiens cDNA clone IMAGE:284142.5'
0230		35426	3.24	4.0E-04	4.0E-04 AI025690.1	EST_HUMAN	0/87h03.s1 Sogres_testis_NHT Homo sapiens cDNA clone IMAGE:1844341 31
9740			1.22	4.0E-04	4.0E-04 AF022855.1	NT	Mus musculus neuropitin-2(a17) mRNA, atternatively spiliced, complete ods
12380	1		2.05	4.0E-04	4.0E-04 AF254822.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, atternatively spiliced
152	12067	25808	3.46	3.0E-04	4L119428.1	EST_HUMAN	DKFZp781,1221_r1 781 (synonym; hemy2) Homo sepiens cDNA clone DKFZp781,1221 5
<u>\$</u>	13003	25844	2.24	3.0E-04 P49259	o49259	SWISSPROT	180 KD SECRETORY PHOSPHOLIPASE AZ RECEPTOR PRECURSOR (PLAZ-R)
8	13629	20300	1.32	3.0E-04 U83991.	1	TN	Human short chain acyl CoA dehydrogenase gene, exons 1 and 2
<u> </u>	14570	27282	1.08	3.0E-04 AI26210	41262100.1		qz28d03.y1 NCI_CGAP_Kd11 Homo sepiens cDNA done IMAGE:2028197 5
286	14584		121	3.0E-04 AI39967	A 399674.1		th:23e02.x1 NCI_CGAP_Pr28 Homo septems cDNA clone IMAGE:2119082.3'
88	1884	28712	3.43	3.0E-04 P25147	25147	П	INTERNALIN B PRECURSOR
200	_ !	28717	0.7	3.0E-04 AA2033	VA203342.1	EST HUMAN	2256a04,r1 Sosres_fetal_tiver_spleen_1NFLS_S1 Home sapiens cDNA clone IMAGE:448478 51
3948		29335	4.07	3.0E-04 P49448		SWISSPROT	QLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)
흏	16778		1.33	3.0E-04/		N	Homo seplens Xq pseudosutoscmal region; segment 1/2
4072	16816		1.12	3.0E-04 E	3.0E-04 BE140809.1	EST_HUMAN_	RC0-HT0014-310599-028 HT0014 Homo sepiens cDNA
4766	17408		4.72	3.0E-04 BE15377	3E163778.1	EST_HUMAN	PAIO-HT0339-190200-007-912 HT0339 Homo sepiens cDNA
4827	17558	30180	0.95	3.0E-04 AW8377	1W837723.1	EST_HUMAN	QV3-DT0045-221299-046-d09 DT0045 Homo sapiens cDNA
5063	17782	30388	0.98	3.0E-04 AA6131		EST HUMAN	nq08g09.s1 NCI_CGAP_Lir1 Homo sapiens cDNA clone IMAGE:1143328 3'
8062	18832		7.86	3.0E-04	1.2	NT	Homo explens chromosome 21 segment HS21C081
8722	19556	32586	2.62	3.0E-04 AL 16327	8.2	LN	Homo saplens chromosome 21 segment HS21C078
7491	20163	33256	0.84	3.0E-04 P23468		SWISSPROT	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA)

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Top Hit Descriptor	FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3)	2x48d08.r1 Soares, testis, NHT Homo sepiens cDNA clone INAGE:795471.6' similer to gb:M62762 VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (HUMAN);	wi75a11.x1 Soares_fthmus_NHFTh Homo sepiens cDNA done IMAGE:2513276.3'	al24g05.s1 Soeres, tests, NHT Homo sepiens cDNA clone 1391298 3' similar to gb:M38072 60S RIBOSOMAL PROTEIN L7A (HUMAN);	GLUTAMIC ACID-RICH PROTEIN PRECURSOR	Homo sapiens adrenergic, alpha -1A-, receptor (ADRA1A), mRNA	nc38e04.r1 NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:1010430 similar to contains L1.t2 L1 repositive element:	Homo sepiens mRNA for KIAA0749 protein, pertial cds	DKFZp547L185_r1 547 (synonym; hfbr1) Hamo sablens cDNA clone DKFZp547L185 5	Homo septens SCG10 lifes-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARERP11 connection consistence).	AU146707 HEMBB1 Hamo seniens CDNA cane HEMBB1001253 3:	Human dystrophin gene	Human dystrophin gene	qh98e11.x1 Soeres_NRT_GBC_S1 Homo sapiens cDNA done IMAGE:1855052 3' similar to contains MER3.b2 MER3 receitive element:	Homo saplens chromosome 21 segment HS21C003	Mus musculus 5 flanking region of Pitc3 gene	Human germiline T-cell receptor beta chain TCRBV1781A1T, TCRBV2S1, TCRBV10S1P, TCRBV2SS1P, TCRBV16S1P, TCRBV16S1, TCRBV11S1A1T, HVB nello, TCRBV28S1P, TCRBV3AS1, TCRBV14S1, TCRBV3S1, TCRBV3S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY7, TRY8, TCRBV1, TCRBV1S1, TCRBV1S2>	am58c09.x1 Johnston frontal contex Homo seplens cDNA clone IMAGE:1539760 31	Homo sepiens tubulin, beta, 4 (TUBB4) mRNA	QV2-BT0636-070500-194-bo7 BT0636 Homo sepiens cDNA	EST380550 MAGE resequences, MAGP Homo sepiens cDNA	Phaseolus vulgaris nitrate reductase (PVNR2) gene, complete cds	yu01e11.r1 Sogree_pinesi_gland_N3HPG Homo sepiens cDNA clone IMAGE:232556 5	yu01e11.r1 Source_pinesi_gland_N3HPG Homo sepiens cDNA clone IMAGE:232656 61	Gailus gallus protessome 28 kDa subunit homolog mRNA, complete cds	Danio rerio hagoromo gene, exons 1 to 6, partial ods
Top Hit Defaberse Source	SWISSPROT	EST_HUMAN	EST_HUMAN	EST HUMAN	SWISSPROT	۲N	FST HIMAN		EST HUMAN		EST HUMAN	LN LN	Į.	EST HUMAN	LN	LN	L L	EST HUMAN	7.	EST HUMAN	EST HUMAN	LN TN	EST_HUMAN	EST_HUMAN	NT	INT
Top Hit Acession No.	>22607	3.0E-04 AA454055.1	3.0E-04 AI992139.1	3.0E-04 AA781201.1	713816	4501980 NT	3 0F-04 AA228301 1	3.0F-04 AB018292.1	3.0E-04 AL134483.1	2 NE-04 AE217708 1	20E-04 AU148707.1	M86524.1	20E-04 M86524.1	N288021.1	20E-04 AL163203.2	20E-04 AF224268.1	J66061.1	N124529.1	5174736 NT	3E082317.1	(W978441.1	J01029.1	196265.1	198285.1	J09226.1	7.1
Most Similar (Top) Hit BLAST E Value	3.0E-04 P22807	3.0E-04	3.05-04	3.0E-04	3.0E-04 P13816	3.0E-04	3.05-04	3.0F-04	3.0E-04	205.04	20E-04	2.0E-04 M86524.	20E-04	2 0E-04 A128802	20E-04/	20E-04/	20E-04 D68061.	20E-04 A1124526	2.0E-04	2.0E-04 BE0823	2.0E-04 AW9784	20E-04 U01029.	2.0E-04 H96265.	2.0E-04 H96265.	2.0E-04 U09226	20E-04 AB03796
Expression Signal	3.23	1.34	0.65	3.73	0.54	1.38	4.84	3.08	2.75	8,0	1.8	10.71	10.71	88	2.18	1.12	4.47	1.11	1.1	1.89	0.79	4.83	1.74	1.74	1.63	1.1
ORF SEQ ID NO:	33983	35673	35943	38220	36367	37408	30817	30818		ACAPAC.	28822	26324	26325				28033	28398	28740	28834	29282		29000	29991		30324
Exan SEQ ID NO:	20851	22471	22726	23003	23141	24154	25386	25230	25000	1306	13251	13656	13656	13911	13917	14503	15295	15752	16088	16186	18842	16864	17355	17355	17474	17721
Probe SEQ ID NO:	8157	0286	10078	10356	10495	11555	11978	12338	12730	174	8	887	288	1156	1163	1824	2581	2368	3328	3429	3862	4122	0Z9 1	4620	4742	4998

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						,	
Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Detabase Source	Top Hit Descriptor
6096		30424	1.04	2.0E-04 P35748	P35748	SWISSPROT	MYOSIN HEAVY CHAIN, SMOOTH MUSCLE ISOFORM (SMMHC)
5457	18256	31148	67.0	2.0E-04	2.0E-04 AV654352.1	EST_HUMAN	AV654352 GLC Homo sepiens cDNA clone GLCDUH10 3'
5460		31160	1.75	2.0E-04	2.0E-04 AIG00862.1	EST HUMAN	tq03b11.x1 NCI_CGAP_Ut3 Homo espiens cDNA done IMAGE:2207709 3'
5964	18459	31373	96'0	2.0E-04	2.0E-04 AA298652.1	EST HUMAN	EST11191 Uterus Homo saplens cDNA 5 end similar to EST containing O family reneet
5857	18644	31584	18.0	2.0E-04	4758179 NT	ĮŅ.	Homo saplens cell cycle progression 3 protein (DNJ3) mRNA
6144	18922	31892	0.59	2.0E-04	2.0E-04 AF140708.1	Į.	Mus musculus G protein coupled receptor gene, complete cds; and unimown gene
7130	19818		2.6	2.0E-04	2.0E-04 AU121712.1	EST HUMAN	AU121712 MAMMA1 Homo septens cDNA clone MAMMA1000798 5
7225	19910		0.55	2.0E-04	2.0E-04 AW860963.1	EST HUMAN	QV0-CT0387-180300-167-610 CT0387 Homo saplens cDNA
7520	20191		14.88	2.0E-04 P08548	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7530			1.42	2.0E-04 P54296	P54296	SWISSPROT	MYOMESIN 2 (M-PROTEIN) (165 KD TITIN-ASSOCIATED PROTEIN) (165 KD CONNECTIN-ASSOCIATED PROTEIN)
7855		33675	1.08	2.0E-04	2.0E-04 U32444.2	Į.	Solarum (yooperstam phytochrome F (PHYF) gene, partial cds
7855	20550	33678	1.06	20E-04	2.0E-04 U32444.2	¥	Scianum (yoperatioum phytochrome F (PHYF) gene, partial cds
							Homo services DNA DI ECA in ORCH 4 reason reasons and the ICA ORCH 9 ORCH 4
8182	20875	34012	1.23	2.0E-04	2.0E-04 AB026898.1	NT	complete cds)
8482	20876	34013	123	2.0E-04	2 DE-04 AB026998 1	5	Homo septens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes,
1	1						
8 8	2138		96.	20E-04	3.1	Į.	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, expn 5
ğ	3		9.0	20E-04	20E-04 X57331.1	П	Humen immunoglobulin C(mu) and C(detta) heavy chain genes (constant regions)
88	21912		0.49	2.0E-04	2.0E-04 AA725700.1		al Zari 2.s1 Soeres_bests_NHT Home septens cDNA clone 1343518 3'
8319	23 88 73 88 88	35158	0.0	20E-04 P18715	P18715	SWISSPROT	GASTRULA ZINC FINGER PROTEIN XLCGF28.1
8875	22625	35719	1.19	20E-04	20E-04 BE149303.1	EST_HUMAN	RC3-HT0254-151089-011-b05 HT0254 Homo sepiens cDNA
89 18	2288	35781	1.77	2.0E-04	2.0E-04 AA405777.1	EST_HUMAN	2466c11.r1 Soeree_tests_NHT Homo sapiens cDNA clone IMAGE:742964 5
10755	23440	30084	5.23	20E-04)	20E-04 AV730373.1	EST_HUMAN	AV730373 HTF Home sepiens cDNA clone HTFAAA01 6
11128	23706		1.61	20E-04	20E-04 AJ243213.1	١	Homo sepiens partial 5-HT4 receptor gene, exons 2 to 5
11278	23837	37229	3.06	2.0E-04	2.0E-04 AI440282.1	EST HUMAN	#01f11.x1 NCI_CGAP_Ges4 Home septens cDNA done IMAGE:2140269 3' straiger to contains Alu repetitive element:
11403	24052	37356	2.88	20E-04/	2.0E-04 AW136740.1	EST HUMAN	UI-H-BI1-edm-0-04-0-UI:s1 NOI CGAP Sub3 Homo serviene aDNA clone MAGE-2717193 3'
11857	24441	37782	2.77	2.0E-04		Г	yb79b10.x5 Strategene overy (#637217) Homo sepiens cDNA clone IMAGE: 773713'
1053	13812	28472	33	1.0E-04 P113 60		TORGSSIMS	RETROVIRUS-RELATED POL POLYPROTEIN (CONTAINS: REVERSE TRANSCRIPTASE; FINDONICS FASE)
1092	13860	20508	474	1.0E-04/	7.1	Т	UI-H-BIO-BED-6-09-0-UI at NCI CGAP Subt Homo sections CONA Arrise IMA DE 2708825 9
1092	13850	20509	4.74	1.0E-04/		Т	UI-H-BIG-88D-9-09-0-UI st NCI CGAP Subt Home seniens of NA Ame IMACE of Mason
						7	COZON /2. TOURISTON CALCO STRUCTURE TO TOUR CONTROL OF THE CONTROL

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Detabese Source	Top Hit Descriptor
1309	14057		3.12	1.0E-04	1.0E-04 U62918.1	NT	Anguilla anguilla dopamine D1A1 receptor (d1A1) gene, complete cds
1623	14370	27058	3.25	1.05-04	1.0E-04 AF148805.1	IN	Kaposi's sercome-associated herpesvirus ORF 88 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, letent ruclear antigen, ORF K14, v-GPCR, putative phosphoribosyfformylglychramidine synthase, and LAMP (LAMP) genes, complete cds
1623	14370	27059	3.25	1.05-04	1.0E-04 AF148805.1	TN	Kaposi's sercome-associated herpesvirus ORF 69 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosyfformylglychramidine synthese, and LAMP (LAMP) genes, complete cds
1854	14592	27308	2.09	1.0E-04	2.1	M	Equus caballus DNA, chromosome 24q14, microsatellite TKY36
3278	16039	28689	1.06	1.0E-04	1.0E-04 Q62203	SWISSPROT	SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
3719	16472	29110	0.91	1.0E-04	1.0E-04 AI440282.1	EST HUMAN	#01f11.xt NCI_CGAP_Gas4 Home saplens cDNA clone IMAGE:2140269.3' similar to contains Ak repetitive element;
4037	16782	29412	211	1.0E-04	1.0E-04 M14042.1	Z V	Mouse alpha 1 type-IV collegen mRNA
4062	16807	29437	1.15	1.0E-04	7.1	EST_HUMAN	AV647727 GLC Homo seplens cDNA clone GLC98D04 3'
5036	17755	30368	1.28	1.0E-04	7862015 NT	TN	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5036	17755	30369	1.28	1.0E-04	7862015 NT	Z	Homo sepiens KIAA0237 gene product (KIAA0237), mRNA
5769	18560	31487	1.49	1.0E-04 P08547	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6834	18623	31556	0.57	1.0E-04	1.0E-04 T19815.1	EST HUMAN	753F Heart Homo sapiens cDNA clone 753
£83	18623	31557	0.57	1.0E-04	1.0E-04 T19815.1	EST_HUMAN	763F Heart Homo saplens cDNA clone 753
6346	19116	32105	0.95	1.0E-04	1.0E-04 AA177111.1	EST_HUMAN	Inc02e12.81 NGI_CGAP_Pr3 Hamo sepiens cDNA clone IMAGE:252
6738	19672	32605	0.92	1.0E-04	1.0E-04 AA564581.1	EST HUMAN	nj25e04.s1 NCI_CGAP_AA1 Homo sepiens cDNA clone IMAGE:983486 3' similer to gic.M97252 KALLMANN SYNDROME PROTEIN PRECURSOR (HUMAN):contains Alu repetitive element:
7086	19776	32841	15.6	1.05-04	1.0E-04 AI251980.1	EST_HUMAN	qv57d10x1 NCI_CQAP_Dv32 Hamo septems cDNA clams IMAGE:19856833'
7470	19776	32841	17.82	1.0E-04	1.0E-04 AI251980.1	EST_HUMAN	qv57df0xf NCI_CGAP_Ox82 Hamo sepiens cDNA clone IMAGE:1985683 3'
7894	20589	33719	96'0	1.0E-04	1.0E-04 AA630453.1	Π	ab94g08.s1 Stratagene lung (#937210) Homo septens oDNA clone (MAGE:854654 3'
8238	21915	35088	2.27	1.0E-04	1.0E-04 A1806220.1	EST_HUMAN	wf28e08.x1 Sceres_NFL_T_GBC_S1 Hamo sepiens cDNA clone IMAGE:2356742.31
9247	21926	35097	1.46	1.0E-04 O88989	088860	SWISSPROT	CYSTATIN-RELATED EPIDIDYMAL SPERMATOGENIC PROTEIN PRECURSOR (CYSTATIN 8)
8325	21992		0.49	1.0E-04	1.0E-04 T77153.1	EST HUMAN	yd72008.r1 Soarse feldil liver spleen 1NFLS Hamo sapiens cDNA done IMAGE:113774 6'
9546	22189	35381	1.86	1.0E-04	10963876	Z	Homo sepiens phospholipid scramblase 1 (PLSCR1), mRNA
10079	22727		2.74	1.0E-04 P08547		SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10115	22763	35975	1	1.0E-04 P08548		SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11312	23971		2.13	1.0E-04 M28587.	1		Mouse alpha leukocyte interferon gene, complete cds
11567	24166	37479	2.05	1.0E-04		,	UI-H-BI1-aew-a-02-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720546 3'
11567	24166	37480	2.05	1.0E-04	19.1	T_HUMAN	UI-H-BI1-aew-a-02-0-UI.s1 NCI_CGAP_Sub3 Homo sepiens cDNA clone IMAGE:2720548 3'
11849	24248	37566	1.76	1.0E-04	1.0E-04 AB032988.1	- LV	Homo sepiens mRNA for KIAA1142 protein, pertial cds

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Table 4
Single Exon Probes Expressed in Brain

Top Hit Descriptor	Homo saplens 22kDa percotsomal membrane protein-like (LOC55895), mRNA	PROTEIN MOV-10	Homo sepiens partial SLC22A3 gene for extransuronal monoamine transporter (EMT), expn 1	LIMULUS CLOTTING FACTOR C PRECURSOR (FC)	LIMULUS CLOTTING FACTOR C PRECURSOR (FC)	Human MLC1emb gene for embryonic myosin afkaline light chain. 3UTR	AV653544 GLC Hamo septens aDNA clane GLCDMA06 3'	Home sepiens TESTIN 2 and TESTIN 3 genes, complete cds. atternatively spliced	Mus musculus gene for celretinin, exon 1	RETINAL-BINDING PROTEIN (RALBP)	RETINAL-BINDING PROTEIN (RALBP)	Human renin (REN) gene, 5' flanking region	RETINAL-BINDING PROTEIN (RALBP)	RETINAL-BINDING PROTEIN (PALBP)	Cryptosporidium pervum leolete Zaire 16 I/Os glycoprotein go 15 gene, pertial cds	Drosophila melanogaster senseless protein (sens) gene, complete cds	Macaca mulatta haptoglobin (HP) gene, 5' region	Homo sapiens PP1200 mRNA, complete ods	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCI EASE!	BETA-GALACTOSIDASE PRECURSOR (LACTASE) (ACID BETA-GALACTOSIDASE)		Germann Milk reportuve elementi;	AMERICAN SOURCE TO COMPANY OF THE SECOND COMPANY COMPANY COMPANY OF THE SECOND	ANALYSIS INC. CONT. CONT. Incline agrants control mange. (40.002.3	Grown Court of the second of the second contains a second to the second of the second	XX24g03.X1 Source NFL T GBC S1 Homo sepiens cDNA clone IMAGE:2814100.31	801461463F1 NIH MGC 66 Hamp seplens cDNA clone IMAGE:3865142 57	601461463F1 NIH_MGC_66 Hamo septens aDNA clone IMAGE:3865142 51	qiDig11.xi Soares_NHMPu_S1 Home septens cDNA olone IMAGE:1879748 3' similar to TR:008632 008632 G YCNF TYROSINE-RICH HAIR PROTEIN	PM4-H70521-120200-001-erio H70521 Homo seniera c-DNA	PM1-HT0521-120200-001-e10 HT0521 Homo sepiene cDNA
Top Hit Database Source	F	SWISSPROT	N.	SWISSPROT	SWISSPROT	N TN	EST_HUMAN	TN	IN.	SWISSPROT	SWISSPROT	Ę	SWISSPROT	SWISSPROT	LN	E	F.	Į.	SWISSPROT	SWISSPROT		EST HUMAN	TOWN TO LEGE		EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN
Top Hit Acession No.	8923891 NT	23249	AJ251884.1	226422	226422	(58855.1	5.0E-05 AV053544.1	5.0E-05 AF280225.1	5.0E-05 AB037984.1	249183	249193	112821.1	49193	49193	4.0E-05 AF164488.1	VF212313.1	J01947.1	\F202635.1	11369	23780	, , ,	4.0E-00 AW 02/946.1	Ţ	Ţ	J248061.1	51.1		3.0E-05 BF037898.1	3.0E-05 AI288919.1		П
 (Top) Hit BLAST E Value	5.0E-05	5.0E-05 P23249	5.0E-06 AJ25186	5.0E-05 Q26422	5.0E-05 Q26422	5.0E-05 X58855.	5.0E-05	5.0E-05	5.0E-05	5.0E-05 P49193	5.0E-05 P49183	4.0E-05 U12821	4.0E-05 P49183	4.0E-05 P49193	4.0E-05/	4.0E-05 AF21231	4.0E-05 U01947	4.0E-05 AF2026	4.0E-05 P11389	4.0E-05 P23780	20.7	4.05-05/4	4 05 05		3.0E-05 AI24806	3.0E-05	3.0E-05	3.0E-05 B	3.0E-05	3.0E-05 B	3.0E-05 BE16921
Expression Signer	1.2	1.1	241	0.72	0.72	13.38	3.75	0.90	0.87	3.64	4.72	3.84	0.73	0.73	1.16	0.75	0.74	7.57	0.47	0.59	9,7	1014	171	-	4.0	0.86	<u>6</u> .	1.01	0.73	7.98	7.98
ORF SEQ ID NO:		28001	28350	30408	30409	30051	31636	31822					20800	29810		30289	32528		35745	36168	00300	BACOS		+	29082	28457	28623	28524		29719	29720
Eten SEQ ID NO:	14583	15206	16710	17783			18688	18855	19916	24810	24810	13032	17185	17185	17551	17681	19503	22101	22550	22953	22.00	246.20	2504		13441	13797	13868	13866	16048	17088	17088
Pro be SEQ ID NO:	1855	2551	3961	5074	5074	5438	2003	8078	7231	12176	12440	2810	4440	4449	4820	4955	6841	9423	98	10306	40000	12.46	12780		88	1037	1100	1109	3287	4340	4349

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III Descentia como como como	ORF SEQ Expression (Top) Hit Acession Signal BLASTE No. Source Source	29798 0.94 3.0E-05 AA398679.1 [EST HUMAN EST78998 Placentia Homo sablens cDNA similar to n53 associated motes	0.94 3.0E-05 AA368679.1 EST HUMAN	0.00 3.0E-05 AL168302.2 NT	SWISSPROT	Г	3.0E-05/AU125721.1 EST_HUMAN	1072102 NT	1.17 3.0E-05 AJ225782.1 NT	1.17 3.0E-05 AJ225782.1 NT	2.33 3.0E-05 BE733157.1 EST_HUMAN	34082 1.47 3.0E-05/AA284049.1 EST HUMAN 2580b05.#1 Strategiene schizo brain S11 Homo septems cDNA cione IMAGE-70/841.31	34630 1.58 3.0E-06/AW770982.1 EST HUMAN hi94e08.x1 NCI CGAP Lu24 Homo septions cDNA clone IMAGE: 300e638 3:	Γ	3.0E-05 P43361 SWISSPROT	- NT	3.0E-05 AA372562.1 EST HUMAN EST84475 Colon adenocarcinoma IV Homo septems cDNA 5' end	1.1 EST_HUMAN	0.98 3.0E-05 Q62918 SWISSPROT	38304 0.96 3.0E-05 Q62918 SWISSPROT PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NEL-LIKE PROTEIN 2)	1.77 3.0E-05 L.77570.1 NT Homo septens DiGeorge syndrome critical region, centromeric end		LN.		7.46 2.0E-05 AA180562.1 EST_HUMAN	1.23 2.0E-05/BE086038.1 EST_HUMAN	0.93 2.0E-05 AF184814.1 NT		눟	0.78 2.0E-05 AL039107.1 [EST_HUMAN DKFZp5881064_r1 568 (synonym: hfld2) Homo septens oDNA clone DKFZp5881064 5:	1.09 2.0E-06 BE378471.1 EST_HUMAN	P P
		29798	29799		30055	26082	30144	31161	32433	32434	33616	34082	34630	34633			35088		36303	36304		27784	28037									31382
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	Probe SEQ ID NO:	4434	4434	4550	4686	4785	4791	5470	0020	6659	7799	8250	8791	8796	8789	8028	8228	9563	10433	10433	12072	2323	2587	į	2718	45134	3343	3362	3485	3787	4843	6672

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5880 6065 1 1 1 1 1 1 1 1 1 1 1 1 1	SEQ 1D NO: NO: 18898 18898 19898 19898 19898 1984 19485 19486 19486 19486 19488 22480 21710 21897 22474 22683	32807 32807 32807 32807 32807 32805 32805 32805 32805 32805 32807 32805 32805 32805 32805 32807 32805 32807	Signal 0.69 0.09 0.76 0.76 0.76 0.09 0.76 0.09 0.76 0.09 0.76 0.68 0.68 0.68 0.68 0.68 0.68 0.68 0.6			Top Hit Defabese Source Source Source Source Source SWISSPROT SWISSPROT SWISSPROT SWISSPROT TIT ST HUMAN ST HUMAN ST HUMAN ST HUMAN ST HUMAN ST HUMAN WISSPROT WISSPROT TIT ST HUMAN WISSPROT TIT ST H	Top Hit Descriptor Homo saplens chromosome 9 duplication of the T ceil receptor beta locus and trypelinogen gene families COTRANSPORTER) REVAL SODIUMDICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER) REVAL SODIUMDICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE OOTRANSPORTER) GOTRANSPORTER) GOTRANSPORTER) GOTRANSPORTER) The High is contained to 11 tropeditive element: Imm08d12 st NG_CGAP_SSI Home supplies cDNA clone IMAGE:1238519 3' Fishcherum mRNA for AARPT protein, partial OGZ710 PRO-POL-DUTPASE POLYPROTEIN: WIGSF07x1 Scares Discriptorate godon_NHOD Home suplens cDNA clone IMAGE:2235003 3' similar to TR:002711 WIGSF07x1 Scares Discriptorate godon_NHOD Home suplens cDNA clone IMAGE:2235003 3' similar to TR:002711 WIGSF07x1 Scares Discriptorate Control IMAGE:1238519 3' Hebrodontus francisci Hoxa410, Hoxa42 (Hoxa42), and Hoxa1 (Hoxa1) gense, complete cds Hebrodontus francisci Hoxa41, Hoxa3 (Hoxa41), Hoxa2 (Hoxa2), and Hoxa1 (Hoxa1) gense, complete cds (Hoxa5), Hoxa4 (Hoxa44), Hoxa3 (Hoxa41), Hoxa2 (Hoxa2), and Hoxa1 (Hoxa1) gense, complete cds Hoxa505:x1 NG_CGAP_GLI Home suplens cDNA clone IMAGE:2103369 3' GDNA clone TCBAP1550 TCBAP2E:1600 Pediento pre-B cell acute lymphobiastic leukemia Baylor-HGSC project=TCBA Home suplens TCBAP2E:1600 Pediento pre-B cell acute lymphobiastic leukemia Baylor-HGSC project=TCBA Home suplens TCBAP2E:1600 Pediento pre-B cell acute lymphobiastic leukemia Baylor-HGSC project=TCBA Home suplens TCBAP2E:1600 Pediento pre-B cell acute lymphobiastic leukemia Baylor-HGSC project=TCBA Home suplens TCBAP2E:1600 Pediento pre-B cell acute lymphobiastic leukemia Baylor-HGSC project=TCBA Home suplens TCBAP2E:1600 Pediento pre-B cell acute lymphobiastic leukemia Baylor-HGSC project=TCBA Home suplens TCBAP2E:1600 Pediento pre-B cell acute lymphobiastic leukemia Baylor-HGSC project=TCBA Home suplens TCBAP2E:1600 Pediento pre-B cell acute lymphobiastic leukemia Baylor-HGSC project=TCBA Home suplens divonednes 21 secure PATCPR (CDS5)
\mathbf{I}^{-1}	23103	36333	0.54	2.0E-05 BF055839.1 2.0E-05 AJ131024.1		T HUMAN	7175g08.y1 NCL CGAP_BrizO Horne septens oDNA done IMAGE:3340578 5
41	23135	36362	1.98	2.0E-05 AJ131024, 2.0E-05 N41751.1	_	HUMAN	Homo seplens clase gene, exon 1-siphs W/91806.1 Shares pleases all the seplents and the seplents are pleases and the seplents and the seplents are pleases and the seplents are pleases and the seplents are pleases and the seplents are pleases and the seplents are pleases and the seplents are pleases and the seplents are pleases and the seplents are pleases and the seplents are pleases and the seplents are pleases and the seplents are pleases and the seplents are pleases and the seplents are pleases and the seplents are pleases and the seplents are pleases are pleases and the seplents are pleases are pleases are pleases and the seplents are pleases

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Single Exort Propes Expressed in Brain	Moet Similar Top Hit Acession Top Hit Acession Signal BLAST E No. Source 1.98 2.0E-05 N41751.1 EST HUMAN welfa06.1 Source, piecenta, 8tobweeks, 2NbHP8toDW Homo sapiens cDNA clone IMAGE:259570 5'	2.42 2.0E-05/A1991026.1 [EST HUMAN wu36h07.x1 Soares Dischgnade colon NHCD Homo sapiens cDNA clone IMAGE:2522077.3"	1.35 2.0E-05 A1463285.1 EST_HUMAN ORP2: FUNCTION UNKNOWN.		2.0E-05 BE175801.1 EST_HUMAN	EST HUMAN	Į.	2.0E-05 D16583.1 NT	1.0E-05 P27448 SWISSPROT	1.0E-05 AL163282.2 NT		¥	1.0E-06 P81274 SWISSPROT	3.2	1.1 EST HUMAN			1 OF OR ARKATAGE STEEL HIMAN 1 recomplished in the contained of the co	1.0E-05 4505844 NT	1.0E-05 P19474 SWISSPROT	27.2 NT	21 EST HUMAN	12.45 1.0E-05/AA236110.1 EST HUMAN repetitive element TAR1 repetitive element TAR1 repetitive element.	0.62 1.0E-05/AV732190.1 EST HUMAN AV732190 HTF Home septems cDNA done HTFBiH01 5'	Г	
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		36363	2	37243 1.	37244	36428 2	* 	2	1		28143			28037	29623			32428 1.	32530			2.	34700 3.	35022 12.	35189 0.	
	Exan ORF SEQ ID NO:	23135 3	19485	23948 3	23948 3	23197 3	25168	25155	25247		15803 . 24	16394 2	16545		16894	16965 2		19415 33	19505			21505	21640 3	21857	22020	
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| Top Hit Descriptor | hd41b02x1 Sogres_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:2912043 3' similar to contains
OFR.tt OFR reportition administration | UHH-BIZ-Soke-OB-OH II 81 NCT COAP State Down control of the state of t | UHHBIZ-40K-0-01:11 NCI CGAP Sub4 Homo seriens cDNA clone INA CE:2724308 3

 | he07c10.x1 NCI_CGAP_Klx12 Homo septens cDNA clone IMAGE::2873010 3' similar to contains L1.t2_L1 repetitive element;
 | Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete ods | Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (FILA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, commissioned | Homo sanians in dimerization makes makes and the sanian sanians and sanians in the sanians of th | #73808.xf NCI CGAP HSC3 Home sentence CNA Appearance of the December of the Conference of the Conferen | DET 1108 At Science placements Birthonesia Statistical Attitution and the second statistics and | Himms design of the control
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cDNA clone IMAGE:1658912.3' similar to contains Alu repetitive element | Homo sapiens chromosome 21 segment HS21C009 | SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED 3Y V-SRC) | SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED 3Y V. SRC) | (intersections and intersection in the control of t | ALTATIVE SERNETHER ONLY DE DEOTETH KINNET RESERVE
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| Expression
Signal | 0.74 | 1.16 | 1.16

 | 1.87
 | 1.07 | 1.97 | 1.38 | 4.8 | 3.53 | 2.82
 | 2.61 | 8.0 | 0.85
 | 13.94
 | 1.1 | 2.60 | 2.69 | 4.3 | 3.46
 | 127 | 0.75 | 0.75 |
| ORF SEQ
ID NO: | 35594 | 35669 | 35670

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 | 36760 | 36761 | 37780 | 28129 | 28498 |
 | 31532 | 32534 | 33099
 | 33450
 | 34197 | 34715 | 34716 | 34976 | 36784
 | 27986 | 36298 | 36299 |
| SEQ ID
NO: | | |

 | 22732
 | 23518 | 23518 | 24438 | 15387 | 15867 | 16350
 | 18604 | 19509 | 20021
 | 20337
 | 27058 | 21572 | 21572 | 21810 | 23538
 | 15597 | 23078 | 23076 |
| Probe
SEQ ID
NO: | 9738 | 9816 | 9816

 | 10084
 | 10836 | 10836 | 11864 | 8248 | 3062 | 3597
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958	13723		2.69	7.0E-06 AA6697;	AA669729.1	EST HUMAN	ab90f10.s1 Strategene lung (#637210) Homo sapiens cDNA clone IMAGE:854251 3' similar to contains MER20.t1 MER20 repetitive element;
1419	14187	26851	3.42	7.0E-06	7682177 NT	NT	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
2876	15843		5.83	7.0E-06 Al36825	Al308252.1	EST HUMAN	qw18g09.x1 NCI_CGAP_UB Homo saplens cDNA cione IMAGE:1991296.3' similar to contains Alu repetitive element.
3551			0.92	7.0E-06 AA3856	AA385542.1	EST_HUMAN	EST99205 Thyroid Hano seplens cDNA 5' end similar to EST containing L1 repeat
2800	18405		5.68	7.0E-06	7.0E-06 AW883141.1	EST_HUMAN	QV2-0T0062-250400-173-h01 OT0062 Hamo sepiens aDNA
5715	18508	31429	1.01	7.0E-06 N98645.	N96645.1	EST_HUMAN	yy65c07.r1 Source_multiple_scleroeis_2Nth-MSP Homo sepiens cDNA clone IMAGE:278412 5
8888	21380	34524	0.7	7.0E-08	11420700 NT	Ę	Homo septens DNA segment, numerous copies, expressed probee (GS1 gene) (DXF88S1E), mRNA
0086	22451		0.45	7.0E-06 Q61147		SWISSPROT	GERULOPLASMIN PRECURSOR (FERROXIDASE)
11930	Ш	30608	2.32	7.0E-06	BF215672.1	EST_HUMAN	601881522F1 NIH_MGC_57 Home septens cDNA clone IMAGE:4083972 5
2018	15884	28320	1.28	6.0E-08	6.0E-06 BE060180.1	EST_HUMAN	QV3-BT0379-010300-105-d11 BT0379 Homo sepiens cDNA
3680		22076	1.08	6.0E-06	6.0E-06 BE069189.1	EST_HUMAN	QV3-BT0379-010300-105-d11 BT0379 Homo sepiens cDNA
4705	15708	28359	1.91	5.0E-06 Q01456	001456	SWISSPROT	OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN)
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5324	18127	30787	1.06	8.0E-06 Q02040		SWISSPROT	PROTEIN XE7
9226			1.48	8.0E-08	8.0E-06 AW801912.1	EST HUMAN	LL5-UM0070-110400-063-g02 UM0070 Homo espiens cDNA
12755	L	30979	2.27	6.0E-06	11418157 NT	L	Homo sepiens calclum chemnel, voltage-dependent, alpha 11 autumit (CACNA1), mRNA
5970	18752	31713	3.27	5.0E-06	5.0E-06 AL 163246.2	LN.	Homo sepiens chromosome 21 segment HS21C048
6245	18019	31883	231	5.0E-06 U07581.	-	Ę	Human ABL gane, exon 1b and intron 1b, and putative M8004 Met protein (M9004 Met) cene, complete cots
7134	19821	32887	1.1	5.0E-06 AB00754	6.1	Ę	Homo septens gene for LECT2, complete cds
8359	21052	34192	0.53	5.0E-06	5.0E-06 AW858972.1	EST HUMAN	RC1-CT0302-120200-013-h02 CT0302 Homo sepiens cDNA
8369	21062	34183	0.53	5.0E-06	5.0E-06 AW856072.1	EST_HUMAN	RC1-CT0302-120200-013-h02 CT0302 Homo sepiens cDNA
10002	22650	35862	6.16	5.05-06	5.0E-06 AA313620.1	EST_HUMAN	EST185496 Colon carchroma (HCC) cell line Homo septens cDNA 5' end
10410	23058	36273	0.45	5.0E-06 P08681		SWISSPROT	COMPLEMENT C2 PRECURSOR (C2/C5 CONVERTASE)
12649	24953	30987	2.83	5.0E-06 A10850-K	A1085045.1	EST HUMAN	HA0877 Human fetal liver oDNA library Homo seplens cDNA
832	13411	28046	Ø.1	4.0E-06 R16287.1	316267.1	EST HUMAN	ya48c03.rt Soares Infant brain 1NIB Home septens cDNA clone IMAGE:53254.5' similar to contains Alu receditive element contains L1 receditive element:
828	13586	28208	7.07	4.0F-06 AW1033	7		xxX8g12.x1 NCI_CQAP_Esc2 Home septens cDNA clone IMAGE:2589574 3' similar to contains Alu receitifue element contains element MFR21 monthly administration.
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	Top Hit Descriptor	tb33e09.x1 NCI_CGAP_HSC2 Hamp sepiens cDNA clone IMAGE:2056168 3'	tb33e09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'	QV2-NT0048-200600-250-h07 NT0046 Homo sapiens dDNA	UHH-BIO-eart-f05-0-UI.s1 NCI_CGAP_Sub1 Homo sepiens cDNA clone IMAGE:27104253'	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds	IL3-CT0214-150200-074-B03 CT0214 Homo sapiens cDNA	WB4c10.x1 NC_CGAP_Bm25 Homo sepiens cDNA done INAGE:2432562.3' similar to contains element	MER22 repetitive element;	TRANSMEMBRANE PROTEASE, SERINE 2	Hamo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region	Hamo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0486	z34b08.s1 Scares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432863 3' similar to	contains L1.t1 £1 repetitive element;	234508.s1 Sceres_fetal_liver_spleen_1NFLS_S1 Homo sepiens cDNA clone IMAGE:432863 3' similar to	contains L1.t1 L1 repositive element;	Homo saplens PP1200 mRNA, complete cds	aix48g11.s1 Soeres_testis_NHT Homo sepiens oDNA clone IMAGE:14092523' similar to contains LTR1.t3 LTR1 repetitive element;	W22205.X1 NCI_CGAP_Ut1 Homo septens cDNA done IMAGE:24256163' similar to TR:060734 060734	LINE-1 LIKE PROTEIN ; contains L1.22 L1 repetitive element;	hq84d12x1 NOL_CGAP_HN13 Hamo septems cDNA clane IMAGE:3124151 3'	hq64d12.x1 NCI_CGAP_HN13 Harro septens cDNA clone IMAGE:3124151 3'	Homo sepiens gene for alpha-1-microglobulin-bitanin, exons 1-5 (encoding alpha-1-mioroglobulin, N- terminus.)	AU159412 THYRO1 Hamp septens aDIVA done THYRO1001602 3'	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	601336213F1 NIH MGC 44 Hamo saplens cDNA clone IMAGE:3890314 5	PAROTID SECRETORY PROTEIN PRECURSOR (PSP.)	RCo-LT0001-261199-011-A03 LT0001 Homo septens cDNA	HOMEOBOX PROTEIN GOOSECOID	POL POLYPROTEIN (CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE)	web4e03.x1 NCI_CGAP_K011 Homo sapiens cDNA clone IMAGE:2297088 3' similar to contains MER30.b1 MER30 repetitive element;
	Top Hit Detabase Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	N	EST HUMAN		EST_HUMAN	SWISSPROT	LN.	<u>L</u> V	<u>FN</u>		EST_HUMAN		EST HUMAN	INT	EST HUMAN		EST HUMAN	EST_HUMAN	EST_HUMAN	LN	EST HUMAN	SWISSPROT	EST HUMAN	SWISSPROT	EST HUMAN	SWISSPROT	SWISSPROT	EST_HUMAN
	Top Hit Acession No.	Al334928.1	4.0E-06 AI334928.1	BF3656121	4.0E-06 AW015401.1	4.0E-06 AF198349.1	4.0E-06 AW848295.1		4.0E-06 AIBB6939.1	015393	4.0E-06 AF009660.1	AJ272285.1	4.0E-08 AB007966.1		3.0E-06 AA700562.1		3.0E-06 AA7005621	3.0E-06 AF202635.1	4A868218.1		41857779.1	3.0E-06 BE047004.1	3.0E-06 BE047094.1	(54816.1	NU159412.1	į.	3.0E-06 BE562984.1	207743	W385262.1		21414	N672138.1
Most Similar	(Top) Hit BLAST E Value	4.0E-06 A133492	4.0E-08	4.0E-06 BF36561	4.0E-06	4.0E-05	4.0E-08		4.0E-08	4.0E-06 015393	4.0E-08	4.0E-06	4.0E-08		3.0E-06		3.0E-06	3.0E-06	3.0E-06 AA86821		3.0E-06 AI85///9	3.0E-08	3.0E-08	3.0E-06 X54816.1	3.0E-06 AU15941	3.0E-06 P08548	3.0E-06	3.0E-06 P07743	3.0E-06 AW3852	2.0E-06 P54368	2.0E-06 P21414	2.0E-06 AI672138
	Expression Signal	4.64	4.64	1.8	217	6.0	1.05		1.89	0.56	3.56	1.24	4.21		1.75	!	1.75	1.44	1.05		607	1.13	1.13	3.74	0.83	2.43	0.83	0.68	3.84	281	4.45	4.8
	ORF SEQ ID NO:			26889	27728	28471	29262		30115	34225	34536	35446	36425		27024	į	27626		28332			20152	29153	29893	31811	-	33801	34413				27838
	SEQ ID NO:	14059	14059	14204	14988	15826	19624		- 1	1	21391	222200	23194		488 888	,	488 888	14989	15888		ייין ייין	18515	16515	17259	18847	19817	20676	21278	24755	13010	14308	15098
	Probe SEQ ID NO:	1311	1311	1457	2281	3060	3874		478	8397	8699	9607	11427		2 2 8 8 8		7.00	283	2022	0	8070	3/83	3783	4524	8088	7129	7981	8684	12340	187	1581	2376

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	Hit Top Hit Descriptor	ROT HISTIDINE-RICH GLYCOPROTEIN PRECURSOR	ROT KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP)	Г	Π	Т	П	1		Т	Т	Т	Г		Т	Homo sections of motion 3 (GPC3) came martial role and flexible research regions	Т		Г	T	ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH	Т	Т	T		208e12.e1 Somes_fetal_liver_spheen_INFLS_S1 Homo sepiens cDNA cione IMAGE:42082.3' similar to contains Alu repositive element:	П
2.6	Top Hit Database Source	SWISSPROT	SWISSPROT	EST HUMAN	EST HUMAN	EST HUMAN	¥	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	ا ا <u>خ</u>	Z	EST HUMAN	EST HUMAN	EST HUMAN	SWISSPROT	TORGREWS	Ę	SWISSPROT	F.	EST HUMAN	EST HUMÀN	SWISSPROT
	Top Hit Acession No.	P04929	P06719	2.0E-08 AV857555.1	2.0E-06 AA173518.1	2.0E-06 AW450215.1	2.0E-06 AB030896.1	2.0E-06 AA974832.1	2.0E-06 AI539448.1	20E-08 AI819424.1	AW869223.1	2.0E-06 T12238.1	2.0E-08 AA772497.1	2.0E-06 H62051.1	2.0E-06 AF003529.1	2.0E-06 AF003529.1	2.0E-06 AI473450.1	2.0E-06 N30678.1	2.0E-06 AV748969.1	23249	076082	1.0E-06 AF084364.1		1.0E-06 AL163278.2	1.0E-08 AA034141.1	A034141.1	27625
	Most Similar (Top) Hit BLAST E Vaiue	2.0E-06 P04929	2.0E-06 P06719	2.0E-08	2.0E-06	2.0E-08	2.0E-08	2.0E-08	2.0E-08	20E-08	2.0E-06	2.0E-08	2.0E-08	2.0E-06	2.0E-06	2.0E-06	2.0E-06	2.05-06	2.0E-06	2.0E-06 P23249	1.0E-06 07e082	1.0E-06/	1.0E-08 P00125	1.0E-06/	1.0E-06	1.0E-06 AAG34141	1.0E-06 P27625
	Expression Signal	2.37	1.68	1.12	1.59	0.82	1.82	0.63	0.83	5.47	1.83	0.57	9.0	1.8	0.82	0.82	0.48	-	0.63	2.1	236	262	1.61	1.87	1.27	1.27	1,34
	ORF SEQ ID NO:	27926	28023	28919	29132	29141	29146		31788	32108		33800		34586	34969	34970		35438		30608	26477	26060	20806	26947	26997	26996	
				_ •	16497		16510	18779	18808	19118	20513	20683	21427	21439	21804	21804	21823	22253	22470	25357	12860	13421	14181	14261	14311	14311	14325
	Probe SEQ ID NO:	2469	2571	3509	3744	3753	3758	2008	6028	6348	7818	7988	8735	8747	9118	9116	9136	0096	9819	12251	32	642	1434	1514	1564	1584	1578

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Probe SEQ ID	Eggn SEQ ID	ORF SEQ	Expression	Most Similar (Top) Hit	Top Hit Acession	Top Hit Databese	Top Hit Descriptor
Ö	ë		Signal	BLAST E Vatue	ď Ž	Source	
11733	24326	37860	1.3	9.0E-07	9.0E-07 AF087913.1	LN	Human endogenous retrovirus HERV-P-T47D
4719	17451	30084	3.26	8.0E-07	8.0E-07 AI288596.1	EST_HUMAN	q82g07.x1 Sogres_NhHMPu_S1 Homo saplens cONA clone IMAGE:1878876.3'
4719	17451	30082	3.26	8.0E-07	8.0E-07 AI288598.1	EST_HUMAN	q82g07.x1 Source_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
96/9	18587		9.43	8.0E-07	8.0E-07 P21414	SWISSPROT	POL POLYPROTEIN (CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE)
7901	20596		8.73	8.0E-07	8.0E-07 AF135416.1	LN	Homo sapiens UDP-glucuronosytransferase gene, complete cds
11622	24219		6.59	8.0E-07	8.0E-07 T07770.1	EST_HUMAN	EST05650 Fetal brain, Stratagene (cat#636206) Homo eaplens cDNA clone HFBEN89
11912	24478		. 8.22	8.0E-07	8.0E-07 AL163280.2	NT	Hamo sapiens chromosome 21 segment HS21C080
1858	14596	27312	0.91	7.0E-07	7.0E-07 AF167341.1	LN.	Homo sapiens membrane interleukin 1 receptor accessory protein (IL1RAP) gene, exons 10 and 11
5432	18231	30044	0.72	7.0E-07	TN 0075009	LN	Homo sepiens ATP-binding cessedte, sub-family A (ABC1), member 8 (ABCA8), mRNA
5432	18231	30945	0.72	7.0E-07	TN 0075000	LN	Homo sepiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
1905	14642	Z22Z	2.98	6.0E-07	6.0E-07 AW855558.1	EST_HUMAN	CM3-CT0277-221089-024-e11 CT0277 Hamo septens cDNA
							Homo seplens HLA class III region containing tenesch X (tenescin-X) gene, pertial cds; cytochrome P450 21- hydroxylase (CYP218), complement component C4 (C48) G11, helicase (SKI2W), RD, complement factor B
2496	15213	27858	4.52	6.0E-07	6.0E-07 AF019413.1	LN LN	(Bf), and complement component C2 (C2) genes.>
3965	16705		1.83	6.0E-07 P41479	P41470	SWISSPROT	HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION
9040	21730	34885	1.52	6.0E-07	6.0E-07 BF001867.1	EST HUMAN	7g94f07x1 NCI_CGAP_Co16 Homo sepiens cDNA clone IMAGE:3314149 3' similar to TR:O75620 O75920 4F5L.;
11836	24420		1.3	8.0E-07		Ī	CM0-BT0281-031199-087-403 BT0281 Homo saplens cDNA
12156	25307		2.28	6.0E-07		EST_HUMAN	CM4-NN1029-250300-121-h12 NN1029 Homo sepiens oDNA
318	13121		1.94	5.0E-07	5.0E-07 Al831893.1	EST_HUMAN	wh64fl0x1 NCI_CGAP_Kld11 Homo sepiens cDNA done IMAGE:2385547 3'
1035	13705		4.25	5.0E-07	5.0E-07 AA380630.1	EST_HUMAN	EST\$\$615 Supt cells Homo sepiens cDNA 6 and
3028	15794		0.88	5.0E-07	5.0E-07 AI831893.1	EST HUMAN	wh64/16.x1 NCL_CGAP_Kd11 Homo seplens cDNA clone IMAGE:2385547 3'
6028	18809	31769	6.0	5.0E-07	5.0E-07 U65067.1	TN	Mus maseculus OG-2 homeodomein protein (OG-2) gene, partial cds
4986	19446	32463	1.00	5.0E-07	5.0E-07 Al393981.1	EST HUMAN	tgodbddLef NCI_CGAP_CL1 Homo sapiens cDNA done IMAGE:2107953 3' similar to contains Alu repetitive alement;
9964	19446	32464	1.69	5.0E-07	5.0E-07 Al393981.1	EST HUMAN	tpotedLat NCI_CGAP_CL1 Homo septens cDNA clone IMAGE:2107963 3' semilar to contains Alu repetitive element.
7248	19833	33008	44	5.0E-07	5.0E-07 AW070885.1	EST HUMAN	xx3444Lti NCI CGAP Bris Homo explore cDNA done MAGE:2568362 3' strillar to gb:X15341 CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER (HUMAN);
8173	20867	33990	0.74	5.0E-07	5.0E-07 Q9WUQ1	SWISSPROT	ADAM-TS 1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 1) (ADAMTS-1) (ADAM-TS-1)
8388	21081		0.82	5.0E-07 P09583	P09583	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
10265	22913	36123	4.94	5.0E-07	5.0E-07 Al908587.1	EST_HUMAN	CM-BT178-220499-014 BT178 Homo sapiens cDNA

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Probe SEQ ID NO:	Eson SEQ ID NO:	ORF SEQ ID NO:	Expression	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10580	23256	36493	1.28	5.0E-07 P08547	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11300	24101	37413	4.04	5.0E-07 P11087	P11087	SWISSPROT	COLLAGEN ALPHA 1(I) CHAIN PRECURSOR
11574	24173		2.62	5.0E-07 AJ27173	6.1	IN	Homo sepiens Xq paeudosutosomal region; segment 1/2
12501	25211		3.48	5.0E-07	5.0E-07 AW862537.1	EST HUMAN	QV0-CT0383-210400-204-b12 CT0383 Homo sepiens cDNA
3961	16729	29364	2.02	4.0E-07	4.0E-07 AW009602.1	EST_HUMAN	ws84h05.x1 NCI_CGAP_Cc3 Homo septens cDNA clone IMAGE:2504697.3'
8202	19769		0.83	4.0E-07	4.0E-07 AJ272285.1	TN	Hamo sepiens SPP2 gans for secreted phosphaprotein 24 precursor, exons 1-8
7167	19854	32923	1.74	4.0E-07 Q9Z2V6	092276	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDA1)
7167	19854		1.74	4.0E-07 09Z2V6	092276	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE IN DA1)
7823	20518	33644	9.0	4.0E-07	4.0E-07 AL163207.2	Į.	Homo sepiens chromosome 21 segment HS21C007
8049	21640	34787	14.3	4.0E-07 AW4191	AW419134.1	EST_HUMAN	xy46g11x1 NOLCGAP_Lu34.1 Hamo septems aDNA clane IMAGE:2836548 3'
10027	22875		74.0	4.0E-07	4.0E-07 BE901975.1	EST_HUMAN	801676748F1 NIH_MGC_21 Hamo septens cDNA clane IMAGE:3959651 5'
10027	22875		27'0	4.0E-07	-	П	801676748F1 NIH MGC 21 Homo septens oDNA dane IMAGE:3959651 5
10223	22871	36084	0.49	4.0E-07 AL 163218	2	Ę	Homo saplens chromosome 21 segment HS21C018
10856	23536	36781	3.14	4.0E-07	-	EST_HUMAN	wi81b08.x1 NCI_CGAP_Kid12 Hamo septens cDNA clone IMAGE:2399703 3'
10856	23536	36782	3.14	4.0E-07		EST_HUMAN	W81b08.x1 NCL CGAP Kid12 Homo sepiens dDNA clone IMAGE.2399703 3'
11184	23840		1.88	4.0E-07	4.0E-07 BE001828.1	EST_HUMAN	PM1-BN0083-030300-003-e12 BN0083 Homo septems cDNA
134	12217	CHRIST	78 0	2 OF 07 1 140740		ţ	Human microfibril-esecciated glycoprotein (MFAP2) gene, putative promoter region and attematively spliced
8	43350	25078	5	2.05.07			
1353	14101	28778	2.67	3 0F-07 M89149	T	1	Human beheria Ay pagakungkungka ragiman 1/2
16222	14369		203	3.0E-07 M64857		Z	Human lolk subgroup I germine game 4 and 2 Vinesian 048 ellale
	!						ni50b09.s1 NCI_CGAP_Ov2 Home septens cDNA done IMAGE:090825 similar to contains Au repetitive
	2,43		1.42	3.0E-07/	2.7	T HUMAN	element, contains L1.t3 L1 repetitive element;
8	5	27749	1.83	3.0E-07 M99149.			Human polymorphic microsetalitie DNA
472	15190	27930	7.61	3.0E-07 BE00607	7.1	EST HUMAN	MR0-BN0115-020300-001-f11 BN0115 Homo sepiens cDNA
2472	15190	27931	7.61	3.0E-07 BE00507	7.1	EST_HUMAN	MR0-BN0116-020300-001-f11 BN0116 Homo septens cDNA
833	15797	28443	1.16	3.0E-07 T84704.1		П	yd50f12.r1 Soares feksi liver spieen 1NFLS Homo saplens cDNA clone IMACE:111695 6
3157	15920	28566	1.45	3.0E-07 P38739		SWISSPROT	HYPOTHETICAL 63.8 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR
4678	17412	30047	7.42	3.0€-07 /	Г	EST HUMAN	AV850201 GLC Homo sepiens cDNA done GLCCCD013'
4711	17443	30075	0.86	3.0E-07 ▶	3.0E-07 AI797236.1	EST HUMAN	we88b12.x1 Somes_NRT_GBC_S1 Homo septens cDNA clone IMAGE:2347967 3*
5004	17727	30330	1.3	3.05-07 157850.1		EST_HUMAN	yc14h09.s1 Strategene lung (#837210) Homo saplens cDNA clone IMAGE:80705.3' similar to similar to gb:M62882 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
5004	1777	30331	1.3	3.0E-07 T67850.	_	EST HUMAN	yc14h09.s1 Stratagene lung (#837210) Homo eaplens cDNA clone IMAGE:80705.3' stmiler to similer to ob:Me2382 ARACHIDONA TE 12-I IPOXYGENASE (HI IMAN)
1						7	

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Probe SEO ID NO: 5580 5883 6883 6883 7408 7408 11856 12791 150 177	Exan SEQ ID NO: NO: 20231 18369 24263 24263 123966 12396 123966 12396 12396 12396 12396 12396 12396 12396 12396 12396 12396 123966 12396	31280 31280 31280 31280 31280 31610	Signal Signal Signal Signal 12.43 12.43 12.43 12.43 14.85 17.75 17	Moet Similer (Top) Hit Top Hit Nature 3.0E-07 (088807 3.0E-07 (088807 3.0E-07 (A/8151) 3.0E-07 (A/8151) 3.0E-07 (A/8151) 3.0E-07 (A/8151) 3.0E-07 (A/8151) 3.0E-07 (A/81584) 3.0E-07 (A/81888) 3.0E-07 (A/81888)	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Top Hit Detabase Source Source Source Source Source SWISSPROT EST HUMAN EST HUMAN SWISSPROT EST HUMAN NT NT NT NT NT NT NT NT NT NT NT NT NT	Top Hit Detachers Source PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4) SWISSPROT WIT-14 PROTEIN PRECURSOR EST_HUMAN OVI-UM0039-200300-115-g02 LIM0038 Homo sepiens cDNA cone IMAGE:1339890 3: EST_HUMAN OVI-UM0039-200300-115-g02 LIM0038 Homo sepiens cDNA cone IMAGE:2281037 3' similar to contains ALL EST_HUMAN W28f11xT NCL CGAP_OA36 Homo sepiens cDNA clone IMAGE:2281037 3' similar to contains ALL EST_HUMAN INTERPRETEDATE OF TRAULATION FACTOR, 64 KD SUBUNIT (CSTF 64 KD SUBUNIT) SWISSPROT CLEAVAGE STIMULATION FACTOR, 64 KD SUBUNIT (CSTF 64 KD SUBUNIT) SWISSPROT CLEAVAGE STIMULATION FACTOR, 64 KD SUBUNIT (CSTF 64 KD SUBUNIT) SWISSPROT Homo sepiens chronosome 8 duplession of the T cell receptor beta locus and trypshogen gene families NT Homo sepiens DiGeorge syndrome critical region, belometic end NT Homo sepiens DiGeorge syndrome critical region, belometic end NT Homo sepiens DiGeorge syndrome critical region, belometic end NT Homo sepiens DiGeorge syndrome critical region, belometic end NT Fuguruthripes belat-cytoplesmic/vescular) actin gene, complete ode
731	13505 13505 13517	28160	2.45	2.0E-07 AF0035 2.0E-07 AF0035 2.0E-07 P11369	2.0E-07 AF003530.1 2.0E-07 AF003530.1 2.0E-07 P11369	NT NT SWISSPROT	Homo septiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions Homo septiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
922 923 1140 1506 3676 5050	13889 13896 14342 16429 17778	28353 28364 28566 27032 29070 30395	3.73 1.37 1.598 1.598 1.593	2.0E-07 AA2232e 2.0E-07 T63042.1 2.0E-07 Q26788 2.0E-07 Q09701 2.0E-07 AF12834	25.	EST_HUMAN EST_HUMAN SWISSPROT SWISSPROT NT EST_HUMAN	208b07.s1 Stratagene NT2 neuronal precursor 937230 Homo sepiens cDNA clone IMAGE:650869 3' similar to gb:L31880 GLYCOPHORIN A PRECURSOR (HUMAN); contains Alu repetitive element; yc15g04.s1 Stratagene h.mg (#637210) Homo sepiens cDNA clone IMAGE:80790 3' similar to contains L1 repetitive element; J6 AUTOANTIGEN HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I Homo sepiens cavecin 1 (CAV1) gene, excn 3 and perital cds xx05h07.x1 Scense_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:2567485 3' similar to WP:C38H2.1 CE00923 PROBABLE RABGAP DOMAINS:

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Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3563	16318	28966	1.15	7.0E-08 P15305	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
10716	23405		1.67	7.0E-08	7.0E-08 AI535743.1	EST_HUMAN	cong3.P11.A5 conorm Homo saplens cDNA 3'
11872	24267	37589	5.17	7.0E-08 U24070.	U24070.1	LN	Rattus norvegicus Munc13-1 mRNA, complete cds
12619	16318		2.98	7.0E-08 P15305	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
12619	16318	28966	2.98	7.0E-08 P15305	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
12690	24975		1.89	7.0E-08 AJ13101	AJ131016.1	NT	Hamo sapiens SCL gene locus
962	13570	26230	2.88	6.0E-08 AL16324	AL163248.2	LN.	Homo sapiens chromosome 21 segment HS21C048
798	13570	26231	2.88	8.0E-08	8.0E-08 AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
2363	15085	27824	2.97	80E-08	6.0E-08 BE144398.1	EST_HUMAN	MR0-HT0168-191199-004-g09 HT0166 Homo septens cDNA
3058	15824	28469	0.81	8.0E-08	7662473 NT	M	Homo sapiens KIAA1074 protein (KIAA1074), mRNA
4222	16963	29588	86.0	B.0E-08 AL16324	AL163248.2	N.	Homo sapiens chromosome 21 segment HS21C048
7851	20546		0.69	6.0E-08 P08547	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
							ob56c05.s1 NCI_CGAP_GCB1 Hamo septens cDNA clone IMAGE:1335368 3' similar to contains
9227	21906		0.56	6.0E-08 AA82707	AA827075.1	EST_HUMAN	MER12.b3 MER12 repetitive element;
-							RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE;
11391	23997	37299	224	5.0E-08 P11369	P11369	SWISSPROT	ENDONUCLEASE
11520	24120		1.33	6.0E-08		LN L	Homo sepiens chromosome 21 segment HS21C009
ಜ	12909	26547	3.72	5.0E-08	5.0E-08 AL 163303.2	L	Homo sapients chromosome 21 segment HS21C103
							nh03b09.s1 NCI_CGAP_Thy1 Homo saplens cDNA clone IMAGE:943193 similar to contains Alu repetitive
RZZ ZZ	14957	27897	1.82	5.0E-08	5.0E-08 AA493851.1	EST HUMAN	oloment,
11814	24477		8.36	5.0E-08 P06681	Posest	SWISSPROT	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
12000	24500	31085		5.0E-08	5.0E-08 AW851878.1	EST_HUMAN	QV0-CT0225-131099-034-e12 CT0225 Homo sapiens oDNA
1754	14496	27185		4.0E-08 P25723	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
1754	14496	27196	76.0	4.0E-08 P25723	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
2888	15655		1.00	4.0E-08	4.0E-08 AL070581.1	EST_HUMAN	DKFZp434J0428_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434J0428 5'
3894	16844	29284	1.04	4.0E-08 U82868.	U82868.1	TN	Homo sapiens shox gene, alternatively spliced products, complete cds
6311	19082	32067	1.08	4.0E-08 P52624	P52624	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
1698	21389	34533	න 0	4.0E-08 O15393	015393	SWISSPROT	TRANSMEMBRANE PROTEASE, SERINE 2
1506	21727	34881	1.05	4.0E-08 L42571.	L42571.1	INT	Cricetulus griseus ribosomal transcription factor (UBF2) mRNA, complete cds
9545	22198		0.71	4.0E-08 P08547	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10228	22876		89'0	4.0E-08	4.0E-08 A1016342.1	EST_HUMAN	ot78d12.s1 Scares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1622903 31
10284	22932	36147	3.87	4.0E-08 A 050027	A[050027.1	EST HUMAN	en22d10.x1 Gessler Wilms turnor Home sapiens cDNA clone IMAGE:1689411 3' similar to contains Aturepoditive element.contains element.
		1				7	

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13424 ZOUGS 13.02 Z.OE-08 AW 886438.1 13735 24.4 Z.OE-08 BE280477.1 14069 Z6743 2.38 Z.OE-08 AL163247.2 14476 12.18 Z.OE-08 BE734871.1	EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN NT EST HUMAN
14069 26743 2.38 2.0E-08/AL163247.2 NT 14776 12.18 2.0E-08/BF734871 FST HIMAN	13-24 ZOUGS 13-02 Z.UE-08 AW 886438:1 EST HUMAN 13735 24-4 ZOE-08 BE280477:1 EST HUMAN
NAMIN TS4 1248 2.0E-08/BE734871 1 FS1 HIMMN	14069 26743 2.38 2.0E-08 AL163247.2 NT
	14476 12.18 2.0E-08/BE734871.1 EST_HUMAN

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Table 4
Single Exon Probes Expressed in Brain

Citigue Lyons Lybrasson II Disant	Most Similar (Top) Hit Acession (Top) Hit Acession Detablesse Signal BLAST E No. Source Surce	35 4.11 2.0E-08 AW270271.1 EST_HUMAN \$\psi49f11.x1 NC _CGAP_HN11 Homo sepiens & ONA clane IMAGE:2743149 3'	20 1.71 2.0E-08 K00216.1 NT Sheep His-#RNA-GUG	28618 7.94	28619 7.94 2.05-08 042280	1.76		11 2.48 2.0E-08 AA459040.1 EST_HUMAN reportitive element;		2.36 2.0E-08 AW572881.1 EST HUMAN	31265 1.19 2.0E-08 AA813204.1 EST_HUMAN	31457 0.83 2.0E-08 AW088624.1 EST_HUMAN	33728 0.92	33832 1.35 2.0E-08 AA490121.1	73 0.9 2.0E-09 AU139978.1 [EST_HUMAN AU139978 PLACE1 Homo saplens cDNA clone PLACE1011719 5		36281 0.79 2.0E-08 N78097.1 EST_HUMAN	A TOMOTIA DO 300 C. O. C	4.54 2.00 M 482584.5 NT	28831 1 16 1 0E D8 1792 SWISSPROT	27211 1.45 1.0E-08 AF125348.1 NT	2.31 1.0E-08 BE141959.1 EST HUMAN	31211 4.85 1.0E-08 AJ010770.1 NT	32 3343 1.26 1.0E-08 P19474 SWISSPROT 52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))	33756 0.52 1.0E-08 AL163302.2 NT		33855 0.54 1.0E-08 AF224669.1 NT	33856 0.64 1.0E-08 AF224659.1 NT	34275 1.94 1.0E-08 AI015304.1 EST_HUMAN	0.45 1.0E-08 P09593 SWISSPROT	28 34958 0.78 1.0E-08 BE072572.1 EST HUMAN PM2-BT0548-210100-004-d02-BT0548 Homo septents cDNA
	ORF SEQ ID NO:			ĺ		 -					_ [31457	33728										31211	33443	33756		33833	33856	34275		34056
	SEQ IO	47 14585	45 15200	15985	L	16591	!	73 17111	_	J	18346	1	3 20508	L.	33 21673	_	16 23062	23767	1	L	L	14777	18310	38 20332	34 20629		20723	. 1	Į		21783
	Probe	1847	2545	3202	3202	3840		4373		4903	5549	5742	7903	8008	8983		10416	10448	12484	1400	1788	2044	5512	7868	Ř	<u> </u>	8028	8028	845	9104	9106

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Table 4
Single Exon Probes Expressed in Brain

) - -	
Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3986	i	35712	1.2	1.0E-08 P79110	P79110	SWISSPROT	TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PROTEIN) (CTP) (TRICARBOXYLATE CARRIER PROTEIN)
10453	23088	36330	0.77	1.0E-08 P99083	P98063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
11285	23946	37241	4.14	1.0E-08	1.0E-08 AF044083.1	¥	Homo sapiens major histocompatibility locus class III region
12282	24715		2.82	1.0E-08	1.0E-08 X51755.1	-N	Human lembda-Immunoglobulin constant region complex (germine)
4218	16959	29583	4.65	9.0E-09	9.0E-09 AL163279.2	LN.	Homo saplens chromosome 21 segment HS21C079
4218	16959	29684	4.65	9.0E-09	9.0E-09 AL163279.2	N	Homo saplens chronosome 21 segment HS21C079
36 67	22610		0.52	9.0E-09	9.0E-09 T97950.1	EST_HUMAN	ye58a12.s1 Soares fetal liver spleen 1NFLS Homo septens cDNA clone IMAGE:121918.3
6890	19150		0.62	8.0E-09	8.0E-09 AIZ70615.1	EST HUMAN	qu86c11.x1 NCI_CGAP_Gas4 Homo saplens cDNA done IMAGE:1978964.3' similar to contains L1.t3 L1 repetitive element:
7164	19851	32920	7.88	8.05-09	8.0F-09.A1183500.1	EST HIMAN	qd42e07.x1 Sceree_fetal_heart_NbHH10W Homo sapiens cDNA done IMAGE:1732164.3' similar to contains MSB1 H MSB1 modellis, algorithms and the contains MSB1 H MSB1 modellis.
7809	20504	33726	2.65	8.0E-09 AW9001	AW900159 1	EST HUMAN	CASOLNATORA ACCIONO 22 AND MANAGE HOUSE ADNA
8887	21678		2.65	8 OF OD	8 0F-09 A 4938997 1	FST HIMAN	774/08 of Scenes NB T CRC of Home control in the Control of the Co
3583	16346	†	1.73	7.0E-09 D86842	D86842.1	Į.	Homo saniems DNA for 3 Lewis and CAA thinks a but within the minetimental sets.
7802	20497		0.61	7.0E-09	7.0E-09 BF108755.1	EST HUMAN	745e10.xt Sciences_NSF_F8_9W_OT_PA_PSt Homo sepiens cDNA clone IMAGE:3524443 3' similar to contains MFR29 b2 MFR29 promittes alarment.
7946	20641	 	0.82	7.0E-09	7.0E-09 AA258200.1		z80c05.r1 Sceree_NhHMPu_S1 Home septems cDNA clone IMAGE:881892 5 similar to contains L1.t2 L1 moetility element:
9159	21829	34963	2.91	7.0E-09 L09709.1	1.09709.1	Т	Hunan Nacsomel membrane diversarities (1 AMPs) wasse Killery and Sankhar main.
10083	22731	35946	1.42	7.0E-00	7.0E-09 BE254850.1	T HUMAN	601111173F1 NIH_MGC_16 Home septens oDNA clone IMAGE:3351834 5
10244	22802		0.5	7.0E-09	7.0E-09 AA058628.1	EST HUMAN	### ## ## ## ## ## ## ## ## ## ## ## ##
10571	23266		1.40	7.0E-09 T97950.1	T97950.1	Т	veS8412.81 Source fetal liver aplean 1NFI S Homo sentens ciDNA close MAAGE 124048 or
2149	14879	-	0.99	8.0E-09/	8.0E-09 AL040439.1	Т	DKFZ0434C0514 rf 434 (swnorum hites) Homo sentene child stene DKFZv434C0644 F
4922	17660	30263	3.12	8.0E-09	8.0E-09 BE188421.1	Т	PM1+T10527-160200-001-005 HT0527 Homo seniore CNA
5296	18101	30760	11.59	6.0E-09	6.0E-09 AW195784.1	T	MBST08 x1 Sources NPL T GBC S1 Homo embiens of NA clares MAAGE 2701/9/1/ 2:
8475	21167	34311	0.93	6.0E-09	6.0E-09 BE161663.1	Т	MR3-HTD448-280300-201-h12-HTD446 Homo sacriens cDNA
9074	21763	34925	1.98	6.0E-09	4503710 NT		Homo seciens fibroblest growth factor recenter 3 (activordinalesis themstrockock Australy (FCED)
10178	22824		3.76	6.0E-09	6.0E-09 AF200923.2	LN PA	Homo sepiens testis-specific kinese substrate (TSKS) gene, complete cds
10632	23324	36561	1.44	6.0E-09 BF10875	5.1	EST_HUMAN	745e10.x1 Soures_NSF_F8_9W_OT_PA_S1 Homo saplens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER29 repetitive element:

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Single Exon Probes Expressed in Brain	Exam ORF SEQ Expression (Top) Hit Acession No. Signal BLASTE No. Source Source	24388 37722 1.37 6.0E-09 C01803.1 EST HUMAS INTRA HUMAS CONTACT HIT IN CHILD STATE CONTACT CON	26818 3.27 5.0E-09 BE149264.1 EST HUMAN	1.06 5.0E-09 AL163284.2 INT	1.73 5.0E-09 AA369454.1	30581 0.76 5.0E-09 U66059.1 NT	34321 0.48	35855 2.22 5.0E-09 AW799667.1 EST HUMAN	2.12 4.0E-09 AL163282.2 NT	2.5 4.0E-09 AL163285.2 NT	8718 NT	27479 2.31 4.0E-09 AF175325.1 NT	27480 2.31 4.0E-09 AF175325.1 NT	4.0E-09 AA350878.1 EST HIMAN	33565 0.59 4.0E-09 AA495747.1	34250 0.62 4.0E-09 T649421 EST HIMAN	36704 2.05 4.0E-09 AL163209.2	36943 1.47 4.0E-09 AI898401.1 EST HUMAN	1.83 4.0E-09 AA195142.1 EST_HUMAN	27810 4.77 3.0E-09 BE222239.1 EST HUMAN	28006 1.2 3.0E.09 BE222230 1 EST LILIMAN	28104 1.13 3.0E-09 P23249 SWISSPROT	28733 112 3 0E.00 BE000000 1 COT LINES	1.08 3.0E.09 AA422724 EST LINAAN	0.7 3.0E-09/X18674.1 NT	29761 3.42 3.0E-09 AF175325.1 NT	29836 1.65 3.0E-09 Q9Y3R6
			L																	27810	28006	28104	28733			29761	28836
	- 0)								╛						- 1			23683	23731	15073	15271	15366	16083	16130	16820	17129	17211
	Probe SEQ ID NO:	11798	1394	1845	6316	5/2/	4	9886	208	\$	1463	2016	2016	2430	7746	8420	10779	11011	11061	2351	2557	2858	3323	3371	4078	4392	4476

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession Na.	Top Hit Database Source	Top Hit Descriptor
7800	20405	33617	1.19		3.0E-09 BE465780.1	EST_HUMAN	be80e02.x1 NCI_CGAP_Kid11 Homo sepiens cDNA clone IMAGE:3194090 3' skniler to TR:O55091 055091 IMPACT PROTEIN.;
10147	22705		1.7	3.0E-09	3.0E-09 AL163247.2	TN	Homo sapiens chromosome 21 segment HS21C047
10945		38873	4.8	3.0E-09	3.0E-09 BF109943.1	EST_HUMAN	772c08.x1 Sogres_NSF_F8_9W_OT_PA_P_S1 Hamo againns cDNA clane IMAGE:3527030 3'
10945	23624	36874	4.8		3.0E-09 BF109943.1	EST_HUMAN	772c08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Hamo sapiens cDNA done IMAGE:3527030 3'
1			2.43		X16674.1	NT	H.saplens PADPRP4 gene for NAD(+) ADP-ribosyltransferase
1236	13984	20053	7.99		2.0E-09 AL163284.2	TN	Homo saplens chromosome 21 segment HS210084
1655	14401		7.46		20E-09 AL118573.1	EST HUMAN	DKFZp781B1710_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761B1710 5
2328	15051	Z7787	1.1	2.0E-09	2.0E-09 Q9Y3R5	SWISSPROT	258.1 KDA PROTEIN C210RF5 (KIAA0833)
3916	16686	20306	3.01	2.0E-09 O80241	060241	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR
5078		30411			M23161.1	NT	Human transposon-like element mRNA
5633	18428	31341	0.55		2.0E-09 A1004062.1	EST_HUMAN	047b09.s1 Soares_testis_NHT Homo sepiens cDNA clone IMAGE:1619897 3'
8028	18838		29.0	2.0E-09	2.0E-09 AL163249.2	LN	Homo sepiens chromosome 21 segment HS210049
6682	19599		0.83	2.0E-09	AA357407.1	EST_HUMAN	EST66142 Kidney IX Homo sapiens cDNA 5 and similar to EST containing L1 repeat
	L						zx63h06.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:796187 5' similar to contains
7351			8.4		2.0E-09 AA481430.1	EST HUMAN	Alu repetitive element;
7423	20100	33188			2.0E-09 W28834.1	EST_HUMAN	52d11 Human retina cDNA randomly primed sublibrary Homo septens cDNA
7117	20381	33494	0.62		2.0E-09 AW862126.1	EST HUMAN	MR1-CT0352-240200-105-b06 CT0352 Homo septens cDNA
8812	21304				AJ271735.1	NT	Homo sepiens Xq pseudoeutosomal region; segment 1/2
11233	23896		1.62		20E-09 AL163248.2	LN	Homo sepiens chromosome 21 segment HS210048
12428	13500		22.07	L	2.0E-09 X16674.1	LN	H.sapiens PADPRP4 gene for NAD(+) ADP-ribosyltransferase
	L					1000	nc11c02.r1 NCI_CGAP_Pr1 Home sapiens cDNA clone IMAGE:1007810 similar to contains Alu repeditive
12490			7.41	Ì	ZUE-UNIAAZZGU7U.1	ES HUMAN	מינוויות ווי
12834	24834		1.75		2.0E-09]U82668.1	LN.	Homo septens shot gene, attentatively spiced products, complete cas
974	13739		0.72		1.0E-09 W78152.1	EST HUMAN	zd79d03.s1 Scares_fetal_heart_NbHH19W Homo saplens cDNA clone fMAGE:348853 3' shrifar to ab:L02832 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
1087	L	26603			5031624 NT	Ę	Home saplens CCAAT-box-binding transcription factor (CBF2) mRNA
1087	_			1.0E-09		N	Homo septens CCAAT-box-binding transcription factor (CBF2) mRNA
1630	14376		1.17		1.0E-09 AJ229041.1	LN	Home saplens 959 to config between AML1 and CBR1 on chromosome 21q22; segment 1/3
							Homo sepiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis Inhibitory
2892					U80017.1	LN.	protein (nalp) and survival motor neuron protein (smn) genes, complete cds
2926		28336			1.0E-09 M28690.1	۲.	Homo sepiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
2926			3.25	ı	1.0E-09 M28699.1	LN	Homo septens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
3034	15800	28446	7.0	1.0E-09	1.0E-09 BE535440.1	EST_HUMAIN	601058602F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445177 5'
!	į	i					

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Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Detabese Source	Top Hit Descriptor
77727	2777		4		1 05 00 \$ 8.710207 4	NALM ILL TAR	ZIS5003.s1 Source_prince_glerid_M3HPG Homo saplens cDNA done IMAGE:414029 3' similar to contains. All meastitus element contains element MFR22 magailities element.
1 2 2	18245	20022			1.05-09 AN 163283 2	LN TN	Hamp septembly chromosome 21 segment HS21C083
240	18532				1.0E-09 U07000.1	NT	Human breatpoint cluster region (BCR) gene, complete cds
8	18833				P20094	SWISSPROT	CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
8280	20083				1.0E-00 Ale88474.1	EST HUMAN	wd39b05.xt Soares, NFL_T_GBC_S1 Homo seplens cDNA done IMAGE;2330481 3' similar to contains MER25.tt MER25 repetitive element;
10212	1				1.0E-09 AL163283.2	NT	Hamo suplens chromosome 21 segment HS21C083
11799	l		1.08		3.2	LN	Homo sapiens chromosome 21 segment HS21C083
12333	25344	30717		Ĺ	11418127 NT	¥	Hamo sepiens GTP binding protein 1 (GTPBP1), mRNA
12503	24867		1.35		1.0E-09 T83176.1	EST_HUMAN	ye24e05.r1 Stratagene lung (#637210) Homo sapiens cDNA clone IMAGE:118688 5'
1286	14038	28707	3.74		9.0E-10 AW867740.1	EST_HUMAN	MR0-SN0040-050500-002-c07 SN0040 Hamo septens cDNA
2838	15808	28256	14.4		9.0E-10 AI870071.1	EST HUMAN	we78h03.x1 Scenes_Dieckgraefe_colon_NHCD Homo sepiens cDNA clone IMAGE:2347253 3' similar to SW:RL29_HUMAN P47914 603 RIBOSOMAL PROTEIN L29 ;contains element PTR5 repetitive element;
6735	19680				9.0E-10 Al452982.1	EST_HUMAN	tig6b09.x1 Soarse_NSF_FB_9W_OT_PA_P_S1 Homo septens cDNA clone IMAGE:2144537 3' stmilar to TR:000372 000372 PUTATIVE P150.;
142	12957	25599	13.27	L	8.0E-10 U83630.2	NT	Homo sepiens MCM4 (MCM4) and DNA-PKcs (PRKDC) genes, partial cds
3337	16097		0.88		8.0E-10 BE080748.1	EST_HUMAN	QV1-BT0631-150200-071-f01 BT0631 Hamo sepiens cDNA
4177	16017	20644	3.17	i	8.0E-10 AA376832.1	EST_HUMAN	EST89584 Small trisetthe Homo saplens cDNA 5' end
59962	22515		2.44		8.0E-10 U36308.2	NT	Homo sapiens lens major intrinsio protein (MIP) gene, complete ods
6885	13460	28107	9.36		7708225 NT	LΝ	Homo sapiens TPA Inducible protein (LOC51589), mRNA
989	13460		98.6	7.0E-10	7708225 NT	LN	Hamo sapiens TPA inducible protein (LOC51596), mRNA
1618	14385	27055	2.24		7.0E-10 Q13342	SWISSPROT	LYSP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SP100)
2013	14748		3.17	7.0E-10 P08548	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
2564	15278		24.23	7.0E-10 P08647	P08647	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3086	15850	28491	2.19		7.0E-10 X00858.1	L	H.seplens DHFR gene, exen 3
2609	18870	31836	4.18		7.0E-10 AA345220.1	EST HUMAN	EST51247 Gall bladder II Homo saplens cDNA 5' end
7316	19990	33078	1.08		7.0E-10 BF352883.1	EST_HUMAN	IL3-HT0619-110700-209-D12 HT0619 Homo seplens cDNA
7558	20228		1.48		7.0E-10 P35084	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
7875	20570					F	Hamo sepiens presentiin-1 gene, exans 1 end 2
7875	20570				7.0E-10 AF029701.2	LΝ	Homo sapiens presentitin-1 gene, excus 1 and 2
10209	22857	36073	1.67		7.0E-10 L08895.1	LN.	Homo septens MADS/MEF2-family transcription factor (MEF2C) mRNA, complete cds

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Table 4
Single Exon Probes Expressed in Brain

	ORF SEQ ID NO: 28132 28132 34518 34519 36373	Expression Signed 3.5 1.21 1.21 1.27 1.27 1.27 1.27 1.27	Moss (75 (75 (75 (75 (75 (75 (75 (75 (75 (75	4. Sinitar AST E No. AST E No. AST E No. 6.0E-10 AJ424405.1 6.0E-10 AA24405.1 6.0E-10 P33730 6.0E-10 P33730 6.0E-10 P33730 6.0E-10 P32730 6.0E-10 AW971923.1 5.0E-10 AW971923.1	Top Hit Database Source Source EST HUMAN EST HUMAN SWISSPROT SWISSPROT EST HUMAN EST HUMAN EST HUMAN	Top Hit Descriptor Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene end C11orf17 gene #02407.x1 NCI_CGAP_Pr28 Homo sepiens dDNA done IMAGE:2085021 3' FC3-C10254-031098-012-g12 C10254 Homo sepiens dDNA E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E) E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E) ENTEROPEPTIDASE PRECURSOR (ENTEROKINASE) EST384012 MAGE resequences, MAGL Homo sepiens dDNA DKFZp434N219_J 434 (synonym: hess) Homo sepiens cDNA done DKFZp434N219 5'
16224 17659 18907 22114 22114 12830	35.289 35.289 35.289	2.5 1.51 1.89 1.89 1.80		6.0E-10 G01033 6.0E-10 AF181897.1 6.0E-10 BF105159.1 6.0E-10 P34678 6.0E-10 P34678		HYPOTHETICAL GENE 48 PROTEIN Homo septens WRN (WRN) gene, complete cds 60/1822164F1 NIH_MGC_75 Homo septens d'ONA clone IMAGE:4042413 5' HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III GOBTOS.XI Scares_placenta_8to&weeks_2NbHP8to&W Homo septens cDNA clone IMAGE:1756049.3' similar to contains LTR8.b.2 LTR8 repetitive element;
13348 14725 15294 19767	25976 27446 28032 32831	0.74 1.31 3.73 26.71	4.0E-10 4.0E-10 4.0E-10	2.4 80.1 3.1		n/84s01.s1 NCI_CGAP_Cos Homo saplens cDNA clone IMAGE:924648.3' hg58g03.x1 NCI_CGAP_GC6 Homo saplens cDNA clone IMAGE:2946844.3' similar to contains Alu repetitive element; Homo saplens ohromosome 21 segment HS21C103 Homo saplens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
22743 22890 13863 14078	36208	0.49 0.89 3.65 4.72	11 }	4.0E-10 AW283243.1 4.0E-10 Al287342.1 3.0E-10 N38113.1 3.0E-10 AY085150.1	EST HUMAN EST HUMAN EST HUMAN NT	UI-H-BI2-ahl-a-07-0-UI.a1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727061 3' eq63h11.x1 Stanley Frontsi SN pool 2 Homo sapiens cDNA clone IMAGE:2725653 yy22706.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:272963 3' similar to contains L1.t1 L1 repetitive element: Homo sarviens extraoeliular chacocodeliular chacocodel
17234 17234 18169 19887 19032	28864 28865 30865 31856 32007	1.04 1.24 2.52 3.43	3.0E-10 AL1632 3.0E-10 N60109 3.0E-10 P20350 3.0E-10 BE3028	33.2	T HUMAN ISSPROT T HUMAN	Homo sepiens chromosome 21 segment HS21C003 Homo sepiens chromosome 21 segment HS21C003 yz11g08.s1 Soeree _multiple_solerosis_ZNIbHMSP Homo sepiens cDNA clone IMAGE:282782.3: RHOMBOID PROTEIN (VEINLET PROTEIN) ba78d08.y1 NIH_MGC_Z0 Homo sepiens cDNA clone IMAGE:2006319.5

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					5	אום דיייים פוה	Single Extended Expressed in plant
Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Vatue	Top Hit Acessian No	Top Hit Defabase Source	Top Hit Descriptor
7880	20324	33432	1.42	3.0E-10	3.0E-10 AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBGD08 5'
7660	20324	33433	1.42	3.0E-10	3.0E-10 AV743302.1	EST_HUMAN	AV743302 CB Hamo sepiens cDNA clone CBFBGD08 5
8629	21321	34463	1.2	3.0E-101H87208	H87208.1	EST HIMAN	ys74b12.s1 Scenes retine N2b4HR Homo sepiens cDNA done IMAGE:220511.3' similar to contains MER29 repositive element:
7408		1	1.58	3.0E-10 AW8507	AW850731.1	EST HUMAN	IL3-CT0219-180200-084-B06 CT0219 Homo septems cDNA
8047	L			3.0E-10 AW8507	AW850731.1	EST_HUMAN	IL3-CT02A9-160200-084-B06 CT02Y9 Homo septens cDNA
9240	21919		92.0	3.0E-10	3.0E-10 AF020503.1	L _Z	Homo septens FRA3B common fractile recton, diadenostine triphosphate hydrolese (FHIT) nerve arm 5
10359			237	3.0E-10 T65891.1	T65891.1	EST HUMAN	yc11e12.r1 Stratagene kmg (#837210) Homo eaplens cDNA clone IMAGE:80398 5
10483	1		1.34	3.0E-10	3.0E-10 AA789294.1	EST HUMAN	nz36g03.s1 NCI_CGAP_GCB1 Homo septens cDNA clone IMAGE:1289908 3'
12584	24907	31003	2.65	3.0E-10 BE1795	BE179517.1	EST_HUMAN	IL3-HT0618-110500-136-E07 HT0818 Homo sepiens cDNA
34	12862	25470	1.67	2.0E-10 P48988	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTICEN B (CENTROMERE PROTEIN B) (CENP-B)
34	12862	25480	1.67	2.0E-10 P48988	P48968	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
	l						Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial ods, neuronal apoptosis inhibitory
3	1		1.96	2.0E-10 U80017.	U80017.1	LN	protein (naip) and survival motor neuron protein (emn) genes, complete ods
2085	15751		1.04	2.0E-10 BF67504	BF675047.1	EST HUMAN	602136640F1 NIH_MGC_83 Hamo septiens cDNA clane IMAGE:4273377 5
5714	18507		2.54	2.0E-10 Q28540	Q28640	SWISSPROT	(HPRG)
							Homo septiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) send cytochrome P450 polypeptide 7 (CYP3A7) genes, complete ods; and cytochrome P450
6156		31900	1.37	2.0E-10	2.0E-10 AF280107.1	F	polypepticle 5 (CYP3A5) gene, pertial cds
7279	19963	33039	6.47	2.0E-10	2.0E-10 BE7910821	EST_HUMAN	801588208F1 NIH_MGC_7 Hamo sepiens cDNA clone IMAGE:3940824 5'
7912	20807	33737	0.48	2.0E-10 P26800	P26800	SWISSPROT	POL POLYPROTEIN (CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H)
7912	20807	33738	0.48	2.0E-10	P28809	SWISSPROT	POL POLYPROTEIN (CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H)
					i		7678d08.X1 NCI_CGAP_KId11 Homo sepiens cDNA clone IMAGE:3842303 3' shrillar to combine L1.t3 L1
920Z	21871	·	08.0	2.0E-10 BF43450	BF434565.1	EST_HUMAN	repetitive element;
11207	23968		1.37	2.0E-10	2.0E-10 AIB62153.1	EST HUMAN	har10f12.x1 Soures_total_fetus_Nb24F8_9w Homo septems cDNA clone IMAGE:2043695 3*
488	14245		1.87	1.0E-10,	1.0E-10 AW867767.1	EST_HUMAN	MR0-SN0038-290300-001-f01 SN0038 Homo sepiens cDNA
1602	14348	27037	3.18	1.0E-10	1.0E-10 AV652123.1	EST_HUMAN	AV652123 GLC Homo sepiens cDNA clone GLCCXA113'
2586	15300		3.16	1.0E-10,	1.0E-10 AW862001.1	EST_HUMAN	QV0-CT0225-191199-068-608 CT0225 Homo sepiens cDNA
3491		28901	0.89	1.0E-10	1.0E-10 AW832912.1	EST_HUMAN	QV2-TT0003-161199-013-g10 TT0003 Hamo sepiens aDNA
3528			0.7	1.0E-10	1.0E-10 AL041685.1	EST_HUMAN	DKFZp434N1317_r1 434 (synonym: https3) Homo saplens cDNA clone DKFZp434N1317 5
3825	16284		1.03	1.0E-10	1.0E-10 AL041685.1	EST HUMAN	DKFZp434N1317_r1 434 (synonym: htes3) Homo septens cDNA clane DKFZp434N1317 5'
3996	16744		6.19	1.0E-10	1.0E-10 AF213884.1	LΝ	Homo saplens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds

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Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signel	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Detabase Source	Top Hit Descriptor
4108	16851	71462	5.1		1.0E-10 U52111.2	TN	Homo septens X28 region neer ALD focus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein Kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4108	16851	25478	5.1		1.0E-10 U52111.2	ŢN	Homo sapiens X29 region neer ALD locus containing duel specificity phosphalase 9 (DUSP9), ribosomal protein L18e (RPL18a), Ca2+/Calmodulin-dependent protein lidnase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), advendeukodystrophy protein >
4113	16856		1.94		1.0E-10 AB031069.1	N	Hamo sapiens PCCX1 mRNA for protein containing CXXC domain 1, complete cds
4149	16891		1.84		1.0E-10 M30629.1	LN LN	Human pregnancy-specific glycoprotein beta-1 (SP1) mRNA, last exon
5085	17804		1.61	1.0E-10	1.0E-10 Al797745.1	EST_HUMAN	we82f04.x1 Source_NFL_T_GBC_S1 Homo septens cDNA clone IMAGE:2347815.3' similar to contains MER31.t1 MER31 repositive element;
67.20	19635	32678	0.06		1.0E-10 AF003528.1	Į.	Homo sepiens X-linked antidrotite ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
7375	20055		0.65		1.0E-10 P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7583	20261	33357	0.55		AU128584.1	EST_HUMAN	AU128584 NT2RP2 Hamo septens dDNA clane NT2RP2003751 5
8138		33968	1.04		1.0E-10 AW408990.1	EST_HUMAN	1B_6A4 Fetal brain library Homo sepiens cDNA
8553	21245		1.07		1.0E-10 Al268340.1	EST_HUMAN	qm04e10.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1880874.3' similar to contains L1.t1 L1 repetitive element;
10102	22750		4.01		1.0E-10 AA081868.1	EST_HUMAN	Z123g08.11 Stratagene neuroepithelium NT2RAMI 937234 Homo sepiens cONA clone IMAGE:548314 5'
10831	23513	36754	2.65		1.0E-10 Al038280.1	EST_HUMAN	oy85h03,x1 Soeres_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:167,2861 3'
11896	17913		1.71	1.0E-10	1.0E-10 X87344.1	Ł	H.sepiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING9, 9, 13 and 14 genes
255	13063	25702	1.59	9.0E-11	9.0E-11 BE145600.1	EST_HUMAN	1L2-HT0203-291099-018-c08 HT0203 Homo sapiens cDNA
2097	14828	27561	6.12		9.0E-11 AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: http://) Hamo septens cDNA clane DKFZp547D225 5'
2097		27562			9.0E-11 AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfbr1) Homo sapiens cDNA clane DKFZp547D225 5
3378	16137	28795	2.45		9.0E-11 AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547D225 5'
3378	16137	28796			9.0E-11 AL134395.1	EST_HUMAN	DKFZp547D225_r1 647 (synonym: http:// Homo saplens cDNA clone DKFZp547D225 6'
4465		29827			9.0E-11 AA775985.1	EST_HUMAN	ae78f01.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:970297 3'
5487	18286		3.83		9.0E-11 BE079780.1	EST_HUMAN	RC8-BT0627-140200-011-E06 BT0627 Homo sapiens cDNA
10054	22702		1.19		9.0E-11 AA324960.1	EST_HUMAN	EST27872 Cerebellum II Homo sapiens cDNA 5' end
10054	22702	35920	1.19		9.0E-11 AA324960.1	EST HUMAN	EST27872 Cerebellum II Hamo saptens cDNA 5' end
12258	24703	31080	3.9		9.0E-11 C16635.1	EST_HUMAN	C16535 Clontech human sorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-508B08 5
3114	15879		8.33		8.0E-11 H19871.1	EST HUMAN	yn53f11.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:172173 3' similer to contains L1 repetitive element;
1	1						

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E	Top Hit Acession No.	Top Hit Detabese Source	Top Hit Descriptor
				A SILVE			
3045	16695	29334	0.7	8.0E-11	A1478617.1	EST_HUMAN	Im54c09.x1 NCL_CGAP_Kid11 Homo sepiens cDNA clone IMAGE:21618363*
4022	16768		4.88	8.0E-11	8.0E-11 N23712.1	EST_HUMAN	yw48e06.st Weizmenn Olfsclary Epithelium Hamo sapiens cDNA clone IMAGE:255298 3'
							x45h11.x1 NCI_CGAP_Bm50 Home sapiens cDNA done IMAGE:2621061 3' similar to contains MER10.t1
8674				8.0E-11	8.0E-11 AW166158.1	П	MER10 repositive element;
1430	14177	26862	1.75	7.0E-11	7.0E-11 AA330642.1	EST_HUMAN	EST34392 Embryo, 8 week I Homo saplens cDNA 5' end
3852	16802	20240	1.83	7.0E-11	7.0E-11 AJ277548.2	Ę	Homo sepiens WEE1 gene for protein kinase and partial ZNF143 gene for zino finger transcription factor
8396	L	34224	2.05	7.0E-11	7.0E-11 AF163864.1	N L	Homo sepiens SNCA isoform (SNCA) gene, complete ods, elternatively epiloed
10128			1.17	7.0E-11 P11380	P11360	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN (CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE)
403		25837		6.0E-11	6.0E-11 M55270.1	N.	Human matrix Gla protein (MGP) gene, complete cds
8	13188		7.01	6.0E-11	6.0E-11 M55270.1	Ę	Human matrix Gla protein (MGP) gene, complete cds
8822	19384	32398	0.67	8.0E-11	6.0E-11 L44140.1	Ę	Homo saptens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenaee (GBPD) gene, complete ode's
7583	1			G.0E-11 P08547	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8262	20958			8.0E-11	6.0E-11 AV727859.1	EST_HUMAN	AV727859 HTC Homo septens aDNA clone HTCASC08 5'
9213	21892			6.0E-11	6.0E-11 BE063509.1	EST_HUMAN	CM0-BT0281-031199-067-e03 BT0281 Homo sepiens cDNA
11	12838	25451	1.49	5.0E-11	5.0E-11 AL163283.2	N	Hamo saplens chromosome 21 segment HS21C083
3359	12838	25451	1.0	5.0E-11	5.0E-11 AL163283.2	Į.	Homo sapiens chromosome 21 segment HS21 C083
4203	16044	129671	1.36	5.0E-11	5.0E-11 P48034	SWISSPROT	ALDEHYDE ÖXIDASE
8423	19191	32187	1.63	5.0E-11	5.0E-11 AL163213.2	N	Homo sapiens chromosome 21 segment HS21C013
7430	20102	33194	14.05	5.0E-11	11416799 NT	LN	Homo sapiens protocacherin beta 3 (PCDHB3), mRNA
1380	14127		1.94	4.0E-11			zu01b12.r1 Soeres_testis_NHT Hamo sepiens cDNA clane IMAGE:730559 5'
2783	15498		7.14	4.0E-11	4.0E-11 BE885900.1	THUMAN	601507531F1 NIH_MGC_71 Hano sapiene cDNA clane IMAGE:3908295 5
2963	15735		1.16	4.0E-11	4.0E-11 AL 163247.2		Homo sapiens chromosome 21 segment HS21C047
4576	17311	20030	0.85	4.0E-11	4.0E-11 D44888.1	EST_HUMAN	HUMSUPY069 Human brain oDNA Homo sepiens oDNA done 069
6384	19153	32153	3.2	4.0E-11 P20095	P20095	SWISSPROT	PRE-MRNA SPLICING FACTOR RNA HELICASE PRP2
8003	10641	3.288R	C	4 0E 44	4 0E-44 88442830 4	POT LINAN	2/36/10.71 Soeres_testis_NHT Homo septens CDNA clone IMAGE:75/7963 5' similar to TR:G1055250
3					W+12000.	LOWDING TO THE	
7274	19958		4.5	4.0E-11	AF224009.1	Ž	Homo septens mennosidase, bela A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8282	21962		1.79	4.0E-11	4.0E-11 BE149425.1	EST_HUMAN	RC1-HT0256-210100-013-108 HT0256 Homo saplens cDNA
9562	22216	35402	6.0	4.0E-11	4.0E-11 Al609753.1	EST HUMAN	tf82g12.x1 NCI_CGAP_Bm23 Homo sepiens cDNA clone IMAGE:2105630 3' similar to WP:ZK353.1 CE00385;

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SEO ID SE	on the Carlot Loves Lybrasses in company	Most Similar Top Hit Acession (Top) Hit Descriptor Top Hit Descriptor Signal BLASTE No. Source	31029 1.47 4.0E-11 11545732 NT	222 26908 2.8 3.0E-11 6679077 Mus musculus expressed in non-metastatic cells 2, protein (NM23B) (Nme2), mRNA	1.04 3.0E-11 AA309248.1 EST_HUMAN	26372 1.97 2.0E-11/A/150502.1 EST_HUMAN	26580 3.99 2.0E-11 R24807.1 [EST_HUMAN]	26581 3.99 2.0E-11 R24807.1 [EST_HUMAN]	27042	554 27045 4.86 2.0E-11 L17432.1 NT COR3'beta (COR3'beta) genes, complete cds		27048 1.21 2.0E-11 AI126371.1 EST_HUMAN	28607 7.58 2.0E-11 P10263 SWISSPROT	28730	POLYPEPTIDE N-ACETYLGALACTOSAMINY LIRANSFERASE (PROTEIN-UDP	28771 0.93 2.0E-11 Q10473 SWISSPROT	1.01 2.0E-11 AF020503.1 . INT	0.72 2.0E-11/AL163227.2 NT	1.77 2.0E-11 BE062558.1 EST_HUMAN	31785 1.02 2.0E-11 AW877806.1 EST_HUMAN	31968 1.87 2.0E-11/AA581028.1 EST_HUMAN	32850) 0.59) 2.0E-11 BF592945.1 EST_HUMAN	177 0.66 20E-11 P37072 SWISSPROT OLFACTORY RECEPTOR-LIKE PROTEIN COR6	1,14	36046 5.44 2.0E-11 Q13606 SWISSPROT	36277 1.12 2.0E-11 AW865874.1 EST_HUMAN	36278 1.12 2.0E-11 AW885874.1 EST HUMAN
10 SE Den 10 SE Den		ORF SEQ ID NO:		26908		\rfloor						27048	28607	28730						31785	31968	32850		<u> </u>	36048		l

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Vælue	Top Hit Acession No.	Top Hit Detabese Source	Top Hit Descriptor
11056	23726	36997	1.48	2.0E-11	2.0E-11 AA035369.1	EST HUMAN	zk27g02.s1 Soares_pregnent_uterus_NbHPU Homo sepiens cDNA clone IMAGE:4717943'
11056	23726	96696	1.48	2.0E-11	2.0E-11 AA035368.1	EST_HUMAN	zk27g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471794 3'
11090	23760	37035	12:1	2.0E-11	2.0E-11 AA281958.1	EST_HUMAN	zs18b04.rl NCI_CGAP_GCB1 Homo septens cDNA clone IMAGE:685519 5
12017	26332		1.54	20E-11	20E-11 AA704195.1	EST_HUMAN	2/7/e03.s1 Scares fetal liver spleen 1NFLS_S1 Hamo sepiens cDNA clone IMAGE:460924 3'
12048	24587		3.54	20E-11		EST_HUMAN	RC0-CN0027-210100-011-c01 CN0027 Homo saplens cDNA
12073	24588	31123	1.87	2.0E-11	2.0E-11 BF377859.1	EST_HUMAN	CM2-TN0140-070900-372-g01 TN0140 Homo sapiens cDNA
12332	24748		2.67	2.0E-11	2.0E-11 D25217.2	TN	Homo sapiens mRNA for KIAA0027 protein, perties cds
12479	24840		3.14	20E-11 P08547	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
12781	25035		3.37	2.0E-11	11417968 NT	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
661	13437	28078	1.34	1.0E-11	1.0E-11 AJ131018.1	TN	Hamo sapiens SCL gene locus
1195	13947	28611	3.35	1.0E-11	1.0E-11 AL 163279.2	TN	Homo sapiens chromosome 21 segment HS21C079
1485	14232		2.38	1.0E-11	1.0E-11 AF119914.1	Z	Hamo saplens PRO3078 mRNA, complete cds
2030	14785	27494	1.13	1.0E-11 P16268	P16268	SWISSPROT	OXYSTEROL-BINDING PROTEIN
2122	14853	27582	2.91	1.0E-11	1.0E-11 AF000573.1	LN.	Homo sapiens homogentisate 1,2-dloxygenase gene, complete cds
3490		28900	12	1.0E-11	1.0E-11 BE004315.1	EST_HUMAN	CA/0-BN0105-170300-292-d12 BN0105 Homo septens cDNA
5249	18055	30683	16.93	1.0E-11	1.0E-11 AL163247.2	LN.	Homo sapiens chromosome 21 segment HS21C047
							7p57d01x1 NCI_CGAP_Pr28 Hamo saplens cDNA clane IMAGE:3649945 3' similar to contains MER10.b3
5741	18533	31456	0.63		BF22264	EST HUMAN	MER to repetitive element;
8101	20795	33926	3.15	1.0E-11	4885546 NT	L	Homo sapiens PHD finger protein 2 (PHF2) mRNA
8480	21172	34317	2.44	1.0E-11	1.0E-11 R13174.1	EST_HUMAN	y73d08.r1 Soares infant brain 1NIB Homo eaplens cDNA clone IMAGE:28166 5'
8946		34782	1.89	1.0E-11	1.0E-11 BF365119.1	EST_HUMAN	QV4-NN1149-250900-423-e03 NN1149 Hamo septens cDNA
8946	21687	34783	1.89	1.0E-11	1.0E-11 BF365119.1	EST_HUMAN	QV4-NN1149-250900-423-a03 NN1149 Homo sepiens cDNA
11257		37212	1.62	1.0E-11	1.0E-11 BF680078.1	EST_HUMAN	802(54807F1 NIH_MGC_83 Hamo sepiens cONA clane IMAGE:4295977 5'
9697	22348	35542	1.07	9.0E-12	9.0E-12 AL 163300.2	L	Homo sapiens chromosome 21 segment HS21C100
9697		35543	1.07	9.0E-12	AL163300.2	NT	Homo sepiens chromosome 21 segment HS21C100
9237			26.0	8.0E-12	8.0E-12 BE074720.1	EST_HUMAN	ILE-BT0578-130300-038-G12 BT0578 Homo septens cDNA
12125	24817		3.91	8.0E-12	8.0E-12 AJ271736.1	NT	Homo saplens Xq pseudoautosomal region; segment 2/2
4613	17348	29982	1.18	7.0E-12	7.0E-12 Q05904	SWISSPROT	34 KD SPICULE MATRIX PROTEIN PRECURSOR (LSM34)
11322	24013	37316	69.6	7.0E-12	7.0E-12 AA704736.1	EST_HUMAN	423g01.s1 Scares fetal liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:4511523'
3535	16291		0.71	6.0E-12	6.0E-12 AV730554.1	EST_HUMAN	AV730554 HTF Homo sapiens cDNA clone HTFAW F08 5'
							nz88f11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1302573 3' similer to contains Alu
4314	17063	29678	8.52	6.0E-12	6.0E-12 AA732516.1	EST HUMAN	repetitive element;
6295	19068	32051	22.0	6 OF-12	6 OF-12 AFG2OFG3 1	Ę	Homo sapters FRA3B common fractile rection, disnernosine hibhosobate hicholese (FHIII) cense secon 5
	1						

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Detabase Source Source Source Source T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN	Top Hit Aces No. AF003249.1 T06673.1 T06673.1 T06673.1 BE047779.1 AL163278.2 AL163278.2 AL163278.2 AL163278.2 AL163278.2 AL16327.1 AL040739.1 AL040739.1 AL040739.1 AL040739.1 AL163303.2 AAT00007.1 ABC45140.1		Signal Signal 1.04 1.04 1.167 1.33 1.62 1.33 1.163 1.1		<u> </u>	SEQ ID NO: 0.0.1 NO: 0.0.2
	-	4.0E-14	7	2000	4	2
		4	1		1	
	Γ	4.0E-12	4.2	36954	L	11019
		4.0E-12	0.87	34418		8587
		4.0E-12	3.2			8141
		-				
7	BF445140.1	4.0E-12	0.72			7519
						!
7		4.0E-12	8.0		_	4577
T	AA700328.1	4.0E-12	4.03	25686		238
7		4.0E-12	42			Ř
	FC 10 180	2.00	E.		1	3
		505-12	470		L	10468
		5.0E-12	0.78			10262
	3.2	5.0E-12	4.45			10175
		5.0E-12	0.96	35161		8323
٥			1			
		5.0E-12	2.83			9006
			0.54			8893
			0.65			8586
		5.0E-12	1.33			8128
						_
	AL040739.1	5.0E-12	1.16			6942
	AL040739.1	€.0E-12	0.94			6033
	AW974760.1	5.0E-12	11.33			6388
	8.2	5.0E-12	6.41			5631
	8.2	6.0E-12	6.41			5931
	6.1		5.03			3713
T_HUMAN	9.1		1.61			3385
	T06573.1		3.62			1020
	AA847898.1		1.67			9374
		6.0E-12	1.04			88
Top Hit Database Source		(Top) Hit BLAST E	Expression Signer	ORF SEQ ID NO:		SEQ ID
gie Exon Prope	IIIO					
	Top Hit Database Source Source Source T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN	Top Hit Acession	Single Exon Prob Most Similar (Top) Hit Pages of Pages of Pages 6.0E-12 AA847898.1 EST HUMAN 6.0E-12 AA847898.1 EST HUMAN 6.0E-12 AL163278.2 NT 6.0E-12 AL40739.1 EST HUMAN 6.0E-12 AL40739.1 EST HUMAN 6.0E-12 AL40739.1 EST HUMAN 6.0E-12 AL40739.1 EST HUMAN 6.0E-12 AL40739.1 EST HUMAN 6.0E-12 AL40739.1 EST HUMAN 6.0E-12 AL40739.1 EST HUMAN 6.0E-12 AL40739.1 EST HUMAN 6.0E-12 AL40739.1 EST HUMAN 6.0E-12 AL40739.1 EST HUMAN 6.0E-12 AL40739.1 EST HUMAN 6.0E-12 AL40739.1 EST HUMAN 6.0E-12 AL40739.1 EST HUMAN 6.0E-12 AL40739.1 EST HUMAN 6.0E-12 AL40739.1 EST HUMAN 6.0E-12 AL40739.1 EST HUMAN 6.0E-12 AA700328.1 IST	Most Similer	Most Similar Top Hit Acession Top Hit Acession Signal Top Hit Acession Top Hit Acession Signal Top Hit Acession SEC ID ORF SEQ Expression Top Hit Acession Dutabase No. Signal I.67 G.0E-12 AF003249.1 NT Dutabase Signal Sign	

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Probe Example 1770
D SEQ ID NO: NO: NO: NO: NO: NO: NO: NO: NO: NO:
Property 124 1111111111111111111111111111111111

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	Top Hit Descriptor	Homo sapiens Xq pseudosutosomal region; segment 2/2	Homo saplens chromosome 21 segment HS21C010	Г	ob 18d02.s1 NCI_CGAP_Kid5 Hamo sepiens cDNA clone IMAGE:132403537		zn88h10.r1 Strategene kmg oarchroma 937218 Homo sapiens cDNA done IMAGE:565315 5' similer to contains THR.t2 THR repetitive element;	wz8602.x1 NCI_CGAP_Bm25 Hamo sepiens cDNA clone IMAGE:2565890 3' similar to TR:075139 075139 KIAA0644 PROTEIN.;	Homo septens X28 region near ALD tocus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMRI), creatina transporter (CRTR),	CDM protein (CDM), adrendeuloodystroptry protein >	EST60487 Activated T-cells XX Homo saplens cDNA 5' and similar to serine protesse P100, Ra- reactive factor		DOS PROMY MAKAN MA LAN DITANA II.	Т	7		Home saplens chromosome 21 segment HS21C048	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cs2-VCalmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), achencieulodystrophy protein >	Denio rento fibrochast growth factor receptor 4 mRNA, complete cds	Horio saplens DNA polymeraes delta email subunit (POLD2) gene, exons 1 through 11 and complete ods	Homo sepiens hypothetical protein PRO2130 (PRO2130), mRNA	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA	nab76/05x1 Sogres_NSF_F8_9W_OT_PA_P_S1 Homo saplens cDNA clone IMAGE: 3'	Homo septens S164 gens, pertial ods; PS1 and hypothetical protein genes, complete ods; and S171 gene, partial ods	Homo sepiens chromosome 21 segment HS21C078
all a line	Top Hit Database Source	LN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN		L _N	EST_HUMAN		EST HUMAN	ESI HUMAN	EST HUMAN	EST HUMAN	ΝŢ	LN.	Į.	 	Ę	N	EST_HUMAN	Ę	NT
5	Top Hit Acession No.	AJ271738.1	3.0E-13 AL163210.2	3.0E-13 BF372062.1	3.0E-13 AA745844.1	3.0E-13 AA134017.1	3.0E-13 AA134017.1	3.0E-13 AW005639.1		U52111.2	3.0E-13 AA352487.1		3.0E-13 AA352487.1		ļ		3.0E-13 AL163248.2	U52111.2	2.0E-13 U23839.1	AF239710.1	8924119 NT	8924119 NT	BF43186	AF109907.1	2.0E-13 AL163278.2
	Most Similer (Top) Hit BLAST E Value	3.0E-13 AJ2717	3.0E-13	3.0E-13	3.0E-13	3.0E-13	3.0E-13	3.0E-13		3.0E-13 U52111	3.0E-13		3.0E-13	3.05-13	3.0E-13	3.0E-13	3.0E-13	2.0E-13 U52111	2.0E-13	2.0E-13 AF2397	2.0E-13	2.0E-13	2.0E-13	2.0E-13 AF1099	2.0E-13
	Expression Signed	1.26	2.47	2.94	2.97	0.59	0.59	0.62	- !	7.67	0.6		9.6	0.72	3.61	3.98	2.29	3.42	2.00	7.8	0.0	6.0	1.13	1.11	1,34
	ORF'SEQ ID NO:	27831		28117		31140	31141	31635		33803	33792		33/03	LORCE		38004	37517	25602	25683	28983	28419	28420	28686	28908	
	SEQ ID NO:		15201	15379	L. 1	18251	18251	18887		20478	20670	l	- 1	- 1		Į	24197	12960	13043	13006	15771	15771	16038	16254	16831
	Probe SEQ ID NO:	2370	2483	2003	3182	5452	5452	5005		7783	7975		2000	200	10675	10075	11598	145	282	1247	3005	3002	3275	3498	4088

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					5	20 TO THE PARTY OF	Origin LAULE TOTAL LAPTOSSOL II DIBILI
Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similer (Top) Hit BLAST E Vælue	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9032	18812	31772	4.7	2.0E-13	2.0E-13 Q06852	SWISSPROT	CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1)
6113	18890		0.58	20E-13	20E-13 X79417.1	TN	S.scrofa rps12 mRNA for ribosomal protein S12
6717	19632		7.15	2.0E-13 X16012	X16912.1	TN	Human PFKL gene for liver-type 8-phosphofructoldnese (EC 2.7.1.11) exon 2
6954	19438	32451	99.0	2.0E-13	10835072 NT	LN	Homo expiens N-myristoyftransferase 1 (NMT1), mRNA
6954	19436		0.65	2.0E-13	10835072 NT	TN	Homo sapiens N-myristoyltransferase 1 (NMT1), mRNA
10355		36219	3.87	2.0E-13	5031896 NT	N	Homo sapiens mab-21 (C. elegans Hike 1 (MAB21L1) mRNA
12105	24602		3.48	2.0E-13	2.0E-13 AW892155.1	EST_HUMAN	CM0-NN0001-100300-274-e11 NN0001 Homo sepiens cDNA
285	13091	25732	1.52	1.0E-13	1.0E-13 S74129.1	LN	FGF-1≖fibroblast growth factor 1 [human, kidney, Genomic, 342 nt, segment 2 of 2]
868	13637	26307	5.64	1.0E-13	1.0E-13 AJ007973.1	INT	Homo sapiens LGMD28 gene
1313	14004	96738	80	4 0E 43	4 0E-43 X87344 4	LZ	H. septens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RINGS, 9, 13 and 14
		200	3	1,00	1		SOURCE OF NICE COAD CROSS Lives and the Coad
2015	14750	27478	2.13	1.0E-13	1.0E-13 AA720574.1	EST_HUMAN	THR repetitive element;
4553	17288	29917	1.04	1.0E-13	1.0E-13 BF340987.1	EST_HUMAN	602038009F1 NCI_CGAP_Bm64 Homo sepiens cDNA done IWAGE:4185866 5'
							nn24d01.s1 NCI_CGAP_Gas1 Homo septens cDNA clone IMAGE:1084801 3' similar to comains Alu
7810	20505	33626	0.78	1.0E-13	1.0E-13 AA577812.1	EST_HUMAN	repetitive element contains element MER24 repetitive element;
							nn24d01.s1 NCI_CGAP_Gas1 Homo septens cDNA clone IMAGE:1084801 3' similar to contains Alu
7810		33627	0.78	1.0E-13 AA5778	121	EST_HUMAN	repetitive element, contains element MER24 repetitive element;
0666			0.79	1.0E-13 015481		SWISSPROT	MELANOMA-ASSOCIATED ANTIGEN B4 (MAGE-B4 ANTIGEN)
10199	Ш	£90 0 £	0.53	1.0E-13	1.0E-13 AF300701.1	N.	Mus musculus ostootesticular protein tyrosine phosphatase mRNA, complete cds
							745610.x1 Sogres_NSF_F8_9W_OT_PA_P_S1 Homo saplens cDNA clone IMAGE:3524443 3' similar to
11352		37345	11.1	1.0E-13	1.0E-13 BF108755.1	EST_HUMAN	contains MER29.bz MER29 repeditive element;
11034	}		2.25	1.0E-13	1.0E-13 AV716377.1	EST_HUMAN	AV715377 DCB Homo saptens cDNA clone DCBAIE03 5
12563	24893		. 2.12	1.0E-13	1.0E-13 AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
							aj24c01.s1 Scares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.t1 MER19
324	13125	25761	1.81	9.0E-14	9.0E-14 AA781159.1	EST_HUMAN	repetitive element ;
							ej24c01.s1 Sceres_testis_NHT Homo sepiens cDNA clone 1391232 3' similar to contains MER19.t1 MER19
325		25762	3.05	9.0E-14	9.0E-14 AA781159.1	EST_HUMAN	repetitive element;
2504			3.66	9.0E-14	9.0E-14 AW861577.1	EST_HUMAN	RC4-CT0322-080100-013-d09 CT0322 Homo sepiens cDNA
2589	15313	28050	1.18	9.0E-14	9.0E-14 AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
2589		28051	1.18	9.0E-14	9.0E-14 AJ133127.1	NT	Homo septens mRNA for sodium-glucose cotransporter (SGLT2 gene)
2758			2.6	9.0E-14	9.0E-14 AB038162.1		Homo sapiens TFF gene cluster for trefoil factor, complete cds
3109	15874		3.96	9.0E-14	8.0E-14 AW513296.1	EST HUMAN	xx054h05x1 NCI_CGAP_Ut1 Homo septens oDNA clone IMAGE:27078333'

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Table 4

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Probe SEQ ID NO:	Eson SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Moet Similar (Top) Hit BLAST E Value	Top Hit Acessian No.	Top Hit Detabase Source	Top Hit Descriptor
4870	17697	30220	0.92		3.0E-14 AW 265354.1	EST_HUMAN	xp45f12.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:Z743343 3' similar to contains Alu repetitive element,contains element MER9 repetitive element;
4873	17600	30222	26'0	3.0E-14	7856884 NT	TN	Homo saplens a disintegrin and metalloproteinese domain 29 (ADAM29), mRNA
9835	18397	32411	1.49		3.0E-14 AH20786.1	EST_HUMAN	te91c12.x1 NCI_CGAP_Pr28 Homo sepiens cDNA done IMAGE:2094070 3' similar to TR:000519 000519 FATTY ACID AMIDE HYDROLASE;
9635	18307	32412	1.40		3.0E-14 AH20786.1	EST HUMAN	teg1c12.X1 NCI_CGAP_Pr28 Homo sepiens cDNA done IMAGE:2084070 3' similar to TR:000519 000519 FATTY ACID AMIDE HYDROLASE.
6744	25099		0.62		3.0E-14 AL163248.2	Į.	Homo saplens chromosome 21 segment H321C048
8686	21378	34522			3.0E-14 N42165.1	EST_HUMAN	yy07b10.r1 Soares melanocyte 2NbHM Homo sepiens oDNA clone IMAGE:270523 51
10914	23594	36840	1.28		3.0E-14 BE888016.1	EST_HUMAN	601511530F1 NIH_MGC_71 Homo septens cDNA clone IMAGE:3913087 6
11201	1821	30220	21.7		3.0E-14 AW263354.1	EST HUMAN	xp45f12.x1 NCI_CGAP_HN11 Home sapiens cDNA chore IMAGE:2743343 3' simitar to contains Alu repetitive element;contains element MER9 repetitive element;
12539	25282			\rfloor_{-}	3.0E-14 AL163285.2	N	Homo sapiens chromosome 21 segment HS21 C085
381	13168	25811	3.71		2.0E-14 AJ271738.1	Z	Homo sapiens Xq pseudoautosomal region; segment 2/2
381	13168		3.71		2.0E-14 AJZ71736.1	LN L	Homo sapiens Xq pseudoautosomal region; segment 2/2
874	15548	26091	30.6		20E-14 AL163303.2	Z	Homo saplens chromosome 21 segment HS21C103
2387	15108		1.49		2.0E-14 AW372868.1	EST_HUMAN	RC5-BT0377-091299-031-D12 BT0377 Hamo sapiens cDNA
2487	15185		2.15	2.0E-14		TN	Homo saplens rhabdoid tumor deletton region protein 1 (RTDR1), mRNA
5228	15245	27983	1.19		20E-14 AL163209.2 NT	LN.	Homo saplens chromosome 21 segment HS21C009
2542	15258		1.14		2 0F-14 BF 272432 1	EST HUMAN	hv80g10.x1 NCI_CGAP_Lu24 Home septens cDNA clone IMAGE:3180738 3' similar to contains Alu receditive element contains OFR.tt OFR receditive element:
2681	l		0.95		2.0E-14 P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6437	18236	30050	8.0		2.0E-14 BF380661.1	EST HUMAN	IL2-UT0072-240800-142-D07 UT0072 Homo sapiens cDNA
							ta78h01 x2 NOL CGAP HSC2 Homo sepiens cDNA clone IMAGE:2050225 3' similar to contains L1.t3 L1
5533					2.0E-14 AB12351.1	EST_HUMAN	repetitive element;
5634		31342			2.0E-14 U01317.1	NT	Human beta globin region on chromosome 11
6784					20E-14 BE000550.1	EST_HUMAN	RC3-BN0072-240200-011-e08 BN0072 Homo sapiens cDNA
9884					4585709 NT	LN.	Homo saplens a disintegrin and metalloproteinase domain 11 (ADAM11) mRNA
7185	19871		1.25	2.0E-14 P56163	P56163	SWISSPROT	ZINC-FINGER PROTEIN NEURO-D4
2072	20084	33167	22.12		2.0E-14 BE158761.1	EST_HUMAN	IL2-HT0397-071299-024-D04 HT0397 Homo sapiens cDNA
7407	20084	33168	22.12		2.0E-14 BE158761.1	EST_HUMAN	IL2-HT0397-071299-024-D04 HT0397 Homo saplens cDNA
9817	22468	35671	0.67	20E-14	20E-14 AI978795.1	EST_HUMAN	wr50g10.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2492034 3' similar to contains Alu repetitive element;
10317	22904	36181	0.53	2.0E-14	2.0E-14 AV741648.1	EST_HUMAN	AV741648 CB Homo sapiens cDNA clone CBFBSF04 5'

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Table 4
Single Exon Probes Expressed in Brain

	ORF SEQ Expression (Top) Hit Acession (Top) Hit Descriptor Signal BLAST E No. Source Surce	8 31549 1.02 6.0E-15 X73462.1 NT O aries mRNA for heir torratin cysteine-rich protein	31550 1.02 6.0E-15 X73462.1 NT	26834 6.63 5.0E-15 AL163208.2 NT	Human hereditary haemochromatosis region, historie 2A-like protein gene, hereditary haemochromatosis 5.0E-15 (1091328.1 NT (CHIA-H) care. Reflect cente. and acclusin physiologic from complete centers.	1.03 6.0E-15 AW296817.1 EST HUMAN	2.4 5.0E-15 AV730056.1 EST HUMAN	25442 2.85 4.0E-15 AL163303.2 NT	32339 0.76 4.0E-15 AB007970.1 NT	33505 3.08 4.0E-15 AJ130894.1 INT	33506 3.08	7.06 3.0E-15 N89452.1 EST HUMAN	0.79 3.0E-15 P92485 SWISSPROT	1.33	32837 2.9 3.0E-15[M27685.1 NT	32938 2.9 3.0E-15 M27685.1 NT	2.51 3.0E-15 AA807128.1 EST_HUMAN	20000 1 1 2 0 0 1 1 1 1 1 1 1 1 1 1 1 1	1.81	1.35 3.0E-15 AW877214.1 EST_HUMAN	25692 3.8 2.0E-15 AF223391.1 NT	Homo sepiens calcium chemnel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	Homo saplens calclum channel alpha1E subunit (CACNA1E) gene, excess 7.49, and partial cds, alternatively spiloed	Homo saplens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, attennatively spliced
-		31540	31550	25834	28212			25442	32339	33505	33506				32837	32238		SCHOOL	2		25692	25738	25789	28910	28911
-	Even SEQ ID NO:		9 18618	1 13186	15400	L	23269	12829			20392	16933	17599			19865	5 22476	28385	1	25058	13052	13157	13157	16256	16256
	Probe SEQ ID NO:	5820	582	404	276	3461	10574	418	6667	10904	10994	4192	4872	6716	7179	7179	9825	10804	12310	12814	243	350	359	3500	3500

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Probe SEQ ID NO:	Econ SEQ ID NO:	ORF SEQ ID NO:	Expression Signel	Most Similer (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Dafabase Source	Top Hit Descriptor
4049	16794	29423	1.08		2.0E-15 AW238499.1	EST_HUMAN	xp28h01.x1 NC_CGAP_HN10 Homo sepiens cDNA clone IMAGE:2741521 3' similar to contains L1.t3 L1 repetitive element;
4580	17315		2.46		2.0E-15 Al806335.1	EST_HUMAN	wf07f06.x1 Socres_NFL_T_GBC_S1 Homo septens cDNA clone IMAGE:2349923 3' similar to TR:Q61043 Q61043 NINEIN ;
6083	18867		0.88		20E-15 BE5623521	EST_HUMAN	801344253F1 NIH_MGC_8 Homo septens cDNA clone IMAGE:3877288 5
6089	18867	31834			2.0E-15 BE562352.1	EST_HUMAN	801344253F1 NIH_MGC_8 Hamo septens cDNA dane IMAGE;3877288 5'
7014	19706		1.5		2.0E-16 AJ400877.1	LN	Homo saplens ASCL3 gene, CEGP1 gene, C11of114 gene, C11of115 gene, C11of116 gene and C11of17 gene
7171	19857	6Z6ZE				EST_HUMAN	477e03.s1 Sceres_fetal_liver_splean_1NFLS_S1 Homo sepiens cDNA clone IMAGE:4809243
7294	19977	33054	5.18		2.0E-15 W05064.1	EST_HUMAN	za78d10.r1 Soures, fetal jung, NbH.19W Home saplens cDNA clone IMAGE:298675 5' similar to WP:F44F4.8 CE02227 TRANSPOSASE
8804	21496	34642	2.86		2.0E-15 D14547.1	L	Human DNA, SINE reportitive element
8971	21661	34811	1	2.0E-15	2.0E-15 AA397758.1	EST_HUMAN	Z77g08.r1 Soures_tests_NHT Homo sapiens cDNA clone IMAGE:728414 5
8971	21881	34812	1	2.0E-15	2.0E-15 AA397758.1	EST_HUMAN	2/77g08.r1 Sceres_testis_NHT Homo septems cONA clone IMAGE:728414 57
8304	21971	35145	1.23		2.0E-15 AW379465.1	EST_HUMAN	CM0-HT0244-201099-078-e12 HT0244 Homo sepiens cDNA
8304	21971	35146	1.23		2.0E-15 AW379465.1	EST_HUMAN	CM0-HT0244-201099-078-612 HT0244 Homo septiens cDNA
10742	23429		5.56	2.0E-15	2.0E-15 AJ271735.1	LN	Homo sepierrs Xq pseudosubsomel region; segment 1/2
12451	25338		204	20E-15	20E-15 U82828.1	LN	Homo sepiens atzoda telengiectasia (ATM) gene, complete cds
12653	16256	28910	3.34	2.0E-15 AF22339	1.1	IN	Homo septens celcium chennel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, attenuatively spliced
12653	16256	28011	3.34	2.0E-15 AF22339	[1	NT	Homo sepiens calcium channel alpha1E subunit (CACNA1E) gene, exms 7.49, and partial cds, afternatively epiced
2777	15482		239	1.0E-15		EST HUMAN	b28h05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similer to TR:Q13539 Q13539 MARINER TRANSPOSASE
3011	15777	28427	1.35	1.0E-15	_	EST HUMAN	hk40e02.y1 NCI_CGAP_Ox34 Homo septens cDNA clone IMAGE:2899162.57
3130	15003	28548	1.29	1.06-15	1.0E-15 P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5138	17856		26.0	1.0E-15		EST_HUMAN	df23e06.y1 Morton Fetal Cochies Homo septens cDNA clone IMAGE:2484202 5
6279	19052	32030	1.74	1.0E-15 T96783.1	196783.1	EST_HUMAN	ye40s10.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120234 3' similar to contains MER6 repetitive element;
6008	19847		2.12	1.0E-15 BE07421	7.1	EST_HUMAN	QV3-BT0569-270100-074-g05 BT0559 Hamo septens cDNA
8131	20825	33961	0.86	1.0E-15/	1.2	Ţ	Homo sepiens chromosome 21 segment HS210080
8310	21012	34149	4.56	1.0E-15			qf88h08.xf Soares_testis_NHT Hamo aspians aDNA clane IMAGE:1755227 3'
8319	21012	34160	4.56	1.0E-15/	1	EST HUMAN	qf88h08.x1 Soares_testis_NHT Homo sepiens cDNA clane IMAGE:1755227 3'
8837	21628	34770	0.67	1.0E-15/	1.0E-15]AL163207.2	M	Hamo saplens chromosome 21 segment HS21C007

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tr31c05x1 NCI_CGAP_0v23 Homo septions cDNA clone IMAGE:2219912 3' similer to contains Alu repetith Mus musculus offactory receptor cluster, OR37A, OR37B, OR37C, OR37E genes and OR37D pseudogene q178a02.x1 NCI_CGAP_Kid3 Homo sepiens d1NA clone IMAGE:1885354 31 similar to contains MER10.t3 q78a02x1 NCI_CGAP_Kid3 Homo sepiens cDNA clone IMAGE:1885354 3' similar to contains MER10.t3 dr37c03.s1 NCI_CGAP_Kid6 Homo septens cDNA clone IMAGE:1459972 3' similar to comtains L1.t3 L1 o80c04.s1 Source_total_fetus_Nb2HF8_9w Homo septens cDNA clone IMAGE:1623078 3' similar to PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4) PROTEIN-ARGININE DEIMINASE TYPE IN (PEPTIDYLARGININE DEIMINASE IN) (PAD-R4) Hamo sepiens cut (Drosophile)-like 1 (CCAAT displacement protein) (CUTL1) mRNA ye28c12.r1 Strategene king (#637210) Homo sepiens cDNA clone IMAGE:119062 5 HSC23F051 normalized trush brain cDNA Homo saplens cDNA clone c.23f05 Homo saplens chromosome 21 segment HS21C046 601885734F1 NIH_MGC_37 Homo saplens cDNA clone IMAGE:4104129 5 Homo sapiens gene for TMEM1 and PWP2,complete and partial cds MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR Hamo seplens chemoldne (C-C modf) receptor 8 (CCR8) mRNA Top Hit Descriptor EST384702 MAGE resequences, MAGL Homo seplens cDNA QV1-UM0036-200300-115-002 UM0036 Homo septens cDNA QV1-UM0036-200300-115-g02 UM0036 Homo septens cDNA PM4-BT0650-010400-002-g09 BT0650 Hamo septens cDNA PM4-BT0650-010400-002-909 BT0650 Homo seplens cDNA Homo sepiens major histocompetibility locus class III region Homo sapiens spermidine synthese (SRM) mRNA DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM Homo saplens GTP binding protein 1 (GTPBP1), mRNA (PEPTIDYLARGININE DEIMINASE TYPE ALPHA) (PEPTIDYLARGININE DEIMINASE TYPE ALPHA) Homo sepiens chromosome 21 segment HS210084 contains element L1 repetitive element; Single Exon Probes Expressed in Brain MER 10 repetitive element; MER10 repetitive element; repositive element; element EST_HUMAN NT EST_HUMAN EST_HUMAN EST HUMAN Top Hit Database SWISSPROT EST_HUMAN EST_HUMAN SWISSPROT EST_HUMAN **EST_HUMAN** EST HUMAN EST HUMAN EST_HUMAN EST HUMAN SWISSPROT EST HUMAN SWISSPROT Source 눋 4885120 NT z 4507208 4503168 Top Hit Acession 11418127 6.0E-18 AW972811.1 1.0E-15|AA864653.1 4.0E-16 AW 707168.1 1.0E-15 AF044083.1 5.0E-16|AA992176.1 5.0E-16 AL 163246.2 AW797168.1 4.0E-16 AL 163284.2 1.0E-15 AI783944.1 9.0E-16 AI244341.1 9.0E-16 AI244341.1 4.0E-16 BE083875.1 5.0E-16 AJ251154.1 BF217368.1 AB001523.1 4.0E-16 BE083875.1 F08688.1 7.0E-16 T94149.1 1.0E-15 Q39575 7.0E-16 088807 7.0E-15 088807 0,10053 5.0E-18 9.0E-18 1.0E-15 9.0E-16 7.0E-16 6.0E-16 4.0E-16 4.0E-18 4.0E-16 BLASTE (Top) H 0.98 1.48 \$ 1 8 8 9,0 3.6 54. 4. 8.38 3.6 0.87 202 3.58 0.71 8 2.17 9 46.62 1.81 1.77 Expression Signal 35042 29830 34774 35370 30806 ORF SEQ 37815 30651 36841 37818 31324 33002 80802 28134 37418 28856 29489 20,000 33001 27840 35806 Ö N Q 21631 22185 SEQ ID 23409 2514B 21877 23595 2422 19928 19926 14223 24105 22 18411 25237 14867 15396 22002 25018 14061 15100 15100 16206 16863 16863 ÿ 9148 8940 9632 10720 SEQ ID 12722 11696 4469 10915 11696 5815 12675 1476 9954 223 2378 7241 2687 11504 2378 3460 7241 7812 12757 4121 233

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9195	21865		1.04	4.0E-16	11423191	L	Homo sapiens hypothetical protein FLJ10024 (FLJ10024), mRNA
11182	23847	37133	1.51	4.0E-16	4.0E-16 AV730030.1	EST_HUMAN	AV730030 HTF Homo sapiens cDNA clone HTFAWA03 5
11851	24435		1.44	4.0E-16	4.0E-16 Q62632	SWISSPROT	FOLLISTATIN-RELATED PROTEIN PRECURSOR
12014	24547			4.0E-16 P08548	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
12109	24005			4.0E-16	6912459 NT	IN	Homo saplens Grb2-associated binder 2 (KIAA0571), mRNA
130	12945			3.0E-18	3.0E-16 AW022862.1.	EST_HUMAN	df45c01.y1 Morton Fetal Cochilea Homo sapiens cDNA clone IMAGE;2486376 5
130	12946	25590	2.03	3.0E-16	3.0E-16 AW022862.1	EST_HUMAN	df45c01.y1 Morton Fetal Oachlea Home sapiens cDNA clone IMAGE:2486376 5
453	13239		1.5	3.0E-16	3.0E-16 AL046445.1	EST_HUMAN	DKFZp434P037_r1 434 (synonym: htes3) Hamo septens aDNA dane DKFZp434P037 5
463	13248		1.5		3.0E-16 AF135446.1	N	Hamo saplens TSX (TSX) pseudogene, exan 5
1435	14182	26867	1.38	3.0E-15	3.0E-16 Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2000	45744	0000	9.70	3 00 40	Oww.	100000000000000000000000000000000000000	ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN
2 2	-	88588	3.78	3.05-16 1-03200	Fuszuu	SWISSPRO	[07.45]
200	-1	20304	19.63	3.0E-16	3.0E-16 T08160.1	EST HUMAN	ES 100000 Infant Brain, Bento Scares Homo septens cDNA clone HIBBA13 5' end
888			0.95	3.0E-16	3.0E-16 U03887.1	NT	Human BXP.20 gene
5196	18004		0.99	3.0E-16	3.0E-16 AA077225.1	EST_HUMAN	7810F02 Chromosome 7 Fetal Brain cDNA Library Homo septens cDNA clone 7B10F02
5529	18327	31230	1.79	3.0E-18	3.0E-16 AF003520.1	L	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
960							em98h05.s1 Strategene echtzo brein S11 Homo sapiens cDNA clone IMAGE:16841853' similar to contains
) (2)	. 1	34387	4.28	3.0E-16	3.0E-16 Al002836.1	EST_HUMAN	THR.b2 THR repetitive element;
9790			0.80	3.0E-16	3.0E-16 BF690617.1	EST_HUMAN	602246538F1 NIH_MGC_62 Hamo sapiens cDNA clane IMAGE:4332032 6
10019	22887	35883	5.67	3.0E-16	3.0E-16 L78810.1	NT	Homo sepiens ADP/ATP certier protein (ANT-2) gene, complete cds
951	13717		1.2	2.0E-16	2.0E-16 AL163279.2	NT	Hamo saplens chromosome 21 segment HS21C079
2385	15106		16.0	20E-16	20E-16 AA621781.1	EST_HUMAN	8f08d04.s1 Soares_lessis_NHT Homo sapiens cDNA clone IMAGE:1030855 3'
7			1.06	2.0E-16	2.0E-16 J03061.1	IN	Human SSAV-related endogenous retrokral LTR-like element
4157	16897	29526	1.16	2.0E-16	2.0E-16 X89211.1	NT	H.saplens DNA for endogenous retrownal like element
							qg56803.x1 Sourse_testis_NHT Homo sapiens cDNA clone IMAGE:1839197 3' similar to contains MER29.t3
4447		29807	0.98	20E-16	2.0E-16 AI208733.1	EST HUMAN	WER29 repetitive element;
5104		30438	0.79	2.0E-16	2.0E-16 BE001178.1	EST_HUMAN	RC3-BT0046-131199-003-H12 BT0046 Homo suplens cDNA
0042	19404	32419	66.0	2.0E-18	2.0E-16 Q31125	SWISSPROT	HISTIDINE-RICH PROTEIN KE4
							#16e11.x1 NO_CGAP_Gas4 Homo sepiens aDNA dane IMAGE-2141708 3' similar to contains element
79/5	20281	33389	0.75	2.0E-18	2.0E-16 AI470723.1	EST_HUMAN	MER33 repositive element ;
7007	_			i d		1	nz47706x5 NCI_CGAP_Pr12 Homo sepiens cDNA cione IMAGE:1290947 similar to TR:054849 054849
) oo	ı	1	7.7°	Z.OE-10	Z.UE-10/AI/3263/.1	ESI HUMAN	INTROTACTION 428 NO PROTEIN, [2] INTOCHOUS MENTALINERY INTERPREDIENT
8028	20752	33883	0.57	2.0E-10	2.0E-16 BE858026.1	EST_HUMAN	7/82/109.X1 NCI_CGAP_Prize Homo septens cDNA cione IMAGE:3303521 3'

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	Top Hit Descriptor	782h09.xt NCI_CGAP_Pr28 Homo sepiens cDNA dane IMAGE:3303521 3'	CM4-PT0034-180200-306-a01 PT0034 Homo septens cDNA	CM4-PT0034-180200-508-s01 PT0034 Homo sapiens cDNA	Homo sapiens pitulitary tumor transforming gene protein (PTTG) gene, complete cds	af39g11.s1 Soeres_total_fetus_NbZHF8_9w Homo saplens cDNA clone IMAGE:1034084 3' similar to	A DESCRIPTION OF A DESCRIPTION OF THE PROPERTY	CVU-ENOT48-0/0/00-233-410 BNO148 Homo septens CUNA	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced	Homo sapiens CCR8 chemoldine receptor (CAMKBR8) gene, complete cds	MITOGEN-ACTIVATED PROTEIN KINASE KINASE KINASE 10 (MIXED LINEAGE KINASE 2) (PROTEIN	KINASE MST)	Homo sapiens COR8 chemokine receptor (CMKBR8) gene, complete cds	QV2-PT0012-040400-124-e06 PT0012 Hamo septems cDNA	CM1-NN1003-200300-153-e01 NN1003 Homo saplens cDNA	the part of the CCAP_CLT Homo sapiens cDNA done IMAGE:21095243' similar to contains MER28.t2	MER28 repetitive element;	xgA9g12x1 NCI_CGAP_Utt Hamo sapiens aDNA done IMAGE:2630850 3' similar to contains OFR.t2 OFR	repolitive element;	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete ods	QV0-OT0032-080300-155-d01 OT0032 Homo sapiens cDNA	Homo sapiens chromosome 21 segment HS21C080	MR0-HT0559-060300-003-e04 HT0559 Homo sepiens cDNA	AV730759 HTF Hamo sepiens cDNA dane HTFAQB07 5'	Mus musculus apolipoprotein B editing complex 2 (Apobec2), mRNA	Homo septens putative MTAP (MTAP) mRNA, partial cds, alternatively spliced	Mus musculus WNT-2 gene, pertial ods; putative ankyrih-related protein and cystic fibrosis transmembrane conductance reminister (CFTR) canase section 1 of 2 of the complete cits: and improve near-	and the second of the second o	RC1-HN0008-220300-021-b04 HN0003 Homo sepiens cDNA	hB1404.x1 Sogres_NFL_T_GBC_S1 Home saplens cDNA clone IMAGE:2978695 3' similar to contains L1.t2.	Figure defical,	MYELOID CHIL SURFACE AN IIGEN COSS PRECOUSOR (GP87)	yournoller! Strategene king (#637210) Homo sepiens cDNA clone IMAGE:79639 5	ycceco4,r1 Sogres fetal liver spicen 1NFLS Homo sapiens cDNA clone IMAGE:109327 5
_	Top Hit Deterbase Source	EST_HUMAN 7	EST_HUMAN C	EST_HUMAN C			Ť	HOMAN	TA L	1 LN		/ISSPROT	IN IN	EST_HUMAN C	EST_HUMAN C		EST_HUMAN N		EST HUMAN IN		EST_HUMAN C		EST_HUMAN N	EST_HUMAN A		I.N.	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \		EST HUMAN	T NAME TO THE	Τ.	Т	Т	EST_HUMAN Y
	Top Hit Acession No.	5	4.1	4.1	1.0E-16 AF200719.1	,	Ţ	7	1.0E-16 AF163864.1					1.1	9.0E-17 AW900048.1		_		7.1	1.1		8.0E-17 AL163280.2	۲.	7.	6753097 NT	7.0E-17 AF218650.1	7 05-47 & 5220843 4	1	6.0E-17 AW983860.1		[2			
	Most Similar (Top) Hit BLAST E Veitue	2.0E-16 BE858026	2.0E-16 AW87721	2.0E-16 AW87721	1.0E-16	100	1.UE-10 AA02838	1.0E-16	1.0E-16/	1.0E-16 U45983.1		1.0E-16 Q02779	1.0E-16 U45983.1	1.0E-18 AW87585	9.0E-17		9.0E-17 A1392964		9.0E-17	9.0E-17 AF200719	8.0E-17	8.0E-17	8.0E-17 BE172081	8.0E-17 AV730758	7.0E-17	7.0E-17	7 0E-47 1	, ,,,,	8.0E-17 /	A 06 47	0.0E-17 AW002//	6.0E-17 P20138	5.0E-17 T64110.1	5.0E-17]
	Expression Signel	0.57	18.0	0.81	1.84	8	8.8	2.37	0.75	27.85		3.39	7.15	1.07	2.11		2.2		4.75	2.47	1.77	0.87	3.7	1.94	3.44	3.3	ď	3	80	ď	5	0.48	2.97	2.09
	ORF SEQ ID NO:	33884	34256		25630				31343		-	32246		35018	29H12								31193				303065	3	25853	24074	STB/C	1	25436	-
	Exem SEQ ID NO:	20752	21118	21118	12992	2	200		18430	19111		19246	10111	21853	16475		18386		20702	22772	13757	16622	25069	19861	14188	18046	10351	1	13011	1009	8	22838	12823	20158
	Probe SEQ ID NO:	8028	8425	8425	180	{	2/2	1983	5635	6341		6 730	7453	9183	3722		6624		8007	10124	268	3872	5496	7175	1441	5240	8836	3	188	Š	177	19180	412	7486

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Probe SEQ ID NO:	Econ SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3626	16379	02062	0.69	4.0E-17	4.0E-17 AA643697.1	EST_HUMAN	ni96e05.s1 NCI_CGAP_Co10 Hamo sepiens aDNA alone IMAGE:1058528 3'
2928	22016	35184	1.07	4.0E-17	4.0E-17 AW129165.1	EST HUMAN	x20e04.x1 NCI_CGAP_Kld8 Homo saplens cDNA clone IMAGE:2818622 3' similar to contains Alu repetitive element;contains MER19.b1 MER19 repetitive element;
11475	24078	37386	2.64	4.0E-17	4.0E-17 AL163247.2	NT	Homo sapiens chromosome 21 segment HS21 C047
12027	24555		1.75	4.0E-17	4.0E-17 Al073546.1	EST_HUMAN	ow5e04.x1 Source, testis, NHT Hamo septens cDNA clone IMAGE:1640286 3' similar to TR:Q16530 Q16530 PMS3 MRNA ;contains MER10.t2 MER10 repetitive element;
1477	14224		1.14	3.0E-17	3.0E-17 D14547.1	LN	Human DNA, SINE repetitive element
2091	14822	27554	1.85	3.0E-17	3.0E-17 AW119123.1	EST_HUMAN	xd89c09.x1 Source_NFL_T_GBC_S1 Homo septems cDNA clone IMAGE:2004784 3'
3188	15951		1.18	3.0E-17 P35410	P35410	SWISSPROT	MAS-RELATED G PROTEIN-COUPLED RECEPTOR MRG
3633			1.34	3.0E-17	3.0E-17 BE3265221	EST_HUMAN	hw05b04.x1 NCI_CGAP_Lu24 Hamo sepiems cDNA olane IMAGE:3181989 3'
3633	16386	28027		3.0E-17	3.0E-17 BE326522.1	EST_HUMAN	hw05b04.x1 NCI_CGAP_Lu24 Hamo sepiens dDNA clane IMAGE:3181889 3'
4970	17695		1.89	3.0E-17	3.0E-17 BF511286.1	EST_HUMAN	UI-H-BI4-ecj-c-06-0-UI.s1 NCI_CGAP_Sub8 Homo sepiens cDNA clone IMAGE:3085043 3'
2	20800	00000	τ. 4.	9.0E-47	3 0E-47 Negas4 4	NAMI ILI LAAN	2x14b02.s.1 Source fetal five spleen 1NFLS Homo septens cDNA clone IMAGE:292491.3' similar to contains PTRA to PTRA manufallum element.
	1			10.0	110000	NO CONTRACTOR	Homo septems DNA, DLEC1 to ORCTL4 cene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 cenes.
1096		35439	6.58	3.0E-17	3.0E-17 AB026898.1	노	complete cds)
10279	22927	38140	1900	3.0E-17	3.0E-17 BF327012.1	EST_HUMAN	QV3-BN0047-270700-283-e12 BN0047 Hamo sepiens cDNA
10279	1		19.0	3.0E-17		EST_HUMAN	QV3-BN0047-270700-283-e12 BN0047 Homo sapiens cDNA
11994			39°E	3.0E-17	11417966	LN	Homo sapiens SEC14 (S. cerevisiae) Like 2 (SEC14L2), mRNA
12764	25023		17.1	3.0E-17	3.0E-17 AV720204.1	EST_HUMAN	AV720204 GLC Homo septens cDNA clone GLCDIF08 5'
970				100			qt63e06.x1 NCI_CGAP_Eso2 Homo saplens cDNA clone IMAGE:1959922 3' similar to contains Alu
3	13144	79/CZ	3	2.05-17	2.0E-17 AIZ/0080.1	EST HOMAN	repetitive etement;
77	13144	26782	247	7. HO C	2 OF 47 A 1970ABA 4	NYM 5	qt63e06x1 NCI_CGAP_Eso2 Homo sepiens cDNA clone IMAGE:1959922 3' similar to contains Alu
286	_			2.0E-17	AA722832 1	FST HIMAN	2081004.81 Scenes fetel heart NhHH19W Homo serviens cDNA clume IMAGE:300751.31
2448		L		2.0E-17	2.0E-17 O28983	SWISSPROT	ZONADHESIN PRECURSOR
2448	l _	37906		2.0E-17 Q28983	028983	SWISSPROT	ZONADHESIN PRECURSOR
							NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN) (NEUROFILAMENT
2830		28343	6.64	2.0E-17 P12038	P12036	SWISSPROT	HEAVY POLYPEPTIDE) (NFH)
5282		30745	1.88	2.0E-17 M27686.	1	IN	Mus musculus ultra high suffur keratin gene, complete cds
· 5282		30748	1.88	2.0E-17 M27885.	1	LN	Mus musculus ultra high sulfur keratin gene, complete cds
6171			204	2.0E-17	3.1	LN	Homo sapiens MHC class 1 region
6308			1.18	2.0E-17	2.0E-17 AL134881.1	EST_HUMAN	DKFZp762J0810_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762J0610 5
7982	20877	33802	1.12	2.0E-17 Q95156	Q95156	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF3
	:						

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[] [[[[[[] [[] [[] [] [] [] [] [] [] []	Top Hit Descriptor	EST13504 Testis tumor Homo sapiens cDNA 5' end similar to similar to glycogenin	600944690F1 NIH_MGC_17 Hamo sepiens cDNA clane IMAGE:2380615 51	Homo sapiens chromosome 21 segment HS210047	Homo sapiens chromosome 21 segment HS21C047	Human CYP19 gene for aromatase cytochrome P-450, promoter region (containing two cis-acting transcriptional nemislative elements)	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)	we94b04.x1 Sogres_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348719.3'	we94b04.x1 Sogres_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348719.3'	MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1)	Homo sapiens Xq pseudoautosomal region; segment 2/2	Homo sapiens chromosome 21 segment HS21 C007	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR	Homo sapiens thrombospondin 2 (THBS2) gene, promoter region and exons 1A and 1B	Homo saplens memosidase, beta A, tysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3	(UBEZAZO) genes, complete cas	YOURD'T'S CORE OF SOME END STREET TO THE STREET STAND STREET SOME OF THE STREET	he38e05x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2921312 3' similar to contains Alu repetitive element;contains LTR8.t1 LTR8 repetitive element;	qe65b05.x1 Soares_fetal_lung_NbHL19W Home sepiens cDNA clone IMAGE:17438253'	qe65b05.x1 Soares_fetal_bung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825 3'	URIDINE PHOSPHORYLASE (UDRPASE)	QV0-BT0283-101289-072-407 BT0263 Homo septens cDNA	QV3-BN0048-220300-129-c10 BN0046 Hamo sepiens cDNA	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE (MLCK) [CONTAINS: TELOKIN]	248f05.s1 Soeres_testis_NHT Home septens cDNA done (MAGE:795489 3' similar to TR:01263081	TAY RATE & Statements (statements (2020) Lamb earliers CDMA close MARCE: 600862.2	A Second Section of The Section of T	yearus XI sommes NST To BYY OI TAY P SI HOME SEPTEMENT CONTROLLY ACCES S	ACOND SAME SPICION (YOUR PLANSMINES INCHEDING 1906 SUBSTAND (FINNS)) INTONA WATCHED A NO. (1904 Part Home series CINA Arts MAGE 2837071 3' similar to Art. 20058 205	RIBOSOMAL PROTEIN L4 (HUMAN);
	Top Hit Acession No.	7 AA300640.1 EST_HUMAN	7 BE299888.1 EST_HUMAN	Γ	7 AL163247.2 NT				7 AI798902.1 EST_HUMAN	7 A1798002.1 EST_HUMAN	7 P08183 SWISSPROT	7 AJ271736.1 NT	7 AL163207.2 NT	7 P02461 SWISSPROT	7 U79410.1 NT				7 AW 468 468.1 EST HUMAN	7 A1185842.1 EST HUMAN	7 AI185642.1 EST HUMAN	7 Q16831 SWISSPROT	7 BE062744.1 EST_HUMAN	7 AW996338.1 EST_HUMAN	7 Q28824 SWISSPROT		T	T	AI4/210/.1		
Top Hit Acession No. No. AA300640.1 BE29888.1 AL163247.2 AL163247.2 AL163247.2 AL163247.2 AL163247.2 AL163247.2 AL163207.2 AU788902.1 AU788902.1 AU788902.1 AU788902.1 AU78410.1 AL163207.2 AU889488.1 AN4684488.1 AN4684488.1 AN468448.1	Most Simila (Top) Hit BLAST E Vatue		L	L												L					Ŀ							ļ			
Most Similar (Top) Hit Top Hit Acesslon PLAST E Value 2.0E-17 AA300640.1 2.0E-17 AL163247.2 2.0E-17 AL163247.2 2.0E-17 AL163247.2 2.0E-17 AL163247.2 2.0E-17 AL163247.2 2.0E-17 AL163247.2 2.0E-17 AL163202.1 1.0E-17 AL163204.1 1.0E-17 AN996638.1	Expression Signal			3.2				0.7			3.66	1.28	2.73	2.3	2.00		1.7	į,	99.0	204	2.04	90.0	1.33	38.0	2.06	27.0	100	20.0	10.0	1.0	16.92
Most Similar Top Hit Accession Signet Top Hit Accession Signet Top Hit Accession Value 1	ORF SEQ ID NO:	34188	35628	35857	35858			36139	36169	36170	26164		27204						-	32327	32328	32730			37304		l		╽.		26778
ORF SEQ Expression (Top) Hit Top Hit Accession Signal BLAST E No. Signal 1 2.0E-17 AA300640.1 35628 2.81 2.0E-17 BE268688.1 3.22 2.0E-17 AL163247.2 36658 3.22 2.0E-17 AL163247.2 36138 0.73 2.0E-17 PD8063 36138 0.73 2.0E-17 PD8063 36138 0.73 2.0E-17 PD8063 36138 0.73 2.0E-17 PD8063 36109 0.49 2.0E-17 PD8063 2.0E-17 AL163207.2 2.0E-17 PD8183 2.0E-17 PD8183 2.0E-17 AL163207.2 2.0E-17 AL163207.2 2.0E-17 AL163207.2 2.0E-17 AL163207.2 2.0E-17 AL163207.2 2.0E-17 AL163207.2 2.0E-17 AL163207.2 2.0E-17 AL163207.2 2.0E-17 AL163207.2 2.0E-17 AL163207.2 2.0E-17 AL163207.2 2.0E-17 AL163207.2 2.0E-17 AL163207.2 2.0E-17 AL163207.2 2.0E-17 AL163207.2 2.0E-17 AL163207.1 3.3232 2.04 1.0E-17 AL163207.1 3.3232 2.04 1.0E-17 AL163207.1 3.3232 2.04 1.0E-17 AL163207.1 3.3232 2.04 1.0E-17 AL163207.1 3.3334 8.0E-18 AL174078.1 2.3232 2.05 3.31 8.0E-18 AL174078.1 2.3232 2.05 3.31 8.0E-18 AL174078.1 2.3232 2.05 3.31 8.0E-18 AL174078.1	SEQ ID NO:	21049	22420	L			Ĺ		22954	22954	13507	14446	14503	14840	15059		\perp		19136	19320	19320	19682			24000		1	1.	[_	1	13140
Exch NO: ORF SEQ Signel Expression Top) Hit Signel Most Similar Top Hit Acession No: Top Hit Acession Available 21046 34188 1 2.0E-17 Avai0640.1 22420 35628 2.81 2.0E-17 Avai0640.1 22456 35657 3.22 2.0E-17 Avai0640.1 22456 36658 3.22 2.0E-17 Avai0640.1 22626 36138 0.73 2.0E-17 Avai040.1 22626 36138 0.73 2.0E-17 Avai040.1 22664 36169 0.73 2.0E-17 Avai040.1 22674 36169 0.73 2.0E-17 Avai040.1 14507 27204 2.0E-17 Avai040.1 14509 27724 2.73 1.0E-17 Post08 14509 27724 2.73 1.0E-17 Avai040.1 16309 27724 2.05 1.0E-17 Avai040.1 16309 27720 2.05 1.0E-17 Avai040.1 16309 27720 2.04 1.0E-17 Avai040.1 16309 27730 0.69 1.0E-17 Avai040.1 2	Probe SEQ ID NO:	8356	9769	9804	9804	10150	10278	10278	10307	10307	733	1703	1761	5100	2335		\$ 5	•	8366	8555	6555	6869	8490	9907	11394	44790	2474	808	9766	3	339

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Probe SEQ (D NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Databese Source	Top Hit Descriptor
339	13140	26777	16.92	7.0E-18	7.0E-18 AW316976.1	EST_HUMAN	xx10b04.x1 NCL_CGAP_Pen1 Homo sepiens cDNA clone IMAGE:2837071 3' similer to gb:L20868 60S RIBOSOMAL PROTEIN L4 (HUMAN);
7343	20024	33100	1.33	7.0E-18	7.0E-18 AW887542.1	EST HUMAN	RC3-OT0061-170300-011-d03 OT0061 Homo septens cDNA
12492	13140	25776	3.41	7.0E-18	7.0E-18 AW316976.1	EST HUMAN	xx10b04.x1 NCI_CGAP_Pan1 Homo septens cDNA clone IMAGE:2837071 3' similar to gb:L20868 80S RIBOSOMAL PROTEIN L4 (HUMAN);
12492	13140	25777	3.41	7.0E-18	7.0E-18 AW316976.1	EST_HUMAN	xx10b04.x1 NGL CGAP_Pen1 Homo sepiens cDNA done IMAGE:2837071.3' similar to gb:1.20868 60S RIBOSOMAL PROTEIN L4 (HUMAN);
3280	18050	28698	÷	8.0E-18	8.0E-18 X71791.2	ĮN.	Rattus norvegicus partial Gdn/Ph-1 gene for glia-derived nexin/protesse nexin I, enhancer region
986	17432		3.02	8.0E-18	6.0E-18 P52181	SWISSPROT	PROTEIN-GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE (TISSUE TRANSGLUTAMINASE) (TGASE C) (TGC)
8148	20842		284	6.0E-18	11428155 NT	Ę	Homo sepiens similar to high-mobility group (nonhistone chromosomal) protein 4 (H. sapiens) (LOC63446), mRNA
8246	20940	34077	0.72	6.0E-18	8.0E-18 AL163210.2	E	Homo sapiens chromosome 21 segment HS21 CO10
11079	23749	37024	19.1	6.0E-18	6.0E-18 AL153246.2	Z	Homo saplens chromosome 21 segment HS21 C046
11300	23960	37.280	1.74	6.0E-18	6.0E-18 X87344.1	Ā	H.sepiens DWA, DMB, HLA-Z1, IPP2, LWP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
12241	24692	31076	3.29	6.0E-18	6.0E-18 U87929.1	LN.	Human accritists hydratase (ACO2) gene, exon 4
1125	13881	28541	21.7	5.0E-18	5.0E-18 AI280214.1	EST_HUMAN	qm65g11xt Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA done IMAGE:1893698.3' similar to contains Alu repetitive element.
5047	17786	30384	96'0	6.0E-18	6.0E-18 D61517.1	EST_HUMAN	HUM411F05B Clontech human fetal brain polyA+ mRNA (#6535) Homo sepiens cONA clone GEN 411F05 5
5191	17999	30622	1.2	5.0E-18	5.0E-18 AF087913.1	N.	Human endogenous retrovirus HERV-P-T470
8620	21312	34454	6.25	5.0E-18		EST_HUMAN	MR0-HT0161-221099-002-006 HT0161 Homo septens cDNA
10899	23579	36828	3.47	5.05-18	10242378 NT	N	Homo sepiens lymphocyte activation-associated protein (LOC51088), mRNA
10899	23579	36829	3.47	5.0E-18	10242378 NT	Ę	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
1238B	24770		9.4	5.0E-18	5.0E-18 AW867182.1	EST_HUMAN	MR1-SN0035-060400-001-g11 SN0035 Homo septens cDNA
12695	24978		4.18	5.0E-18	5.0E-18 AV550547.1	EST HUMAN	AV650547 GLC Homo septens aDNA clone GLCCGA023'
121	12939	25580	1.37	4.0E-18	4.0E-18 BE044076.1	EST_HUMAN	ho36h04.x1 NCL_CGAP_Ut1 Homo sepiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3 MER29 repetitive element;
121	12939	25581	1.37	4.0E-18	4.0E-18 BE044076.1	EST_HUMAN	ho36h04.x1 NCL_CGAP_Ut1 Homo esplens cDNA clone IMAGE:3039511.3' eknilar to contains MER29.b3
1711	14454	27153	1.19	4.0E-18	_		nq24f11.s1 NCI_CGAP_Co10 Homo sepiens cDNA clone IMAGE:1144845 3' similar to qb:M28328 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
1882	14619		1.12	4.0E-18	4.0E-18 AI738592.1	EST_HUMAN	wi33h08.x1 NCI_CGAP_Co16 Homo septens cDNA clone IMAGE:2392095 3"

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Probe SEQ ID NO:	Exam SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Vaitue	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2198	14927	27662	1.33	4.0E-18 Q06430	008430	SWISSPROT	N-ACETYLLACTOSAMINIDE BETA-1, 6-N-ACETYLGLUCOSAMINYLTRANSFERASE (N-ACETYLGLUCOSAMINYLTRANSFERASE) (1-BRANCHING ENZYME) (1GNT)
2198	14927	27663	1.33	4.0E-18 Q06430	008430	SWISSPROT	N-ACETYLLACTOSAMINIDE BETA-1, B-N-ACETYLGLUCOSAMINYTTRANSFERASE (N-ACETYLGLUCOSAMINYLTRANSFERASE) (1-BRANCHING ENZYME) (1GNT)
3772	16524	29162	89'0		4.0E-18 AI581586.1	EST HUMAN	ar83b06.x1 Barstead colon HPLRB7 Homo sepiene cDNA clone IMAGE:2173139 3' strailer to contains Alu repetitive element:
6279	18084		2.24	4.0E-18	4.0E-18 AI017585.1	EST HUMAN	ou23e06.x1 Sogres NPL T GBC S1 Homo septems cDNA clone IMAGE-1627138 31
\$279	18084	30741	2.24	4.0E-18	4.0E-18 AI017565.1	EST_HUMAN	out2808.x1 Sogres_NPL_T_GBC_S1 Hamp septems cDNA clone IMAGE:1627138 3'
7745	20441		0.63	4.0E-18	4.0E-18 AA746811.1	EST_HUMAN	m64e08.s1 NCI_CGAP_AIM Homo sepiens cDNA clone IMAGE:1200998 similar to contains L1.t2 L1 repetitive element;
10927	23607	36858	8.76	4.0E-18	4.0E-18 AA371807.1	EST_HUMAN	EST83633 Pituttary gland, subtracted (protectin/growth hormone) Il Homo septens oDNA 5' end similar to EST containing O family repeat
828	13500	28270	1.68	3.0E-18	3.0E-18 AA814196.1	EST HUMAN	ob23h11.s1 NCI_CCAP_Kid5 Homo septens cDNA clone IMAGE:1324581 3' similar to SW:RS5_HUMAN P46782.40S RIBOSOMAL PROTEIN S5.
606	13675		3.47	3.0E-18	3.0E-18 BE088634.1	EST HUMAN	CM0-BT0690-210300-298-g07 BT0690 Homo sapiens cDNA
3931	16681		1.47	3.0E-18		IN	Homo seplens chromosome 21 segment H321C047
9730	19564		5.64	3.0E-18	3.0E-19 BE001671.1	EST HUMAN	PMO-BN0081-100300-001-b08 BN0081 Hamo sapiens cDNA
10844	23528	36799	1.61	3.0€-18		EST_HUMAN	801884856F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103652 5
12497	24852		6.14	3.0E-18	3.0E-18 AW022015.1	EST_HUMAN	d/31h12.y1 Morton Fetal Coohlee Homo sepiens cDNA clone IMAGE:2485126 5
244	13063	25693	4.42	2.0E-18	20.1	EST HUMAN	QV1-LT0036-150200-070-e07 LT0036 Homo saplens cDNA
138	13886		62.83	2.0E-18	2.0E-18 BE256097.1	EST_HUMAN	801114352F1 NIH_MGC_16 Hamo suplems cDNA clane IMAGE:3356044 67
5326	18129		3.19	2.0E-18 AA86861	0.1	EST_HUMAN	ak53e07.s1 Scense testis. NHT Hamo suptens cDNA clone IMAGE:1400652 3' stmitar to TR:014577 014577 BAC CLONE RG114A06 FROM 7031, COMPLETE SEQUENCE.
52,10	18218	30927	3.08	2.0E-18 D14547.1		NT	Human DNA, SINE repetitive element
5410	18218	30828	3.68	2.0E-18		LN	Human DNA, SINE repositive element
2788	18570		1.68	2.0E-18 BF34722	1	Г	802021164F1 NCI CGAP Brn67 Homo septents cDNA clore IMAGE-4159670 5
8073	18852	31817	0.77	2.0E-18 X60459.1			Human IFNAR gene for interferon alpha/beta receptor
8	18852	31818	0.77	2.0E-18)		N.	Human IFNAR gene for interferon alpha/beta receptor
9185	18962	31935	1.04	2.0E-18	1	EST HUMAN	IL3HT0619-220700-222-C12 HT0619 Homo saplens cDNA
8228	19000	31977	5.18	20E-18	2.0E-18 AW665853.1	EST_HUMAN	hB4g01.x1 Soarse_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:2979684.3' similar to contains MER19.t2 MER19 repetitive element;
7336	20018	33086	0.81	2.0E-18 AA457619		EST_HUMAN	ae89d11.r1 Strategene fetal refine \$37202 Homo sapiens CDNA clone IMAGE:838485 5' similar to TR:001634 G61634 POLYPEPTIDE PR77:
8047	20741	33873	0.47	2.0E-18 BE439524	7.		HTM1-160F1 HTM1 Homo sepiens cDNA

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similer (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Defebese Source	Top Hit Descriptor
8	22595	35798	1.86		2.0E-18 AW151673.1	EST_HUMAN	x67e10.x1 NCI_COAP_Gas4 Homo sapiens cDNA done IMAGE:2623146 3' similar to contains MER10.t2 MER10 repetitive element;
9947	22595	35799	1.88		20E-18 AW151673.1	EST_HUMAN	A67e10x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.t2 MER10 repeditive element;
10894	23574	36824	И		2.0E-18 AW470791.1	EST_HUMAN	ha33d06.x1 NCI_CGAP_Kid12 Homo septens cDNA clone IMAGE:2875499 3' similar to contains THR.b3 THR repetitive element;
11736	24329	37063	3.91		2.0E-18 AW151299.1	EST_HUMAN	xg47e09.x1 NCI_CGAP_Ut1 Homo sepiens cDNA clone IMAGE:2630728 3' similar to contains MER8.b2 MER8 repetitive element;
12174	13886		1,45		2.0E-18 BE258097.1	EST HUMAN	601114352F1 NIH_MGC_16 Homo saplens cDNA clone IMAGE:3355044 5'
4382	17119		1.02		1.0E-18 T95406.1	EST_HUMAN	ye43g05.r1 Soares fetal liver spleen 1NFLS Homo seplens dDNA done IMAGE:120536 5' similar to contains L1 repetitive element;
5271	18077	30707	3.63		1.0E-18 AV653405.1	EST_HUMAN	AV663405 GLC Homo sapiens cDNA clone GLCDKE113'
5483	18282	31180	2.94		1.0E-18 D00099.1	TN	Homo eaplens mRNA for Na,K-ATPase alpha-subunit, complete cds
5483	18282	31181	2.94		1.0E-18 D00099.1	TN	Homo sepiens mRNA for Na,K-ATPase alpha-subunit, complete cds
සහ	19133	32128	1.83		1.0E-18 AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
8341	21034	34171	1.43		1.0E-18 Al148288.1	EST_HUMAN	oz69d09.x1 Soaras_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:16805693 3' similar to contains L1.t1 L1 repetitive element;
97.00	22450	36863	4		1.0E-18 U91328.1	Ę	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, end eodkum phosphate transporter (NPT3) gene, complete ods
12130	24621	31092	4.23		1.0E-18 AF003529.1	Z	Horno septens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
532	13316	25052	5.34		9.0E-19 AA281981.1	EST_HUMAN	2111008.11 NCI_OGAP_GCB1 Homo sepiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element;
88	13316	22952	3.24		9.0E-19 AA281961.1	EST HUMAN	211d08.11 NCI_CQAP_GCB1 Homo sepiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element;
7747	20443		4.47		9.0E-19 F08688.1	EST HUMAN	HSC23F051 normalized Infant brain cDNA Homo sapiens cDNA clone c-23f05
8288	21280	34419	2.54		9.0E-19 AL163203.2	Ę	Homo sepiens chromosome 21 segment HS21 0003
8288	21280	34420	2.54		9.0E-19 AL163203.2	NT	Homo eaplens chromosome 21 segment HS21C003
11072	23742	37018	4.82		9.0E-19 AB032969.1	LNT	Homo sapiens mRNA for KIAA1143 protein, pertial cds
11901	13316	25952	1.88		9.0E-19 AA281961.1	EST HUMAN	z11d06.r1 NCI_CGAP_GC81 Homo saplens cDNA clone IMAGE:712811 5' similar to contains MER19.t2 MER19 repetitive element;
1026	13786		1.25		8.0E-19 AW974902.1	EST_HUMAN	EST387007 MAGE resequences, MAGN Homo saplens cDNA
4372	l		1.04		P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8048	20742	33874	0.92		8.0E-19 BE158936.1	EST HUMAN	MR0+IT0404-210200-001-g08 HT0404 Hamo septens cDNA

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	Homo sapiens DEAD/H (Asp-GtL-Ala-Asp/His) box polypeptide 6 (RNA helicase, 54iO) (DDX8) mRNA	Rattus novegicus cp151 mRNA, partial cds	BETA CRYSTALLIN A2	tb01c08.x1 NCI_CGAP_Lu26 Homo septens cDNA clone MAAGE:2052302.3°	zf60b01.s1 Sceres_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:43514531	PM0-CT0248-131089-001-g01 CT0248 Hamo septens cDNA	OLFACTORY RECEPTOR 6 (M50)	OLFACTORY RECEPTOR 6 (M50)	Homo sapiens Xq pseudoeutosomel region; segment 1/2	DKFZp762F192_71 762 (synonym: trmei2) Homo septems cDNA clone DKFZp762F192 5*	ZONA PELLUCIDA SPERM-BINDING PROTEIN B PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP-X) (RC55)	Homo saplens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exon 14	x87b02x1 Sceres_NRL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2884171 3' similar to contains element MSR1 receitive element.	Homo sepiens mRNA, chromosome 1 specific transcript KIAA0501	802130810F1 NIH MGC_56 Hamo saplens cDNA clane IMAGE:4287674 5	Homo saplens mannosidase, beta A, Iyeosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds	BETA-2 ADRENERGIC RECEPTOR	BETA-2 ADRENERGIC RECEPTOR	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 8)	LIM-ONLY PROTEIN 8 (TRIPLE LIM DOMAIN PROTEIN 6)	AV708136 ADC Homo septens cDNA clone ADCAMA11 5'	Homo sepiens NPD008 protein (NPD008) mRNA, complete cds	Homo septens similar to aldo-keto reductase family 1, member B11 (aldose reductase-like) (H. sepiens) (LOC63222), mRNA	M.musculus mRNA for TPCR33 protein	Homo seplens phorbolin I protein (PBI) mRNA, complete cds	Homo sepiens chromosome 21 segment HS21C001	qo01e02x1 NCI_CGAP_Kld5 Homo sapiens cDNA done IMAGE:1915898 3' similier to TR:Q69386 Q69386 POLENV GENE;	AV731382 HTF Homo septems cDNA clone HTFAZCO6 5
Jie Exon Probe	Top Hit Detabase Source		NT.	SWISSPROT B	EST_HUMAN TO	EST HUMAN 2	Г	SWISSPROT O	ISSPROT	Ī	EST HUMAN D	SWISSPROT Z		EST HUMAN	Ť	T HUMAN	Į.	ISSPROT	Т	SWISSPROT LI	SWISSPROT LI	EST_HUMAN A					Ĭ	GST_HUMAN PC	EST_HUMAN A
Sing	Top Hit Acession No.	4758139 NT	7.0E-19 AF092090.1		7.0E-19 Ats44951.1	7.0E-19 AA705684.1	6.0E-19 AW852930.1			8.0E-19 AJ271735.1	6.0E-19 AL120817.1		5.	1.50	Ī							3.0E-19 AV708136.1	3.0E-19 AF223467.1	11432214 NT	3.0E-19 X89885.1	2.	12		2.0E-19 AV731382.1
	Moet Similar (Top) Hit BLAST E Value	7.0E-19	7.0E-19	7.0E-19 P26444	7.0E-19	7.0E-19	6.0E-19	6.0E-19 P34986	6.0E-19 P34986	6.0E-19	6.0E-19	5.0E-19 Q00193	5.0E-19	5.0E-19	4.0E-19	4.0E-19	4.0E-19	3.0E-19 Q28997	3.0E-19 Q28997	3.0E-19 043900	3.0E-19 043900	3.0€-19	3.0E-19	3.0E-19	3.0E-19	3.0E-19	20E-19 AL16320	2.0E-19	2.0E-19
	Expression Signal	1.51	2.34	6.0	0.51	2.05	1.34	1.36	1.36	1.3	1.04	5.36	1.03	7.45	1.88	1.02	76.0	2.	104	96.0	0.99	1.12	0.64	2.79	1.15	23.34	21.33	1.03	0.57
	ORF SEQ ID NO:	27708	32129	32969	35758			29795	29798		30301	31485	36191	37431	25958	28136	30773	29219	28220	20822	29623	29777	 		33548		28017		31706
	Exan SEQ ID NO:	14970	19134	19885	22500	25397	16513	17168	17166	17479	17892	18558	22971	24125	13324	15398	18115	16584	16584	16004	16994	17150	18006	19968	20430	24700	15279	17148	18745
	Probe SEQ ID NO:	2242	6364	7199	9911	12036	3781	4430	4430	4747	4987	5767	10324	11525	54.	2689	5311	3833	3833	4253	4263	4413	5198	7283	8328	12264	2565	4411	5963

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Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exem SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Detabese Source	Top Hit Descriptor
7238	19923	32668	SØ:0	2.0E-19	7857286 NT	TN	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
8228	20822	34061	80.8	2.0E-19	2.0E-19 AA012854.1	EST_HUMAN	2834c09.rf Soares retina N2b4HR Homo sapiens cDNA clone iMAGE:360880 51
6088	L.	32008		20E-19 Q95155	Q95155	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF2
11820	24413	37750	1.33	2.0E-19	2.0E-19 BF330867.1	EST_HUMAN	RC3-BT0333-250800-114-f04 BT0333 Homo saplene cDNA
11829	24413	37751	1.33	20E-19	20E-19 BF330867.1	EST_HUMAN	RC3-BT0333-250800-114-f04 BT0333 Homo sepiens cDNA
469	13255		1.87	1.0E-19	1.0E-19 BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo saplens cDNA clone IMAGE:3638310 5'
							yo79g07.r1 Soeres adult brain N2b4HB55Y Homo sepiens cDNA clone IMAGE:184188 5' similar to contains
2161	14891	27626	1.58	1.0E-19	1.0E-19 H30795.1	EST_HUMAN	MER10 repetitive element;
2723	15430		787	1.0E-19	1.0E-19 D38044.1	N	Human gene for Ahreceptor, exon 7-9
2851	15810		4.95	1.0E-19	4758977 NT	F	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
3304	16154	WUBBC	6.6	4 OF 40	1 OE-40 4 4 83 4067 4	FOT H. MAN	e496/12.51 Sources_bests_NHT Homo sepiens cDNA clone IMAGE:1393631.3' similar to contains MER37.12 MER37 recently a former to
202			1	4 01 40		LN	promoter representation of the confirmation of
3	1	21120		-30E-18		2	ci yearangas cutinomas secretificada conference con estada est us cara, pes usa cas
4110	25419		0.83	1.0E-19	1.0E-19 AA595527.1	EST HUMAN	nh22d03.s1 NCI_CCAP_Pr1 Hamo septens cDNA clone IMAGE:953093 similar to contains L1.t1 L1 repetitive element;
7528		33283	0.86	1.0E-19	1.0E-19 U08813.1	L	Onctolegus cuniculus Ne+/glucose cotransporter-related protein mRNA, complete cds
7528		33294	0.86		1.0E-19 U08813.1	Ę	Oryctolagus cuniculus Na+fglucose cotransporter-related protein mRNA, complete ods
7895			0.93		1.0E-19 AF200719.1	۲N	Homo sepiens pituitary tumor transforming gene protein (PTTG) gene, complete ods
8349	21042	34179	1.75	1.0E-19	1.0E-19 M64657.1	L	Rabbit phosphorylase kinase beta subunit mRNA, complete cds
							ye/2b02.rt Soares fetal liver spicen 1NFLS Homo sepiens dDNA clone IMAGE:123243 5' similar to contains
88 88	21332		2.64	1.0E-19	1.0E-19 T99920.1	EST_HUMAN	OFR repositive element;
8849	22301		0.46	1.0E-19	1.0E-19 U60822.1	M	Human dystrophin (DMD) gene, exons 7, 8 and 9, and pertial cds
10087	22735		23.03	1.0E-19	1.0E-19 AW812259.1	EST_HUMAN	RC0-ST0174-191099-031-b05 ST0174 Homo sepiens cDNA
10097	22745	35960	1.46	1.0E-19	1.0E-19 N44631.1	EST_HUMAN	yy31e09.r1 Source melancoyte 2NbHM Homo saplens cDNA clone IMAGE:272872 5
	72070	0	,	10,	,,	ļ	Homo septens MAGE-82 (MAGE-82), MAGE-83 (MAGE-83), MAGE-84 (MAGE-84), and MAGE-81
3	1000		66.	1.05-19	1.0E-19 043163.1	Z !	(MYCE-51) genes, compless ous
8840	18314	1	2.58	8.0E-20	7867288 NT	F	Mus musculus keratin-esecoteled protein 9-1 (Krtap9-1), mRNA
8 8			2.56	8.0E-20	7057286 NT	NT	Mus muscukus keretin-essociated protein 9-1 (Krtep9-1), mRNA
7418		33180	1.34	8.0E-20	8.0E-20 AI221371.1	EST HUMAN	qg8df09.x1 Soeres_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:1842089.3'
7418	20005	33181	1.34	8.0E-20	8.0E-20 AI221371.1	EST_HUMAN	qg88f09.x1 Soeres_NFL_T_GBC_S1 Home sepiens cDNA olane IMAGE:1842099 3'
3270	16031	28082	1.41	7.0E-20	7.0E-20 BF326455.1	EST HUMAN	PMA-AN0096-050900-003-e04 AN0088 Homo saplens cDNA
888	17972	30529	6.29	7.0E-20	7.0E-20 AL138120.1	EST_HUMAN	DKFZp547D092_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547D092 5'
36	21087	34222	877 (1	7.05-20	7 OF-20 AA567857 1	NAMI IH TRA	n/48c04.s1 NCI_CGAP_Pr4 Homo septems cDNA clone IMAGE:1043718 similar to contains MER29.b2 MER29 promitties element
	1				•		

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Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similer (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8394	21087	34223	12.48	7.0E-20	7.0E-20 AA557657.1	EST HUMAN	nl46c04.s1 NCI_CGAP_Pr4 Homo saplens cDNA clone IMAGE:1043718 similar to contains MER29.b2 MER29 repetitive element;
11714	24308		1.86	7.0E-20	6912833 NT	Ϋ́	Homo sepions ribosomal protein L13a (RPL13A), mRNA
3543	16298	28949	3.52	6.0E-20 P39188		SWISSPROT	ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY
4239		29605		6.0E-20	6.0E-20 BE622434.1	EST_HUMAN	801441231F1 NIH_MGC_72 Homo saplems cDNA clone IMAGE:3916231 5
4556			1.18	6.0E-20	6.0E-20 AV726123.1	EST_HUMAN	AV725123 HTC Homo sepiens cDNA clone HTCBTA01 5
7015	19707	32763	1.07	5.0E-20	5.0E-20 AF075301.1	EST_HUMAN	AF075301 Human fetal liver cDNA library Homo sapiens cDNA clone HA0250
7846	20541	33668	5.28	5.0E-20	5.0E-20 W90525.1	EST HUMAN	zh78d08.st Soares fetal Itver spleen_1NFLS_S1 Homo sapiens cDNA cione iMAGE:418191 3' similar to contains MER30.t1 MER30 repelitive element;
7846	20541	33669	; ; ; ;	5.0E-20	5.0E-20 W90525.1	EST HUMAN	Zh78d08.s1 Scares fetal jiver spleen_1NFLS_S1 Homo sepiens cDNA clone IMAGE:418191 3' similar to contains MER30.t1 MER30 repetitive element:
8002	26902	33825		5.0E-20	5.0E-20 BE165980.1	EST HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens aDNA
8734	21428	34672	2.54	5.0E-20	5.0E-20 AB028174.1	NT	Mus musculus MMAN-g mRNA, complete cds
8734		34573	2.54	5.0E-20	5.0E-20 AB028174.1	Ę	Mus musculus MMAN-g mRNA, complete cds
9345			0.94	5.0E-20 C60809	08090	SWISSPROT	HYPOTHETICAL PROTEIN DJ845024.1
1616	14363	27054	1.34	4.0E-20	4.0E-20 AL163247.2	TN	Homo saplens chromosome 21 segment HS21C047
2029	18359		0.8	4.0E-20 Q89880	ූ	SWISSPROT	HISTONE HZB C (HZB/C)
7828	_[5.15	4.0E-20		EST_HUMAN	t264g03.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clane IMAGE:2283396 3'
10398	\perp	36259	1.33	4.0E-20	4.0E-20 AW837469.1	EST HUMAN	QV3-DT0043-090200-080-c04 DT0043 Homo saplens cDNA
2135		27595	1.02	3.0E-20	.1	NT	Human BXP21 gene
4185	16926	29557	1.29	3.0E-20 P23273	P23273	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN 114
4582	17317	29944	1.05	3.0E-20	3.0E-20 AA037616.1	EST HUMAN	2/36b12.s1 Source_progrant_ulerus_NbHPU Homo sepiens cDNA clone IMAGE:484995 3' straitar to contains L1.t3 L1 repotitive element:
8833	21525		2.95	3.0E-20 D14547.1		Ţ	Human DNA, SINE repetitive element
10219	22867	36078	0.63	3.0E-20	3.0E-20 BF185264.1	EST_HUMAN	601843561F1 NIH_MGC_54 Homo sepiens cDNA clone IMAGE:4084343 5
10561	23257		1.87	3.0E-20 P11369	911369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN (CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
11496	24097	37408	1.5	3.0E-20	3.0E-20 AI284244.1	EST_HUMAN	q70d02x1 NC_CGAP_Kid3 Homo sepiens cDNA clone IMAGE:1864803 3' similar to contains Alu repetitive element;
11498	24097	37409	1.5	3.0E-20		EST HUMAN	q70d02x1 NC_CGAP_Kkt3 Homo saplens dDNA clone IMAGE:1864803 3' similar to contains Alu repetitive element:
12051	24560	31118	2.65	3.0E-20	Į	П	601514180F1 NIH_MGC_71 Hamo saplens cDNA clone IMAGE:3915522 57
811	13582		3.12	2.06-20 /	2.0E-20 AW303868.1	EST_HUMAN	x24e10.x1 NCI_CGAP_Ut4 Homo septens cDNA done IMAGE:2761098 3' similar to SW:RS5_MOUSE P97461 40S RIBOSOMAL PROTEIN S5.;

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Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Vatue	Top Hit Acessian Na.	Top Hit Detabase Source	. Top Hit Descriptor
1089	13847	26505	3.37		2.0E-20 AA516335.1	EST_HUMAN	ng69h09.s1 NCI_CGAP_Lip2 Hamo sapiens cDNA clone IMAGE:940097 similar to TR:G1224066 G1224066 ORF2: FUNCTION UNKNOWN.;
1089	13847	26506	3.37		2.0E-20 AA516335.1	EST_HUMAN	ng69h09.s1 NCI_CQAP_LIp2 Hamo sepiens cDNA clone IMAGE:940097 similar to TR:G1224066 G1224086 ORF2: FUNCTION UNKNOWN.;
2820	13582		2.38		2.0E-20 AW303888.1	EST_HUMAN	x24e10.x1 NCI_CGAP_Ut4 Homo septens cDNA clone IMAGE:2761098 3' similar to SW:RS5_MOUSE P97461 40S RIBOSOMAL PROTEIN S6.;
4893		30238	4.97		2.0E-20 Q28983	SWISSPROT	ZONADHESIN PRECURSOR
4893		30239				SWISSPROT	ZONADHESIN PRECURSOR
2009	17786		5.98	2.0E-20	5174538 NT	NT	Homo sapiens malete dehydrogenase 1, NAD (soluble) (MDH1) mRNA
8017		33843	0.81	2.0E-20	2.0E-20 AA309457.1	EST_HUMAN	EST180326 Liver III Homo sepiens cDNA 6' end
6806					2.0E-20 D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
808	21778	34943	8.6		2.0E-20 D10083.1	NT	Homo saplens RGH1 gene, retrovirus-like element
12426	li	30895			2.0E-20 H56371.1	EST_HUMAN	CHR220310 Chromosome 22 exon Homo sepiens aDNA done C22_391 51
12815	25057		1.39	2.0E-20	11437152 NT	M	Homo sepiens heperin-binding growth factor binding protein (HBP17), mRNA
-			-			İ	Z11d08.r1 NCI_CGAP_GCB1 Homo sepiens cDNA clone IMAGE:712811 5' elmiller to contains MER19.t2
2807	15525	27468	3.71	1.0E-20	1.0E-20 AA281981.1	EST_HUMAN	MER19 repetitive element;
•		Į					hr84b08.x1 NCI_CGAP_K011 Homo septens cDNA clone IMAGE.3135155 3' similer to contains L1.t2 L1
240	╝	71/67	-		1.0E-20 BF115158.1	EST HUMAN	repetitive element;
8	_1	32568	0.75		AF049567	EST_HUMAN	AF049567 Human activated dendritic cell mRNA Homo sapiens cDNA clone GA06
9061	21750	34909	2.04	1.0E-20	11418491 NT	NT	Homo saplens Autosomel Highly Conserved Protein (AHCP), mRNA
11541	24141	37450	2.62		1.0F-20 AF223301.1	Ę	Homo sepiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, attematively soliced
							INCI COAP BY Home series CONA close IMAGE 728804 similar to contains 14 21 4
12171	24051	·	5.7	1.0E-20	1.0E-20 AA420453.1	EST_HUMAN	repositive element;
2913	15679		96.0		9.0E-21 AJ003514.1	EST_HUMAN	AJ003514 Selected chromosome 21 cDNA library Homo septens cDNA clone MPIpt 2-8,121
11904	24489		2.52	9.0E-21	9.0E-21 AW898189.1	EST_HUMAN	RC3-NN0068-090500-021-b03 NN0068 Homo sepiens cDNA
8711	21403		2.15		8.0E-21 AW674891.1	EST HUMAN	5630e02.71 NIH_MGC_10 Home septens d'DNA done IMAGE:2864714 5' similar le SW:NIAM_HUMAN 085189 NADH-UBIQUINONE OXIDOREDUCTASE ASHI SUBUNIT PRECURSOR:
11528	24128	37432	3.52		8.0E-21 AA809411.1	Γ	ob71f08.st NCI_CGAP_GCB1 Hamp septens cDNA clone IMAGE:1336835.3'
12064	24679		4.49	8.0E-21 O21330	1	SWISSPROT	ATP SYNTHASE A CHAIN (PROTEIN 6)
2061	14793	27518	1.62	7.0E-21 P15800	P15800	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
2061	14703	27519	1.62	7.0E-21 P15800		SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
3689	16442	29083	0.69	7.0E-21	2.		Homo saplens chromosome 21 segment HS21C100
4228	10909		5.58	7.0E-21	7.0E-21 AA046502.1	EST HUMAN	zk67a06.r1 Scares_pregnant_uterus_NbHPU Homo seplens cDNA clone IMAGE:487858 5'

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						Service Land	Lyon I know Lybressed III Drail
Probe SEQ ID NO:	Exan SEQ (D NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.		Top Hit Descriptor
6340	19110	32100	0.79		7.0E-21 AL163218.2	M	Homo sapiens chromosome 21 segment HS210018
8287	20981	34121	1.53		7.0E-21 AJ277657.1	듈	Homo sapiens dNT-2 gene for mitochondrial 5(3) decaynibonucleotidase (dNT-2 gene), exons 1-5
8576					7.0E-21 D14718.1	N	Human chromosomal protein HMG1 related gene
10013	22661	35877			7.0E-21 AW850822.1	EST_HUMAN	RC0-CT0301-271199-031-F03 CT0301 Homo sepiens cDNA
10594	23288	38525	2.19		7.0F-24 AA723404 1	EST HUMAN	2g/3d03.st Scaree_fetal_heart_NbHH19W Home septens cONA clone IMAGE:398981.3' similar to de-M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);contains THR.3 OFR receditive element:
11234	L	ĺ_			7708988 NT	N	Homo sapiens PTD013 protein (PTD013), mRNA
4083		29454			6.0E-21 BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiene cDNA clone IMAGE:3638310 5
9034			9.0		8.0E-21 BE162737.1	EST_HUMAN	PM1-HT0454-080100-002-h09 HT0454 Homo sapiens cDNA
£063			4.0		5902031 NT	l.	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
4330	17069	29807			5.0E-21 BE968839.1	EST_HUMAN	601649871F1 NIH_MGC_74 Homo saplens cDNA clone IMAGE:3933880 5
4749	17481	30112	5.58		4885474 NT	1 .	Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA
0665	19582		6.0		5.0E-21 AW440884.1	EST_HUMAN	he05e10.x1 NCI_CGAP_CML1 Hamo seplens cDNA clane IMAGE:2918154 3'
RO47	40 <i>0</i> 854	OUZGE	88 0		7 903 43 8350 K 30 9	MAAMIL TOT	7/83d11.x1 NCI_CGAP_Pr28 Homo septens cDNA clone IMAGE:3303573 3' similer to contains OFR.t1
10474	1_				Colfen	SWISSPROT	ZINC FINGER PROTFIN GLI (GLI-1)
10474	23120	38350			505-21 091690	SWISSPROT	ZNC FINGER PROTEIN GLI (GLL1)
11986	١.				5.0E-21 AA383574.1	EST HUMAN	272c04.r1 Sogres, testis, NHT Hamo septens cDNA done IMAGE:727878 5
							0085608.s1 NCI_CGAP_Kid5 Hamo sepiens cDNA clone IMAGE:1573094 3' similar to TR:Q16530 Q16530
1727		27168			4.0E-21 AA970713.1	EST_HUMAN	PMS3 MRNA; contains OFR.t1 OFR repetitive element;
6772	19516	32544	3.27		4.0E-21 AB019576.1	ᅜ	Rattus norvegicus mRNA for rTIM, complete ods
8	22332	35527	0.03		4.0F-24 Up1328 1	. F	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) cene. RoRat dans, and sodium phosphate transporter (NPT3) cene, complete cds.
9705	L		0.7		22	¥	Homo saciens chromosome 21 segment HS21 0002
1829			9.0 19.0		AA218891.1	EST HUMAN	zq15d06.s1 Stratagene fetal retina 937202 Homo saplens cDNA clone IMAGE:6297713'
2272	14998	27736	1.24		3.0E-21 AL163201.2	N	Homo sepiens chromosome 21 segment HS21C001
3078	15843	28485	4.31	3.0E-21	3.0E-21 AJ007973.1	IN	Homo saplens LGMD2B gene
5412	18211	30919	0.68		3.0E-21 AJ277567.1	IN	Homo sapiens dNT-2 gene for mitochondrial 5(3)-decoynbonucleotidase (dNT-2 gene), exons 1-5
5412	18211	30820	0.68		3.0E-24 A.1277557.1		Homo septens dNT-2 gene for mitochondrial 5/31-decovribonucleoficiase (dNT-2 gene) acons 1-5
	•						

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similer (Top) Hit BLAST E. Value	Top Hit Acession No.	Top Hit Detelbase Source	Top Hit Descriptor
5652	18447		0.65		3.0E-21 AV681044.1	EST HUMAN	AV861044 GLC Homo septens aDNA dane GLCGOA103'
9800	18864		2.3	3.0E-21	3.0E-21 BF184739.1	EST_HUMAN	801844465F1 NIH_MGC_54 Hamo sapiens cDNA clone IMAGE:4064945 5'
88	19451	32460	7.69	3.0E-21	3.0E-21 BF3610G3.1	EST_HUMAN	RC1-OT0083-100800-019-008 OT0083 Homo sapiens cDNA
2695	22245	35429	1.15		3.0E-21 AW897760.1	EST_HUMAN	CM1-NN0063-280400-203-h08 NN0063 Homo septems oDNA
12533	25327	30714	2.88	3.0E-21		NT	Homo sapiens chromosome 21 segment HS21C013
141	12958		17.18			EST_HUMAN	QV3-HT0458-170200-090-g12 HT0458 Homo septems cDNA
914	13681	26342	1.85			NT	Homo saplens mRNA for KIAA0397 protein, partial cds
718	13681	26343	1.85		2.0E-21 AB007857.2	NT	Hamo sapiens mRNA for KIAA0397 protein, partial cds
1192	13944		2.75		20E-21 BE084410.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
2844	15354	86082	1.98	2.05-21 0.28983	0.28983	SWISSPROT	ZONADHESIN PRECURSOR
2844	15354	28099	1.98	2.0E-21 Q28983	028983	SWISSPROT	ZONADHESIN PRECURSOR
	l				,		ts20f03.x1 NCI_CGAP_Pan1 Homo sepiens cDNA clone IMAGE:2230109 3' similar to TR:Q99854 Q99854
88			1.64	2.0E-21		EST HUMAN	HYPOTHETICAL STATE PROTEIN:
5489	18288	31184	0.68	2.0E-21	2.0E-21 AA027211.1	EST_HUMAN	ze97a12.r1 Sceres_fetal_heart_NbH19W Home septens cDNA chore IMAGE:366910 5
5489		31185	89.0		2.0E-21 AA027211.1	EST_HUMAN	ze97a12.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:366910 5
8170	20864	96688	9.0		20E-21 AJ010770.1		Homo sapiens hyperion gene, exons 1-50
8261	20955	34094	6.16		20E-21 BE141785.1	EST_HUMAN	QV0-HT0103-091199-050-g11 HT0103 Homo sepiens cDNA
8722	21414	34557	3.74		2.0E-21 AU136779.1	EST_HUMAN	AU136779 PLACE1 Homo septens cDNA clone PLACE1005052 5
, 000,	1				7 200 700 100	1447 H H 1 4-4-1	httpsg01.xf NCI_CGAP_Kid13 Home septens cDNA done IMAGE:3146256 3' similar to contains MER29.b3
58 25	╛		1.00		DESCRIPT.	ES LOWER	TILLIAND INCOME TO SECURITION OF
11289					20E-21 BE973829.1	EST_HUMAN	6016806336F1 NIH_MGC_83 Home sapiens cDNA clone IMAGE:3951008 5
11289	23960	37247	1.3		2.0E-21 BE973829.1	EST_HUMAN	601680636F1 NIH_MGC_83 Home septents cDNA clone iMAGE:3951008 5
12272	24712		9.87		20E-21 AF176815.1	NŢ	Homo septens putetive 8-hydroxyguanine DNA glycosylase gene, complete cds
							n49co4.s1 NCI_CGAP_Pr4 Homo sepiens cDNA clone IMAGE:1043718 similar to contains MER29.b2
1233		20052	4.6	ľ	1.0E-21 AA557657.1	EST HUMAN	MERZ9 fepeditive element ;
1381			2.62	1.05-21	1.0E-21 AI601264.1	EST_HUMAN	#88412.x1 Bersteed colon HPLRB7 Homo septens cDNA clone IMAGE.2152343 S1
6396	19165		2.74	1.0E-21	1.0E-21 AL079752.1	EST_HUMAN	DKFZp43410830_r1 434 (synonym; htes3) Homo explens cDNA clone DKFZp43410830 5
							qg47e05x1 Soares_testis_NHT Homo suplens cDNA clone IMAGE:1838336 3' stmiler to gb:M84241 QM
7092	19781	32847	6.6		1.0E-21 A1223104.1	EST_HUMAN	PROTEIN (HUMAN);
10484	23130		1.07	1.0E-21	TN 8600573	NT	Homo saplens SET domain and mariner transposase fusion gene (SETMAR) mRNA
4487	75625	7.7700	7		0 0E-20 A 1703438 4	NVMIH 183	1254e.03.X1 NCL_CGAP_Kid11 Homo sepiens cDNA clone IMAGE:2296204.3' similer to TR:Q15408 Q15408 NEI ITRA I PROTESSE ARCE SUBJUIT.
8502	L.					LN L	Homo sablena chromosome 21 segment HS21C001
8502		1		0 0F-22	,	LN	Homo sanlens chromosome 21 segment HS21C001
	2:167		1,500	20.0	!		

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					-S	gle Exon Pro	Single Exon Probes Expressed in Brain
Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3414	16172	L	4.41	2.0E-22	TA SAGADAS INT	L ₂	
4200	16941	29567	1.17	2.0E-22	AW8177	EST HIMAN	Inditio sapiens protein kinase, AMP-activated, gamma 3 non-catalytic subunit (PRKAG3), mRNA
5784	25075	31476	1.18		2.0F-22 W30458 4	TOT LIBRARY	202001.1 Source senescent fibrioblasts_NbHSF Homo sepiens cDNA clone IMAGE:322873 5' similar to
5084	18862	31828	3.58			EST HUMAN	BOOLINOOP (SOOD ONE HIS THOUSE IN THOUSE IN THE CURSOR (HUMAN);
9602	22255	35440	1.53	2.0E-22	-	EST HIMAN	q/76h06xf Soeres NhHMPu_S1 Homo saplens cDNA clone IMAGE:1878299 3' similar to contains
9696		35540	0.60	20E-22		EST HIMAN	MILITARED MICHAEL REPORTING CONTROLL CONTROL CONTROLL CONTROLL CONTROL CONTROL CONTROL CONTROL CONTROLL CONTROL CONTROL CONTROL C
9696		35541	0.69	205-22	2,1	EST HUMAN	INVALIDATION OF A PARTY From Septens CDNA clone IMAGE: 1219269 3'
11761		37684	1.88	20E-22	Š	EST HIMAN	he24ft/k v1 NC CCAD K1420 L
11872	[30983	3.71	2.0E-22		LN	Homo sapless chromosoms 24 across 1624 2004
1871		27320	1.79	1.0E-22	7.1	EST HUMAN	PMA SN0000 01000 D02 SN0000 H
2588	\perp	28038	1.1	1.0E-22		L	Human familial Attebrace descriptions against a september of the september
3405		28814	1.37	1.0E-22		Ę	Human DMA CIME A Library (Library Complete ods
7641	20306	33415	0.89	1.0E-22	5	EST HUMAN	MRO-BTRASO 22020 003 FOZ BITARE I
10451	23097	36328	67.0	1.0E-22		1 -	9209b07.x1 NCI_CGAP_CIL.1 Homo saplens cDNA clone INACE:2020661.3' similar to contains MER29.b2
10451	23097	36329	ç	1 0 5		7	micros repoutre erament; q209b07x1 NCI_CQAP_CL1 Homo sepiens cDNA clone IMAGE:2020981 3' similar to contains MER29.b3
12704	24984		5.89	9 OF 23	Ţ	EST HUMAN	MEKZV repetitive element;
3557	16312	28959	Q. O	A OF 22	T	NOMAIN	ILZ-UMUVG-UVGH-UBT-11 UMM076 Homo septems cDNA
3305	18065		2.55	7.0F-23	T	ROT CIBAAN	Genus gallus Dech2 protein (Dech2) mRNA, complete cds AV647246 Cl. Cl.
10068	23642	36895	4.16	7.0E-23	5031952	- LONG	Home and the All the A
3427	16184		1.72	6.0E-23	AF19933		Rolling Septemble Notice (U. meternogester) Hits protein (NOT68L) mRNA
4235	16976	29601	1.39	8.0E-23			Homo serience characters of the complete cds
12005	24540	31105	1.5	6.0E-23	,		Homo septents mennosides at a segment noot total MANBA) gene, and ubliquitin-conjugating enzyme E2D 3 (UBEDD3) genes, convince consideration of the section
12005	24540	31106	1.5	6.0E-23			Homo septems mennoeldase, beta A, Iyacecmal (MANIBA) gene, and ublquith-conjugating enzyme E2D 3 (UBE2D3) genes, complete cits
12192	24063	31067	3.28	6.0E-23	6.0E-23 AI209130.1	EST_HUMAN	9959003.x1 Soeres_testis_NHT Homo septens dDNA clone IMAGE:1839460 3' similar to SW:MV10_MOUSE P22240 PROTEIN MOV-10.
5358	18160	30844	4.09	6.0E-23 U82671.2		Ę	Homo septens chromosome Xq28 metenome antigen femity A2a (MAGEA2A), metenome antigen family A12 (MAGEA12), metenome antigen family A2b (MAGEA2B), metenome antigen family A3 (MAGEA3), catractin (CALT), NAD(P)H dehydrocenses, like protein (NACH), NAD(P)H dehydrocenses, like protein (NACH)

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Top Hit Acessian Detablese Top Hit Descriptor No. Source	NT	179818.1 NT Pongo pygmaeus olfactory receptor (PPY118) gene, pertial cds	.1832Z7.2 NT Homo saplens chromosome 21 segment HS21C027	.163227.2 NT Homo sapiens chromosome 21 segment HS21C027	5.1 EST HUMAN	0684.1 NT Human endogenoue retroviral element HC2	M	W897827.1 EST_HUMAN RC3-NN0066-270400-011-h01 NN0068 Homo sapiens cDNA	289880.1 NT Homo saplens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene	LN.	2105 SWISSPROT TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)	SWISSPROT	1 EST_HUMAN	1 EST HUMAN	EST_HUMAN	99831.1 [EST_HUMAN yr18a02.r1 Soares fetal liver spieen 1NFLS Homo sepiens cDNA clone IMAGE::205418 5'	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide	Į,	2 NT	TN	INT	2 NT	.163210.2 NT Homo sapiens chromosome 21 segment HS21C010	3378471.1 EST_HUMAN 601236455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608653 5'		.1 EST HUMAN	.1 EST_HUMAN	409643.1 EST_HUMAN 001301762F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636254 5'	ab75a08.e1 Stratagene fetal retine 937202 Homo capiens cDNA clone IMAGE:852758 3' similer to TR:E19822 E19822 CA PROTEIN:	122027 NT
Top Hiit Acess Na.	5.0E-23 AF179818.1	5.0E-23 AF179818.1	3.0E-23 AL163227.2		ari i	270664.1	270664.1	3.0E-23 AW897927.1	2.0E-23 AJ289880.1	20E-23 M55270.1	P22105	P22105	2.0E-23 AI201458.1	2.0E-23 BE165980.1	H59931.1	H59831.1				2.0E-23 M32658.1	2.0E-23 AF009660.1	1.0E-23 AL163252.2	1.0E-23 AL163210.2	1.0E-23 BE378471.1		1.0E-23 AA448097.1	1.0E-23 BE409643.1	1.0E-23 BE409043.1	9.0E-24 AA663213.1	11422
Most Similar (Top) HR BLAST E Value	6.0E-23	5.05-23	3.05-23	3.05-23	3.0E-23	3.0E-23 Z70664.1	3.0E-23 Z70664.1	3.05-23	2.06-23	20E-23	20E-23 P22105	2.0E-23 P22105	2.0E-23	20E-23	2.0E-23 H59931.1	2.0E-23 H59931.1		2.0E-23	2.0E-23	2.0E-23	205-23	1.0E-23	1.06-23	1.0E-23		1.0E-23	1.0E-23	1.0E-23	9.0E-24	8.0E-24
Expression Signal	3.83	3.37	1.34	1.34	4.1	2.96	2.96	1.18	4.25	3.87	1.98	1.98	1.46	3.35	3.65	3.65		4.3	1.21	2.45	2.87	1.1	5.56	3.28		4.6	2.05	2.05	1.84	1.53
ORF SEQ ID NO:	31863	31863	32108	32107	33558	35045	35046		39068		28243	28244			28346	28347			34579			29857						36504	<u> </u>	32121
Econ SEQ ID NO:	25086	25086	19117	10117	20434	21879	21879	22863	13420	15520	15503	15503	16123		16707	16707		- 1		24530	24960	17228	17448	19382				23205	13322	L
Probe SEQ ID NO:	6145	7337	6347	6347	7738	9148	9148	10215	651	1120	27798	2798	3364	3705	3958	3958		7772	8742	11991	12508	4492	4714	9820		8254	10570	10570	539	6357

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9EQ ID 3E NO: 7 3853 3853 10 10536 2 10536 3953 7 7857 7857	Exan SEQ ID NO: 10603 17806 13465 13465 13580 16703 20321	ORF SEQ ID NO: 26256 33430	Expression Signal 1.49 0.95 1.33 2.72 2.72 2.72 0.58	Most Similar (Top) Hit BLAST E Value 7.0E-24 / 7.0E-24 / 6.0E-24 / 6.0E-24 / 5.0E-24 /	t Similer Top Hit Acession AST E No. AST E No. AGUE 7.0E-24 AWG37954.1 7.0E-24 ALG39498.1 7.0E-24 AB001421.1 6.0E-24 AB001421.1 6.0E-24 ALG32903.1 6.0E-24 AF223391.1	Top Hit Detabase Source Source EST_HUMAN EST_HUMAN NT NT	Top Hit Descriptor QV0-DT0047-170200-122-e08 DT0047 Homo septens cDNA DKFZp434A2311_T1434 (synonym: htes3) Homo septens cDNA clone DKFZp434A2311 57 xv17f03.x1 Soares_NFL_T_GBC_S1 Homo septens cDNA clone IMAGE:2813405 3' similar to contains Alu repetitive element; contains Alu RE19.t2 MER19.t2 MER19 repetitive element; omplete cds Macaca fuscala mRNA for 1 sestis-Specific Protein Y (TSPY), complete cds Homo septens chromosome 21 segment HS210049 Homo septens 959 kb config between AML1 and CBR1 on chromosome 21q22, segment 3/3 Homo septens calcium charmel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced.
6840 6840 11133 12361 12565	24194 18628 21273 23801 24765 24851	37513 31663 34411 37078 31062 30996	3.86 1.35 1.85 4.89	5.0E-24 AW5142 4.0E-24 AM5137 4.0E-24 AW8137 4.0E-24 AB02901 4.0E-24 AB02901 4.0E-24	5.0E-24 AW514229.1 ES 4.0E-24 AW813711.1 ES 4.0E-24 BES44822.1 ES 4.0E-24 AB029016.1 NT 6.0E-24 AB029016.1 NT	T HUMAN T HUMAN	Indianos XI Social March 1 Control Septembrication and the invitation of the control of the cont
8322 8377 8365 12438 2246 3779	21015 21070 21840 24808 15069 16531	35414 31045 Z7806 33135	285 1.57 4.33 4.33 1.41 1.41 1.01	3.0E-24 AW6148 3.0E-24 AL16325 3.0E-24 BF12778 2.0E-24 AA16753 2.0E-24 AW6981 2.0E-24 AF08682	3.0E-24 AW614871.1 3.0E-24 AW662076.1 3.0E-24 AL163252.2 3.0E-24 BF127782.1 2.0E-24 AA167539.1 2.0E-24 AW698189.1	EST HUMAN NT EST HUMAN EST HUMAN EST HUMAN EST HUMAN	MER29 repetitive element; MER29 repetitive element; EST374149 MAGE resequences, MAGG Homo septens cDNA Homo septens chromosome 21 segment HS21C052 B01810449F1 NIH_MGC_46 Homo septens cDNA done IMAGE:4063396 5' pq11f02.r1 Stretagene fetal retina 637202 Homo septens cDNA done IMAGE:609161 5' RC3-NN0088-090500-021-b03 NN0088 Homo septens cDNA Mus musculus rho/rec-interacting citron kinase (Critk) mRNA, complete cds
	20059 21331 22405 22405 22409 24409 25377	33476 34476 35611 35611 37744 37745	0.98 0.94 0.94 1.31 1.31 1.47	2.0E-24 AL119155 2.0E-24 H69214.1 2.0E-24 H6921756 2.0E-24 AW8688 2.0E-24 AW8688 2.0E-24 AW8688 2.0E-24 AW8688	20E-24 AJ003538.1 20E-24 AL119158.1 20E-24 H69214.1 20E-24 AI621759.1 20E-24 AI621759.1 20E-24 AW868552.1 20E-24 AW868552.1 20E-24 AW868552.1	T HUMAN T HUMAN T HUMAN T HUMAN	AJ003636 Selected chromosome 21 cDNA library Homo sepiens cDNA clone MPlp12-5H13 DKFZp761L1712_r1 761 (synonym: harny2) Homo sepiens cDNA clone DKFZp761L1712 5' YR2b09.r1 Soeres fetal liver spieen 1NFLS Homo sepiens cDNA clone IMAGE:212729 5' similar to contains MER28 repetitive element; #17809.x1 NCI_CGAP_Kid11 Homo sepiens cDNA clone IMAGE:2138008 3' #17809.x1 NCI_CGAP_Kid11 Homo sepiens cDNA clone IMAGE:2138008 3' MR1-SN0083-040500-001-a08 SN0083 Homo sepiens cDNA MR1-SN0083-040500-001-a08 SN0083 Homo sepiens cDNA Human O family dispersed repeat element

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M87h08.x1 Schneider fetal brain 00004 Homo sepiens cDNA clone IMAGE:27832953' stmilar to gb:K00568 eu87h08.x1 Schneider fetal brein 00004 Homo sepiens cDNA clone IMAGE:2783295 3' stmiller to gb:K00558 hi51h12.x1 Source_NR__T_GBC_S1 Homo sepiens cDNA clone IMAGE;2975879.3' similar to TR:078040 076040 ORF2: FUNCTION UNKNOWN.; nee03c07.x1 NCI_CGAP_Pr28 Homo explens cDNA done IMAGE:3253644 3' similar to contains OFR.t1 #49c04.x1 NCI_CGAP_Lu19 Homo sepiens cDNA clone IMAGE:2408150 3' similar to contains THR.b2 Hamo seplens WAGE-B2 (WAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (WAGE-B4), and MAGE-B1 Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 ADP, ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE 11751F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J1751 5' similar to DKFZp508C2146_r1 508 (synonym: hfld2) Homo septens cDNA done DKFZp586C2146 57 CHR220032 Chromosome 22 exan Homo sepiens cDNA clone C22_45 61 Top Hit Descriptor RC6-FN0138-110800-022-A02 FN0138 Homo septens cDNA WR3-HT0487-150200-113-g01 HT0487 Homo sepiens cDNA PM2-SN0018-220300-002-607 SN0018 Homo septems cDNA CM1-CT0315-091299-063-d07 CT0315 Homo seplens cDNA MR4-BT0398-250800-204-d08 BT0398 Homo seplens cDNA CM1-CT0315-091299-083-d07 CT0315 Homo saplens cDNA AV732214 HTF Homo sepiens cDNA clone HTFBCB08 6 AV723365 HTB Homo septens cDNA clone HTBAHE02 5 Homo sapiens Xq pseudoautosomal region; segment 1/2 Homo sapiens chromosome 21 segment HS21C027 Human nucleoter protein (B23) mRNA, complete cds Homo saplens WRN (WRN) gene, complete cds NUCLEOTIDE TRANSLOCATOR 3) (ANT 3) Human mRNA for KIAA0231 gene, pertial cds Human endogenous retroviral element HC2 TUBULIN ALPHA-1 CHAIN (HUMAN); TUBULIN ALPHA-1 CHAIN (HUMAN); (MAGE-B1) genes, complete cds (MAGE-B1) genes, complete cde REPETITIVE ELEMENT L1 THR repettive element; OFR repetitive element EST_HUMAN NT EST_HUMAN EST HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST HUMAN EST_HUMAN EST HUMAN HUMAN **EST HUMAN** EST_HUMAN EST_HUMAN EST_HUMAN SWISSPROT EST HUMAN EST_HUMAN Database 발 Source EST F 눋 눋 눋 눌 눋 Top Hit Acession 8.0E-27 AW162737.1 8.0E-27 AW162737.1 8.0E-27 AW884776.1 1.0E-26 BE165980.1 1.0E-26 AL038487.1 9.0E-27 BF445558.1 8.0E-27 AW857579.1 7.0E-27 AW 629172.1 AL163227.2 8.0E-27 AF181897.1 8.0E-27 AV732214.1 AW857579. ģ BE928580.1 9.0E-27 BF371227. B.0E-27 AIB31462.1 7.0E-27 AV723365.1 7.0E-27 AJ271735.1 1.0E-28 H55093.1 9.0E-27 U93163.1 8.0E-27 N84970.1 7.0E-27 D89984.1 6.0E-27 U93163.1 M28697. 8.0E-27 P12238 8.0E-27 8.0E-27 7.0E-27 6.0E-27 Aost Simila 8.0E-27 BLASTE # (B) Value 3.53 221 5.72 3.83 59.39 50.30 4.14 1.02 Ξ 4.33 1,37 18. 0.81 228 1.19 1.51 1.51 4.20 1.57 2.12 2.75 Expression Signal ORFSEQ 25,450 26819 22820 28594 28762 31317 34961 34962 36558 37728 ÖΝΩ SEQ ID 23492 25395 20156 19574 22082 12837 14142 <u>0</u> 2452 14142 14893 18404 19429 21797 21797 1344 21448 16107 24843 13327 17957 1750 2334 23320 24394 ÿ 12348 6740 10809 SEO ID 7484 8203 11875 1395 10 1398 2164 3180 88 3348 3 6881 6647 9109 9109 2030 8756 138 899 10650 12484 10627

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Most Similar Top Hit Acession (Top) Hit Top Hit Acession Database Signal BLASTE No. Signal Place Source	35996 2.82 5.0E-27 BF666614.1 EST_HUMAN	35997 2.82	32421 1.65 4.0E-27 9910569 NT	35 1.07 4.0E-27 AL 163209.2 NT Homo sapiens chromosome 21 segment HS21C009	1.54	35491 0.7 4.0E-27 AW880850.1 EST_HUMAN	37525 1.98 4.0E-27 X89211.1	06 27499 4.01 3.0E-27 X80958.1 NT Rrethus RYA3 mRNA for a potential ligand-binding protein	79 29604 1.06 3.0E-27 BE071924.1 EST_HUMAN PM0-BT0527-090100-001-411 BT0527 Homo saplens cDNA	88 30697 6.24 3.0E-27 AA077705.1 EST_HUMAN 7844C08 Chromosome 7 Febs Brain cDNA Library Homo sepiens cDNA clone 7844C08	33475 0.63 3.0E-27 BE670351.1 EST_HUMAN	35256 2.93 3.0E-27 BF035327.1		R 40	NOWOT 154 1.54 1.55 1.55 1.55 1.55 1.55 1.55	10.39 2.0E-27 AW628172.1 EST_HUMAN	28632 1.96 2.0E-27 AF111167.2 INT Homo saplens Jun dimerization protein gene, pertial ods; cfoe gene, complete ods; and unknown gene	28633 1.96 2.0E-27.AF111167.2 NT	20385 1.36 2.0E-27 AF000388.1 NT	32353 0.01 2.0E-27 H02855 1 EST HUMAN	33810 1.65 2.0E-27 AI898347.1 EST HUMAN		2.3 2.0E-27 AA551527.1 EST_HUMAN	35536 0.76 2.0E-27 X60658.1 NT	35782 1.28 2.0E-27 M78500.1 EST_HUMAN		30802 4.11 2.0E-27 AU121686.1 EST_HUMAN	25 3.31 2.0E-27 AA565345.1 EST_HUMAN ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);	12 1.51 1.0E-27 AL 163246.2 NT Homo saplens chromosome 21 segment HS21C046
	35996	35997	32421			35491	37525	27499	29604	30697	33475	35256	25487			_	28632	28633	20385	32358	33810	,		35536	35782	35783	36802		
SEQ ID NO:	7 22785	7 22785	2 19407	0 20535		4 22298	4 24203	14708	3 16979	18068	3 20361	5 22084	12868	14825		15872	15981	15981	16755	18340				- 1			23555		Ш
Probe SEQ ID NO:	10137	10137	6645	7840	7883	9644	11604	2034	4238	5262	7698	9205	40	1888		3107	3218	3218	4000	6577	7989		9168	999	9935	9935	10875	11489	426

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						1	
Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similer (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Detabase Source	Top Hit Descriptor
976	13741	26404	1.34	1.0E-27	1.0E-27 AB026898.1	늏	Hamo sepiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4061	16806		86.0		1.0E-27 BE350127.1	EST_HUMAN	ht09g01.x1 NCI_CGAP_Kid13 Homo saplens cDNA clone IMAGE:3146256.3' similar to contains MER29.b3 MER29 repetitive element;
6448		32215	6.26	1.0E-27	0005856 NT	N P	Homo sepiens Retine-derived POU-domain factor-1 (RPF-1), mRNA
6771	19515	32542	1.96	1.0E-27	1.0E-27 F30158.1	EST_HUMAN	HSPD20461 HM3 Homo seplens cDNA clone e40000e5C10
6771	19515	32543	1.96		1.0E-27 F30158.1	EST_HUMAN	HSPD20461 HM3 Homo sepiens cDNA clane s4000095C10
8208	21200	34346	0.98		1.0E-27 AB007923.1	Ł	Homo sepiens mRNA for KIAA0454 protein, partial ods
8884			2.26		-	EST_HUMAN	RC8-BT0627-140200-011-E06 BT0627 Homo sepiens cDNA
8822		35463	2.55			۲	Human mRNA for KIAA0260 gene, partial cds
11704	24299	37825	3.51		1.0E-27 AF111083.1	NT.	Bos teurus letrophilin 3 spilce versent bbeh mRNA, complete cds
497	130064		700	90 100	7 00000 0	TOT THE PART	hw17c11.x1 NCI_CGAP_Lu24 Homo septens cDNA clane IMAGE:3183188 3' similar to TR:Q07314 Q07314 SECRETED NEI IDEXNA III AI DAY A DOESNI III AI DAY A
2 8	L	25747	334	4.0E-28	9.0E-28 BE348369.1	EST HUMAN	AL128280 NT2824 Home contains ANA Alone NT282400000000000000000000000000000000000
1020			200	20.00	A A 4 7 40 70 4	FOT LINAN	THE CASE OF THE STATE OF THE ST
41054			20.0	8.UE-20	8.UE-20 AA1/40/0.1	EST LITERAL	CAD 19, A 1 CANDO 372 AND TAINS SO ZUZ THORIS SERVING CONTROL OF THE INFORMACE OF THE CAD THORIS SO AND THIS SOURCE.
Cal	1		60.4	X.UE-26	W.UE-26 Br3//639.1	ESI_HOMAN	CMZ-11N0140-0/CSCO-5/Z-201 INO140 HOMS SERVERS CONA
1228	25245		2.46	8.0E-28	8.0E-28 AW157571.1	EST HUMAN	au83h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782911 3' similar to TR:060302 060302 KIAAD555 PROTEIN, ;contains element MER22 repetitive element;
1158	1	26678	7.89	7.0E-28	AU142750	EST_HUMAN	AU142750 Y79AA1 Homo sepiens cDNA clone Y79AA1000824 6
11142			3.36	7.0E-28	11417868 NT	ᅜ	Homo sapiens gamma-giutamytransferase-like activity 1 (GGTLA1), mRNA
11910	24474		2.78	7.0E-28	7.0E-28 AV735348.1	EST_HUMAN	AV735348 CB Homo sepiens cDNA clone CBFAKA12 51
8817	21509		26.0	6.0E-28	6.0E-28 AF016052.1	NT	Hamo saplens zinc finger protein ZNF191 (ZNF191) gene, complete cds
10508	24872		300	90	A 1 E 0 1 E 0 1	1444 LT TOT	ae80e03.r1 NCI_CGAP_GCB1 Homo eaplens cDNA clone IMAGE:825340 5' similar to contains Alu
				2	Tana and	NUMBER	words.07 vt NCI C3AP Part Home and service collection (NACE: 246590 3" smiles to containe THD ht
310	13114	٠.	4.10	5.0E-28	5.0E-28 AI921003.1	EST HUMAN	THR repetitive element;
3990	16738	29372	1.44	5.0E-28	5.0E-28 R79782.1	EST HUMAN	y80/10.r1 Soarse placents Nb2HP Homo septens cDNA clone IMAGE:146443 5'
	45340	20007	9	i i	7 000000	100	xr333c99.x1 NCI_CGAP_Kd11 Homo septens cDNA clone IMAGE:2695504 3' straiter to SW:GG85_HUMAN
3	١	/0007	00.	4.UE-20	4.UE-20 AW (93000.1	ES L'HOMAN	COON & COLCINARY.
2076	- 1	28380	0.78	4.0E-28	4505316 NT	NT	Homo sepiens myosin phosphatase, target subunit 1 (MYPT1), mRNA
3108	15871	28511	2.52	4.0E-28	4.0E-29 BE409100.1	EST HUMAN	601300703F1 NIH_MGC_21 Homo sapiens cDNA done IMAGE:3635305 5'
7230	19915	32088	8:	4.06-28	4.0E-28 AI108941.1	EST_HUMAN	qf80110.x1 Soares_bests_NHT Homo septens cDNA clone IMAGE:1755019.3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Detabese Source	Top Hit Descriptor
10774	23457		3.08		4.0E-28 AF029308.1	IN TA	Home sapiens chromosome 9 duplication of the T cell receptor bata from and transferons asses femalises
10928	23608		17.24		4.0E-28 AB038241.1	F	Felis catus GAPDH mRNA for ghoeraldehyde-3-phosphate dehydrogenase, complete cds.
10850	19915	32968	4.75		4.0E-28 AI198941.1	EST HUMAN	q98910.x1 Source, bestis, NHT Homo septems CDNA clone IMAGE:1755019.3' striker to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HIMAAN).
12312	24734		1.84	4.0E-28	L	EST_HUMAN	RC3-CT0254-240400-210-f12 CT0254 Homo seciens cDNA
1280	14009		2.88	3.0E-28		Ę	Homo septiens metalloprobasse-like, disintegrin-like, cysteine-rich protein 2 epsilon (ADAM22) mRNA, complete cds
5051	17770		1.05	3.0E-28	3.0E-28 AF009660.1	TN	Homo septens T cell recentur beta locus. TORRV7S14.2 to TORRV1952 and an
8728	21418	34562	1.89	3.0E-28	3.0E-28 BF354030.1	T HUMAN	MR3-HT0713-280500-013-00 HT0713 Home services cDNA
10863	23533	36778	2.09	3.0E-28	3.0E-28 U53588.1	Т	Hamo saplens MHC class 1 region
1234	24751		3.62	3.0E-28	3.0E-28 AI831991 1	FST HIMAN	wjekro7 x I NCI_CGAP_Lym12 Homo sepiens cDNA clone IMAGE:2410885 3' similer to contains Alumentellus signatures clones in the contains Alumentellus signatures clones in the contains and the con
87	12913	25561	10.6	2.0E-28	2.0E-28 BE062167.1	Т	RCI-BT0254-20000-016-RT0264-Lives and an action of the
1023	13783	28444	0.86	2.0E-28	4501912 NT	1	Homo sepiens a disintentin and metallicandariases domain 23 (ADAM23) mRNA
1142	13897	28558	16.03	2.0E-28	Y11107.3	TN	Homo saplens (TGB4 cene for integrin beta 4 subunit sema 3.41
2481	15199	27839	2.1	2.0E-28	2.0E-28 A1348634.1	EST HUMAN	poS5b06.x1 NCI_CGAP_Lu5 Homo saplens cDNA clone IMAGE:1910483 3' similar to containe L1.b2 L1 repeditive element;
6215	18080	31986	133	2.05-28	2 0E-28 BF224402 1		ir76c03x1 NG_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134404 3' similar to contains LOR1.b1
6238	19012		5.07	2.0E-28	5	T	801814198F1 NIH MGC 54 Homo senione of NA chara IMAGE: Anabres 51
7943	20638	33706	0.71	2.0E-28		Π	Sus scrofa domestica submadiary accornich mRNA complain cris
88	22137		5.54	2.0E-28		EST_HUMAN	EST384394 MAGE resequences, MAGL Homo sapiens cDNA
11014	24212	37536	28	2.0E-28	2.0E-28 AF224889.1	LN	Homo septens mennosidase, beta A, Iyaosomai (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete order.
12322	24741	 -	222	2.0E-28		T HUMAN	V78009 If Somes Infart hash full Home sentens of NA Acres 1440 Acres infart hash full Home sentens of NA Acres 1440 Acres infart hash full hash fu
1461	14208	26805	284	1.0E-28	-		Human gene for Abracactor, and 7-9
2217	14945	27685	237	1.0E-28	3.1	T HUMAN	QV1-BT0821-120900-360-b03 BT0821 Homo seniens cDNA
7769	20455		3.2	1.0E-28	11429885 NT		Homo sapiens similar to ribosomal protein 12 (H. Saniens) // O.O. R. A. D. A. A. A. A. A. A. A. A. A. A. A. A. A.
7047	20612		3.3	1.05-28	N 5022708		Homo septens hypothetical protein FLJ10968 (FLJ10968), mRNA
947'8	21848	35014	28.	1.0E-28/	1.0E-28 AA308744.1	EST HUMAN	EST178815 HCC cell line (melastasis to liver in mouse) II Homo sepiens cDNA 5' end similar to similar to refinding I TR
8778	22427	35633	8.73	1.0E-28	1768431		Homo sapiens dennie akthemytrensfersee like echt/ky / (GCT) A1 mDNA
8778	22427	35634	8.Y	1.0E-28	4758431 NT		Homo sepiens germa-glutamytransferase-like activity 1 (GGTLA1), mRNA

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	Top Hit Descriptor	AN AU148358 NT2RM4 Homo sapiens cDNA done NT2RM4002148 3'		Γ		L	Т	Т		Т	T	Г		П	1			Homo sapiens PTS dere for 6-purity of tetrah directions available of	Т	Г	Human gens for Ah-receptor, each 7-9		Т		$\overline{}$			П
,	Top Hit Detabase Source	EST HUMAN	EST HUMAN	Ϋ́	EST HUMAN	SWISSPROT	EST HUMAN	Έ	EST HIMAN	FST HIMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	Ę	LN	EST HUMAN	EST_HUMAN	INT	EST HUMAN	Ę	EST HUMAN	EST HUMAN	, L	EST HUMAN	N N
	Top Hit Acession No.	1.0E-28 AU149356.1	1.0E-28 AA054182.1	1.0E-28 AL163247.2	9.0E-29 AW 663987.1	000130	7.0E-29 AW968447.1	7.0E-29 AJ132352.1	6.0E-29 AI936748.1	6.0E-29 BE940436.1	6.0E-29 BF568097.1	5.0E-20 AW887541.1	4.0E-29 A1752367.1	4.0E-29 BE164930.1	4.0E-29 AI678101.1	AI878101.1		1.1	-	3.1		3.0E-29 AW303317.1	Γ	3.0E-20 BE350127.1	_		4.	
	Most Similar (Top) Hit BLAST E Value	1.0E-28	1.0E-28	1.0E-28	9.0E-29	8.0E-29 Cx00130	7.0E-20	7.0E-29	6.0E-29	6.0E-29	6.0E-29	5.0E-20	4.0E-29	4.0E-29	4.0E-29	4.0E-29 AI878101	4.0E-29 J04988.1	3.0E-29	3.0E-20	3.0E-29 L	3.0E-29 D38044.1	3.0E-20/	3.0E-29	3.0E-29	3.0E-29 AA403053	3.0E-29 D63882.1	3.0E-29 AA016177	2.0E-29 AF084869
	Expression Signal	0.63	7.79	1,88	3.18	3.32	1.37	7.13	16.86	8.09	1.72	5.38	20.	7.91	0.55	0.55	6.21	1.4	1.07	1.18	2.87	8.	1.87	0.61	1.47	1.53	7.53	1.72
	ORF SEQ ID NO:				30603		27034		25989	-		 			33797	33798	34480	29751	30054	31564	34405	35034			37185			25900
	Exan SEQ ID NO:				25346	24806	14344	25045	13361	24869	24717	21322	15989	18704	20674	20674	21336	17118	17418	18820	21324	21880	22109	22509	23898	24900	25378	13285
	Probe SEQ ID NO:	10422	11915	12651	12749	12436	1598	12794	581	12201	12286	9630	3226	5919	27.67	7979	8844	4381	4684	88	8832	9200	9431	6 888	11235	12102	12799	8

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SFO D NO: 0 NO: 0	Single Exon Probes Expressed in Brain	Exon ORF SEQ Expression (Top) Hit Acession No. Signal BLASTE No. Source Source	13265 25901 1.72 2.0E-29 AF084869.1 NT Homo septens envelope protein RIC-6 (erv) dens complete cds	14270 26955 6.62 2.0E-29 AIX63804.1 EST HUMAN	14270 29956 6.62 2.0E-29 Al963604.1 EST HIMAN	16987 29610 1.63 2.0E-29 AL163268.2 NT	18527 31449 0.99 2.0E-29 A1082459.1 EST HUMAN		П	33608 1.16 2.0E-29 BE867157.1 EST HUMAN	34313 0.63 2.0E-29 10567821 NT	34314 0.63 2.0E-29 10567821 NT	35241 3.61 2.0E-29 AL163248.2 NT	35242 3.61 2.0E-29 AL163248.2 NT	35999 3.61 2.0E-29 AL163248.2 NT	36000 3.61 2.0E-29 AL163248.2 NT	36804 1.31 2.0E-29 BF025947.1 EST_HUMAN	2.04 2.0E-29 11425108 NT	1.73 2.0E-29 AW880701.1 EST HUMAN	34527 7.37 1.0E-29 AW983880.1 EST_HUMAN	23164 30391 0.85 1.0E-29 X00658.1 NT R.rettue RYA3 mRNA for a potential ligand-binding protein	19254 32255 2.97 9.0E-30 AA781245 1 EST LITIMAN NAFEN INDIAN ANEBA INDIANA ANEBA INDIAN ANEBA INDIAN ANEBA INDIAN ANEBA INDIAN ANEBA INDIAN ANEBA INDIAN ANEBA INDIAN ANEBA INDIAN ANEBA INDIAN ANEBA INDIAN ANEBA INDIAN ANEBA INDIAN ANEBA INDIAN ANEBA INDIAN ANEBA INDIAN ANEBA INDIAN ANEBA INDIAN ANEBA INDIAN ANEBA INDIAN ANEBA IN	9.0E-30 11422745 NT	8.94 8.0E-30 F08688.1 EST HUMAN	33004 3.72 8.0E-30 AA383873.1 EST HUMAN	EST HUMAN	1.03 7.0E-30 BE091133.1 EST HUMAN	27209 1.73 6.0E-30 D25303.1 NT	28598 2.3 6.0E-30 BE008026.1 EST HUMAIN	1 NT
	-		13265	14270	14270	16987	18527	18865	18865	20571	21169	21169	22070	22070	22787	22787	23567	24063	24100	21383	23.104	18254	24531	19001	20862	21275	14251	14508	15948	23083

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Table 4
Single Exon Probes Expressed in Brain

	Most Similar Top Hit Acession (Top) Hit Top Hit Acession Database ID No. Signel Value Value	97 3.38 6.0E-30 X51755.1 NT Human lambda-inmunoglobulin constant region complex (germline)	28376 28.19 5.0E-30 AI399982.1 EST HUMAN	6.44 6.0E-30 U87931.1 NT	1.95 5.0E-30 AL163278.2 NT	37047 2.47 5.0E-30 AL163210.2 NT	37048 2.47 5.0E-30 AL163210.2 NT	27599 1.72 4.0E-30 AW937471.1 EST HUMAN	27800 1.72 4.0E-30 AW837471.1 EST HUMAN	30500 0.63 4.0E-30 P11369 SWISSPROT	34641 2.82 4.0E-30 AW812488.1 EST HUMAN	2.11 3.0E-30 A1338551.1 EST HIMAN	29128 0.93 3.0E-30 AF128893.1 NT	0.58 3.0E-30 AF078779.1 INT	0.48 3.0E-30 AF078779.1 INT	36200 1.7 3.0E-30 BE350127.1 EST HUMAN	36342 0.53 3.0E-30 AB032989.1 NT	36343 0.53 3.0E-30 AB032969.1 NT	37116 2.48 3.0E-30 P34056 SWISSPROT	26077 0.92 2.0E-30 AW867315.1 EST_HUMAN	3.11 2.0E-30 F08688.1 EST_HUMAN	26896 5.31 2.0E-30 BE175877.1 EST_HUMAN	28165 8 2.0E-30 BE765232.1 EST_HUMAN	28331 6.39 2.0E-30 AF114156.1 NT	29160 2.26 2.0E-30 AW 206581.1 EST HUMAN	30005 1.51 2.0E-30 BE298945.1 EST HUMAN	30086 1.51 2.0E-30 BE298945.1 EST HUMAN	32435 0.55 2.0E-30 BF306337.1 EST HUMAN	34208 0.45 2.0E-30 AA019103.1 EST HUMAN	34265 4.86 2.0E-30 C18839.1 EST_HUMAN
	ORF SEQ ID NO:		_								34641		29128			36200	36342	36343	37116	28077		26896	28165	28331	29160	30005	30086	32435	34208	34265
-	SEQ ID NO:	17897	16742		2 23485			14869	14800	3 17925	3 21495	13885	16483		5 21078	3 22880	5 23111	[_[┙	1	_1		17459	- [1	21128
	Probe SEQ ID NO:	12769	3994	5150	10802	11103	11103	2139	2139	6756	8803	1129	3740	7852	8386	10333	10465	10465	11168	88	1062	1462	2728	2820	3769	4727	4727	886	8375	8435

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i		¥	\\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\	1	<u></u>	Т	Τ	Т	T	Т	Т	T	Τ	Т	Ţ	<u>ل</u>	ω ω	Т	7	Т	Т	Т	Т	Т	T	T	T
Chigh Lyon I lobes Lynessed III Digit	Top Hit Descriptor	7637c12.x1 NCI_CGAP_Lu24 Homo sepiens cDNA cione IMAGE:3284682 3° similier to SW:DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR;	7e87c12.x1 NCI_CGAP_Lu24 Homo septens cDNA clone IMAGE:3284692 3' similar to SW:DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE (UBIOUINONE) FLAVOPROTEIN SUBLINIT PRECLIPSOR	EST383857 MAGE resequences, MAGL Homo serviens clowa	ha33d65.x1 NCI_CGAP_Kid12 Homo sepiens cDNA clone INAGE:2875499 3' similar to contains THR.b3 THR recettive element:	C18639 Human placenta cDNA (TFullwara) Homo sapiens cDNA clone (3FN-570CD1 57	hd30b04.x1 Source_NR_T_GBC_S1 Homo septens cDNA clone IMAGE:2910901.3' similar to contains MER1.t3 MER1 MER1 receitibre element:	Homo sapiens chromosome 21 segment HS210003	8C77b08.s1 Stratagene Jung (#937210) Homo septems cDNA close IMAGE 968500 31	602022560F1 NCI CGAP Bri67 Homo seciens cDNA clone INAGE-4157204 5	EST186868 HCC cell line (matastasis to liver in mouse) II Homo serolens cDNA 5' end	601809932F1 NIH MGC 18 Homo explens cDNA clone IMAGE:4040694 51	CHR220532 Chromosome 22 exon Homo sepiens cDNA clone C22 728 51	yc55e06.r1 Strategene liver (#637224) Homo septens cDNA clone IMAGE:85570.5'	yc65e06.rl Stratagene Iver (#037224) Homo saplens cONA clone IMAGE:85570 5	Y99b08.r1 Scenes Infant brain 1NIB Homo sepiens cDNA clone IMAGE:30566 5' similar to gb:X12953 RAS- RELATED PROTEIN RAB-2 (HUMAN);	y/99b08.rf Scence infant brain 1NIB Homo sapiens oDNA clone IMAGE:30666 6' similar to gb:X12963 RAS- BELATED DECITEIN DARD 2 / HIMAN).	HSCOSE022 roomself and bright Area And House and an ability of the Areas of	Refuls normalists but shake four named for channel mDMA complete out	Homo septems hypothetical protein FI (20420) FI (20420)	Homo saplens chromosome 21 segment HS2(2008	OLFACTORY RECEPTOR 15 (OR3)	OLFACTORY RECEPTOR 16 (OR3)	hw05e11.x1 NCI CGAP Lu24 Homo sepiens cDNA clone IMAGF:3182012.3	hw05a11.x1 NCI_CGAP_Lu24 Homo saplens cDNA clone IMAGE:318201231	Homo sepiens V1-vescular vesconesain receptor AVPR1A gene, promoter region and pertial cola	Homo sapiens V1-vascular vasopressin receptor AVPR1A gene, promoter region and partial cds
מין היוסעד סופ	Top Hit Detabese Source	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	NT	EST HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	TOT LIMAN	Т	Т			SWISSPROT	SWISSPROT	EST HUMAN	EST_HUMAN		L
5	Top Hit Acession No.	2.0E-30 BE870817.1	2.0E-30 BE670617.1	2.0E-30 AW971588.1	2.0E-30 AW470791.1		1.0E-30 AW 468897.1	2	1.0E-30 AA684377.1	1.0E-30 BF347728.1	1.0E-30 AA315045.1	3F183230.1	155593.1					,	150	888	L163208.2			_			
	Most Similar (Top) Hit BLAST E Value	2.05-30	20E-30	20E-30,	20E-30	1.0E-30 C18939.1	1.0E-30	1.0E-30 AL163203	1.0E-30/	1.0E-30 E	1.0E-30./	1.0E-30 BF183230.	1.0E-30 H55593.1	9.0E-31 T73025.1	9.0E-31 T73025.1	9.0E-31 R18214.1	0 0F-31 R18214 1	9.0E-31 738283 1	9.0E-31	8.0E-31	8.0E-31 AL163208.	8.0E-31 P23275	8.0E-31 P23275	7.0E-31 BE326517.	7.0E-31 BE328517.	7.0E-31 AF208541.1	7.0E-31 AF208541.
	Expression Signal	3.61	3.61	3.62	7.37	16.33	2.34	2.62	7.16	2.01	0.94	2.46	6.95	0.81	0.81	0.81	0.84	8	0.48	2.41	4.6	1.43	1.43	3.29	3.20	98.0	96.0
	ORF SEQ ID NO:	34368	34387	35741	35839	25720	25942	26122	27875	27921	28461	33366		29135	29138	34053	34054		34369	20473		30213	30214	28123	28124	34130	34131
	Exan SEQ ID NO:	21225	21225	22547	22630	13087	13309	13474	14837	15182	15818	20290	25268	16501	16601	20917	20017	21214	21218	13813	15135	17500	17590	15383	15383	20894	20904
	Probe SEQ ID NO:	8533	8533	2686	9962	280	525	669	2200	2464	3050	7624	12581	3748	3748	8223	823	8522	8624	1054	2414	4861	4861	2074	2674	888	8300

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Table 4
Single Exon Probes Expressed in Brain

LIBIG III DASSAIDYT SOTOL LIGYT SIBILIO	Top Hit Acession Database Top Hit Descriptor Source	7.0E-31 BE408611.1 EST HUMAN 1901304125F1 NIH MGC 21 Homo services CINA close 1440 E-292840 F1	Ψ	Homo saplens calclum channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively soliced	NT NT	EST HUMAN	3.1 EST HUMAN	TN		EST HUMAN	1 NT	SWISSPROT	Π	5730038/NT	AJ230125.1 NT	11430273 NT	al I was concer	TM 64200204	AL 163206	<u> </u>	2.1 EST HUMAN	SWISSPROT	1 EST HUMAN	Т	1.1 EST HUMAN	1 EST HUMAN	1 EST_HUMAN	$\Gamma^{}$
STOLLING SISTER		1.1 EST HUMAN	N.	<u> </u>	NT NT	EST HUMAN	EST HUMAN	TN	K	EST HUMAN	N.	SWISSPROT	2 NT	730038/NT	N.	430273 NT	11 0 00000	Angoog MT	NT NT	<u> </u>	1 EST HUMAN	SWISSPROT	1 EST HUMAN	- Z	1.1 EST HUMAN	1 EST HUMAN	1 EST_HUMAN	EST HUMAN
	Most Similar (Top) Hit BLAST E Value											4.0E-31 Q10473	4.0E-31 AL1				200.04		3.0E-31 AL1	3.0E-31 D14523.1	3.0E-31 AA4	3.0E-31 P11174	3.0E-31 BF035327	3.0E-31 ABO	2.0E-31 AW83817	20E-31 Al393388.	20E-31 AL119245	2.0E-31 AA4
	Signel	16.0	1 2.28	2.68	4.37	90.0	1.96		3.58	0.73	5.18	0.94	1.57	1.23	1.86	1.86	42.00		2	.9	0.54	2.04	3.65	1.68	1.37			4.01
-	ORF SEQ ID NO:	9	31044	-6	1	34062	1	25840	25641			27040					32000			35312	36371				27358	27677	27800	27898
	0)	8 21836	_ :	16420	3 20747	20923	25195		13000	21037	13362		14550	15497		24828	19924	1	_	l	П	23224					15062	15161
	Probe SEQ ID NO:	9166	12434	3867	8053	8229	12169	187	187	8344	582	1606	1810	2792	12205	12457	7239	7303	8061	9479	10408	10527	11101	12810	1910	23.1	2330	2442

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						Igie exon Pro	Single Exon Probes Expressed in Brain							
Probe SEQ ID NO:	Esch SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor							
6193	18001	30624	0.81	2.0E-31	2.0E-31 AW 44496.1	EST_HUMAN	Ul-H-Bi3-ekb-f-09-0-Ul.s1 NCI_CGAP_Sub5 Hamo sablens cDNA clone IMAGE:2733833 3'							
5624	18421	31334	3.57	2.0E-31	2.0E-31 BE350127.1	EST_HUMAN	ht09g01.x1 NCI_CGAP_Kid13 Homo sepiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element;							
8975			2.05	2.0E-31	2.0E-31 AA877764.1	EST HUMAN	int08f04.s1 NCI_CGAP_Co10 Home septens cDNA done IMAGE:1161055 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE EI FAHENT COAIPI ETE COAISENSI IS SECULENCE.							
9107			3.64	2.0E-31	7881535 NT	INT	Homo saplens B9 protein (B9), mRNA							
9086		35681		2.0E-31	AV71094	EST HUMAN	AV710848 Cu Homo sepiens cDNA clone CuAAL B07 5							
9086		35062	0.94	2.0E-31	8.1	EST HUMAN	AV710948 Cu Homo serviens cONA clone CuAAI B07 5							
8973		35829	2.35	20E-31		EST HUMAN	601304125F1 NIH MGC 21 Homo septems cONA close IMAGE 36288310 K							
8075		35830	2.35	2.0E-31		EST_HUMAN	801304125F1 NIH MGC 21 Homo sepiens CONA clone IMAGE:3638310 S							
12/4	24632		1.58	2.0E-31	2.0E-31 AF148512.1	LN	Homo saplens hexokinase II gene, promoter region							
12279	25413		1.75	2.0E-31	2.0E-31 AI114527.1	EST_HUMAN	HA1110 Human fetal liver cDNA library Homo sapiens cDNA							
5	12842	25456	11.09	1.0F-34	1.05-31 [183183.1	F	Homo septions MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1							
1658	14404	27092	1.35	1.0E-31	1.0E-31 095371	SWISSPROT	OLFACTORY RECEPTOR 2C1							
1658	14404 404	27093	1.35	1.0E-31 095371	095371	SWISSPROT	OLFACTORY RECEPTOR 2C1							
1658	14404	27094	1.35	1.0E-31	1.0E-31 095371	SWISSPROT	OLFACTORY RECEPTOR 2C1							
4592	17327	28952	1.15	1.0E-31	1.0E-31 AL134376.1	EST HUMAN	DKFZ05478235 rf 547 (synonym: hfbrt) Home sentene child class DKE725470235 st							
4592	17327	20053	1.15	1.0E-31		EST HUMAN	DKFZ05478235 rf 547 (synonym: hfbrt) Home sentiese child chire DKFZ-6470235 st							
6210		30840	3.79	1.0E-31	1.0E-31 AW391679.1	EST HUMAN	MR3-ST0220-151289-028-608 1 ST0220 Homo seriens chwa							
8	18822	31782	2.2	1.0E-31	1.0E-31 AF048727.1	L.	Homo saplens minisabilitie cebi repest region							
7188	19875	32948	1	1.0E-31	1.0E-31 AF128145.1	LΝ	Bos faurus xenoblotic/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds							
10136	22784	35095	0.51	1.0E-31	1.0E-31 U93163.1	Ę	Homo septiens MAGE-82 (MAGE-82), MAGE-83 (MAGE-83), MAGE-84 (MAGE-84), and MAGE-81 (MAGE-81) genes, complete cds							
10833	23515	36757	2.7	1.0E-31	1.0E-31 Al086434.1	EST_HUMAN	qr21h03.x1 NCI_CGAP_Bm25 Homo septions cDNA clone IMAGE:1750709 3' similier to TR:Q16595 Q16595 FRATAXIN.;							
11830	24414	37752	1.48	1.05-31	1.05-31 U00001.1	l- Z	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV18S1P, TCRBV15S1, TCRBV14S1, TCRBV18S1P, TCRBV14S1, TCRBV18S1, 6542	19307	32312	2.38	9.0E-32,	9.0E-32 AV723976.1	T	AV723976 HTB Homo seniers CDNA clave HTBAACAA F
7492	20164		0.96	9.0E-32		1430822 NT	Homo saplens hypothetical protein FL14294 (FL14294) m3NA							
2070	14802	27530	2.48	8.0E-32	8.0E-32 Al056770.1		oc15a09x1 Sogree_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675384.3*							

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L							
Probe SEQ ID NO:	Esch SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6394	18194	30887	76.0	8.0E-32	8.0E-32 AW997214.1	EST_HUMAN	RC2-BN0048-200300-015-e04 BN0048 Homo sapiens cDNA
4807	17538	30161	0.98	7.0E-32 P52591	P52591	SWISSPROT	NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PROTEIN OF 121 KD) (P145)
12122	24614		8.19	7.0E-32 X17283.	X17283.1	ĬN	Human chromosome 22 immunoglobulin V(K)I gene, part. with 5' breakpoint between orphon and neighbouring non-amplified region
2735	15442	28180	1.01	6.0E-32 Ald7810.	AM78104.1	EST HIMAN	tm34e10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2159694 3' similar to contains MER29.t3 MER29 parentitive element :
7286			1.47	6.0E-32 BE88801	BE888016,1	EST HUMAN	601611630F1 NIH MGC 71 Homo septems of NIA clone IMAGE 3913087 51
1011	13771	28431	16.78	5.0E-32	5.0E-32 AF116627.1	N	Homo septens PRO1181 mRNA, complete cds
910	13677		1.78	4.0E-32	4.0E-32 AL163246.2	NT	Hamo sepiens chromosome 21 segment HS21C046
5148	17867		0.91	4.0E-32 AI98558	AI985563.1	EST HUMAN	ws08h12x1 NCI_CGAP_Kid11 Homo septens cDNA clone IMAGE:2496647 3' similar to contains MER18.b3 MER18 repetitive element;
7503		33266	2.94	4.0E-32	11432574 NT	¥	Homo sepiens AT-binding transcription factor 1 (ATBF1), mRNA
7503		33267	2.94	4.0E-32	11432574 NT	¥	Homo sapiene AT-binding transcription factor 1 (ATBF1), mRNA
8257	20951		1.2	4.0E-32 BE0644	BE064410.1	EST HUMAN	RC4-BT0311-141198-011-h06 BT0311 Homo sepiens cDNA
443	13229	25872	3.7	3.0E-32 Y17293.	_	1	Homo sepiens FLL1 gene, pertiei
1437		28870	80.8	3.0E-32,	3.0E-32 AV731600.1	EST HUMAN	AV731500 HTF Hamo septens cDNA clone HTFAKC07 6"
828		35135	8.38	3.0E-32	3.0E-32 AV758634.1	EST_HUMAN	AV758634 BM Hamo sepiens cDNA clane BMFBBH12.5'
8 28	21961	35136	8.38	3.0E-32	AV758634.1	EST_HUMAN	AV758634 BM Hamo septens cDNA clone BMFBBH12 5'
10843	23525	36788	3.57	3.0F.30	3 0F-32 AA777R21 1	EST HIMAN	ZIGEO7.81 Scenes_fetal_liver_splean_1NFLS_S1 Hamo sepiens cDNA clone IMAGE:448500 3' similar to
12148			3.51	3.05-32			601156285F1 NIH, MGC 21 Homo saplens cDNA clone IMAGE:3139701 5'
12507	17800	30598	2.97	3.0E-32	6174574 NT		Homo saplens myelold/lymphold or mbced-lineage leukemia (trithorax (Drosophila) homolog); transboated to, 4 (MLLT4) mPNA
12607	17890	30587	2.97	3.0E-32	5174574 NT		Homo septens myeloid/lymphold or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MILT4) mRNA
12666	24956		2.27	3.0E-32	3.0E-32 BE279086.1	T HUMAN	601156286F1 NIH MGC 21 Homo sapiens CDNA clone IMAGE:3139701 F/
6158	18835	31902	0.81	2.0E-32 M35418.	_	П	Human cell 12-liboxygenase mPNA, complete cds
6387	19156	32155	5.32	2.0E-32 Z38133.1		NT	H. saplens mRNA for myosin
6387		32156	5.32	2.0E-32 Z38133.1		Į,	H. sepiens mRNA for myosin
8178		34003	2.28	20E-32	2.0E-32 AA114294.1	EST HUMAN	2708008.rl Stratagene HeLa cell s3 837216 Homo sabiens cDNA clone IMAGE:583150 51
8178]	34004	2.26	2.0E-32/	4.1		Zn66c08.r1 Strategene Hel.a cell s3 937216 Homo septens cDNA ctone IMAGE:563150 5
11850	24443	37784	2.96	20E-32 T18862.1		EST_HUMAN	bf 2058t Testis 1 Homo sepiens cDNA clone bf 2058
12783	25022	30961	2.42	2.0E-32 AV73644	9.1	EST_HUMAN	AV738449 CB Homo septens cDNA done CBFBIA08 5'

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Shighe Explicased III brail	Exam ORF SEQ Expression (Top) Hit Top Hit Acession ID NO: Signal BLASTE No. Source Source	14996 1.29 5.0E-33 AL 163285.2 NT Hano sepiens chromosome 21 segment HS21C085	EST HUMAN	9.1 EST HUMAN	2.16 4.0E-33 AL163207.2 NT	738987 NT	15140 2.02 4.0E-33 AA629621.1 EST HUMAN contains Alu repetitive element contains MER28 b2 MER28 bz MER	4.15 4.0E-33 AL163210.2 NT	2.15 4.0E-33 AW 203340.1 EST_HUMAN	24.73 4.0E-33 AA053053.1 EST_HUMAN	32057 0.87 4.0E-33 8393994 NT	0.87 4.0E-33 8393994 NT	13825 5.6 3.0E-33 BE350127.1 EST HUMAN MER29 repetitive element:	3.0E-33.BE350127.1 EST HUMAN	0.92 3.0E-33 AV647851.1 EST_HUMAN		qb67g03.x1 Soeres_fetal_heart_NbHH19W Homo septems cDNA done IMAGE:1705204.3' similar to 3.21 2.0E-33 A190189.1 EST HUMAN contains OFR.t1 OFR receditive element:	2.0E-33 BE169039.1 EST_HUMAN	30265 28.91 2.0E-33 AA62683.1 EST HUMAN	20E-33 11421332 NT	30386 2.75 2.0E-33 11421332 NT	1.81 2.0E-33 AI277492.1 EST_HUMAN	2.18 2.0E-33 A1052256.1 EST HUMAN gb:M29636 TRANSLATIONAL INITIATION FACTOR 2 BETA SUBUNIT (HUMAN):	36384 1.48 2.0E-33 11421332 NT	2.0E-33 11421332 NT	1.20 2.0E-33 AA463647.1 EST HUMAN
		9			3		0						15	10	2									i		
-1	8 0.0 다 다 :	1499	2279	2270	1396	1485	15140	1526	1718	18122	19072	19072	13825	13825	15595	22985	12843	17122	17853	17753	17753	19099	21688	23159	23159	23716
			10148	10148		2121	2419			5318	6530	6280	1087	1068	2451	10338	102	4385	4925	5033	5033	82	8886		10513	11046

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	ORF SEQ Expression (Top) Hit Top Hit Acession ID NO: Signel BLAST E No. Source	1.16 1.0E-33 AF003528.1 NT regions	1.0E-33 4502556 NT		Z	Z	T HUMAN	LN.	1.0E-33 AI927191.1 EST HUMAN		4.07 1.0E-33 AF-003528.1 NT	1.0E-33 AV727809.1 EST_HUMAN	1.81 9.0E-34 AJ271736.1 INT	0.98 8.0E-34 8922751 NT	0.66 8.0E-34 BE069882.1 EST_HUMAN	20858 2.27 7.0E-34 170845-1 EST_HUMAN 10415605.11 Soares fetal lives spleen 1NFLS Homo eaclers GDNA clone IMAGE: 1083.20 5	0.58 7.0E-34 T70845.1 EST HUMAN	3.05 7.0E-34 H12866.1 EST_HUMAN	2.3 6.0E-34 U10991.1 NT	2.3 6.0E-34 U10991.1 INT	6.0E-34 U03686.1 NT	2.9 5.0E-34 · 7706500 NT	3.81 6.0E-34 U30883.1 NT	1.37 5.0E-34 AF078779.1 NT	5.0E-34 AB037856.1 NT	1.79 6.0E-34 AL 163209.2 NT	27449 1.84 4.0E-34 A1804887.1 EST HUMAN IB94009.XI NCI CGAP Pr28 Home explens cDNA clone IMAGE: 2246164.31	1.1 EST HUMAN	4.0E-34 BF209778.1 EST HUMAN	¥	:1 EST HUMAN	
			30485	31198	33067		37261	37581			04000	STUCO		27631	33468	26858	26858		25884	25885	31107											
-	Exan SEQ ID NO:	12835	17873	18289		25432	23953	24259	24790	40004	L		25054	14897	20323	14173	14173	24662	13243	13243	24544	14611	17725	21457	23246	23882	14727	18561	21627	18916	23770	21541
	Probe SEQ ID NO:	8	5156	5501	7307	8920	11202	11663	12407	49570	2000	12002	12/80	2188	889V	1.28 82	88	238	₹	458	184	1873	88	8/62	105.50 000	11210	<u>\$</u>	2 <u>/</u> 2	8636	6438	11100	8850

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ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Tap Hit Acession No.	Top Hit Databese Source	Top Hit Descriptor
34688	1.18	2.05-34	2.0E-34 AI678101.1	EST_HUMAN	wd35g06.x1 Soeres_NRL_T_GBC_S1 Homo explens cDNA clone IMAGE:2330170 3' similar to contains MER29.t2 MER29 repetitive element;
37057	1.34	2.0E-34	2.0E-34 P51805	SWISSPROT	PLEXIN 4 PRECURSOR (TRANSMEMBRANE PROTEIN SEX)
37058	1.34	2.0E-34	2.0E-34 P51805	SWISSPROT	PLEXIN 4 PRECURSOR (TRANSMEMBRANE PROTEIN SEX)
28928	6.63	1.0E-34	1.0E-34 P12238	SWISSPROT	ADP,ATP CARRIER PROTEIN, LIVER ISOFORM 12 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
29055	1.32	1.0E-34	1.0E-34 AF003528.1	Į.	Homo septens X-kn/cod anhidrotitic ectodermel dysplasia protein gene (EDA), exon 2 and flanking repeat regions
29425		1.0E-34	1.0E-34 AYD09397.1	ĮN.	Hamo sapiens WNT3 precursor (WNT3) mRNA, complete cds
29426	26.0	1.0E-34	1.0E-34 AY008397.1	N	Homo sepiens WNT3 precursor (WNT3) mRNA, complete cds
	3.44	1.0E-34	1.0E-34 BE071414.1	EST_HUMAN	RC2-BT0506-240400-016-h08 BT0506 Hamo sepiens cDNA
31788	2.05	1.0E-34	1.0E-34 BE874052.1	EST_HUMAN	601484430F1 NIH_MGC_69 Homo septens cDNA clone IMAGE:3886999 5'
31789	2.05	1.0E-34	1.0E-34 BEB74052.1	EST HUMAN	801484430F1 NIH_MGC_69 Homo septens cDNA clone IMAGE:3886969 5
35076	0.45	1.0E-34	1.0E-34 P23266	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN F6
35434	1.7	1.0E-34	1.0E-34 AL038635.1	EST_HUMAN	DKFZp564A1563_71 564 (synonym: hfbr2) Homo sapiens cDNA clone DKFZp564A1563 5'
37083	1.39	1.0E-34	1.0E-34 BE781790.1	EST_HUMAN	601470592F1 NIH_MGC_67 Hamo septems cDNA clare IMAGE:3873478 5
37084	1.39	1.0E-34	1.0E-34 BE781790.1	EST HUMAN	801470592F1 NIH_MGC_67 Homo septens cDNA clore IMAGE:3873478 5
37100	1.82	1.0E-34	11439599 NT	NT	Homo sapiens nucleobindin 2 (NUCB2), mRNA
	1.65	1.0E-34	1.0E-34 AA807097.1	EST_HUMAN	oc31c11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA done IMAGE:1351316 3' similer to gb:X68203 TYROSINE-PROTEIN KINASE RECEPTOR FLT4 PRECURSOR (HUMAN);
	422	1.0E-34	20	Į,	Homo sapiens chromosome 21 segment HS21C010
29029	1.2	9.0E-35	9.0E-35 AW663302.1	EST HUMAN	hh77b06.y1 NCI_CGAP_GU1 Homo sepiens aDNA clane IMAGE:2268787 5'
	7.71	8.0E-35	9031190 NT	Z.	Homo eaplens prohibitin (PHB) mRNA
27171	3.43	8.0E-35	8.0E-35 BF580637.1	EST_HUMAN	nas33s08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA done IMAGE:3258134 3' similar to TR:075912 075912 DIACYLGLYCEROL KINASE IOTA.;
	,				nes33s08.xt NCI_CGAP_Kid11 Homo sepiens cDNA clone IMAGE:3258134.3' similar to TR:075912
27172	3.43	8.0E-35	8.0E-35 BF589837.1	EST HUMAN	O75012 DIACYLOLYCEROL KINASE IOTA.;
30170	2.69	8.0E-35	8.0E-35 BF183195.1	EST HUMAN	601809588F1 NIH_MGC_18 Homo septems CDNA clone IMAGE:4040324 6
38522	2.42	8.0E-35	8.0E-35 BE378480.1	EST HUMAN	601238468F1 NIH_MGC_44 Homo sepiens cDNA done IMAGE:3608513 5'
	3.95	8.0E-35	8.0E-35 BF509282.1	EST HUMAN	602/84624T1 NIH_MGC_42 Homo sepiens cDNA done IMAGE:4300660 3'
32163	2.06	7.0E-35	11425417 NT	K	Homo saplens phosphatidy/finositol grycan, class L (PIGL), mRNA
26815		8.0E-35	AA757115.1	EST_HUMAN	an53h03.s1 Soares_bedts_NHT Homo septems cONA clone 1309397.3'
27409		₫.0E-35	6005975 NT	NT	Homo septens zinc finger protein 208 (ZNF208), mRNA
29406	0.84	6.0E-35	6.0E-35 AW 297191.1	EST_HUMAN	UHH-BW0-aid-d-09-0-Ul.s1 NCI_CGAP_Sub8 Hamo sepiens cDNA clane IMAGE:2731433 31

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										end metadin genes, complete ondin3 (THBS3) gene, pertial			' similar to	' similar to	MAGE:428015 5'		241236 5' similar to contains	on 2 and flanking repeat	similar to contains MER29.b3	34L148 5	405 3' similar to contains Alu			strailer to TR:Q9QZH7	Hindler to TR:090ZH7
	Top Hit Descriptor	Homo saplens triple functional domain (PTPRF interacting) (TRIO), mRNA	H.saplens mRNA for novel T-cell activation protein	H.sapiens mRNA for novel T-cell activation protein	Human mRNA for KIAA0388 gene, partial cds	Homo septens mRNA for KIAA1365 protein, pertiel cds	H.sapiens immunoglobulin kappa light chain variable region L14	Homo sapiens mRNA for KIAA0408 protein, pertial cds	Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA	Hamo sapiens cli/2 kinase (CLK2), propin1, cote1, glucocerebrosidase (GBA), and metadin genes, complete cds; metadin pseudogene and glucocerebrosidase pseudogene; and thrombospondin3 (THBS3) gene, partial	spo	601431984F1 NIH_MGC_72 Hamo sapiens aDNA dane IMAGE:3917229 5'	qg38c05.x1 Soares_lesdis_NHT Homo septens cDNA clone IMAGE:1837448 3' similiar to SW:7249_HUMAN Q92539 HYPOTHETICAL PROTEIN KIAA0249; ;	qg38c05.x1 Scares_testis_NHT Homo septens cDNA clone tNAGE:1837448 3' similiar to SW:?249_HUMAN Q92539 HYPOTHETICAL PROTEIN KIAA0249; ;	zh84f12.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cONA clone IMAGE:428015 5	601109719F1 NIH_MGC_16 Homo septens cDNA clane IMAGE:3350405 5'	yu88a07.r1 Soares fetal ilver spieen 1NFLS Homo septens cDNA clone IMAGE:241236 5' similar to contains PTR5 repetitive element;	Homo sapiens X-inted anhidrotite ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions	ht09g01.x1 NG_CGAP_Kid13 Homo septens cDNA clone IMAGE:3146256.3' similar to contains MER29.b3 MER29 repetitive element :	DKFZp434L148_r1 434 (synonym: https3) Homo septens cDNA clone DKFZp434L148 5	xx17f03.x1 Socres_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:2813405 3' striller to contains Alu repetitive element;contains MER19.t2 MER19 repetitive element;	601125260F1 NIH_MGC_8 Homo saplens cDNA clone IMAGE:3345063 5	Homo sapiens phospholipid scramblese 1 gene, complete cds	7n25e09.x1 NCI_CGAP_Lu24 Homo sepiens cDNA clone IMAGE:3565361 3' similer to TR:Q9QZH7 Q9QZH7 F-BOX PROTEN FBL2.;	7n25e09.x1 NCI_CGAP_Lu24 Homo equiens cDNA clone IMAGE:3565361 3' similar to TR:Q9QZH7
	Top Hit Database Source	TA	NT	NT	LN LN	LN.	LN LN	N	L _V			EST_HUMAN	EST_HUMAN	EST_HUMAN	Г	EST_HUMAN	EST_HUMAN	Į.	T HUMAN	Т		EST_HUMAN		EST_HUMAN	
	Тop Hit Acession No.	6005921 NT			6.0E-35 AB002364.1	6.0E-35 AB037786.1		5.0E-35 AB007866.2	6912639 NT			5.0E-35 BE890992.1	1	4	5	_		4.0E-35 AF003528.1	,	-	_	-	_	•	,
:	Most Similer (Top) Hit BLAST E Value	6.0E-35	6.0E-35 X94232.1	6.0E-35 X94232.1	6.0E-35	6.0E-35	5.0E-35 X63392.1	5.0E-35	5.0E-35		5.0E-35	5.0E-35	5.0E-35 AI208765.	5.0E-35 AI208765	5.0E-35 AA001786	4.0E-35 BE257907	4.0E-35 H91193.1	4.0E-35/	4.0E-35 BE350127	4.0E-35/	4.0E-35 AW30331	3.0E-35 BE268182	3.0E-35 AF224492	3.0E-35 BF433100	
	Expression Signal	3.84	66.0	66.0	0.86	3.17	1.36	1.07	1.7		1.7	3.99	2.35	2.35	2.46	16.86	4.87	0.72	181	8.88	1.38	7.78	1.5	31.47	;
	ORF SEQ ID NO:	33615	34445	34446	35403	35656	27148	28232	28424		20746		33936	33937		26845	. 27265			34248	37848	27006		30690	3000
	s <u>⊆</u>	20483	21302	21302	22218	22454	14447	15492	15775		17113	20778	20803	20803	23798	14161	14551	17485	10706	21109	24322	14320	15055	18062	8
	Exan SEQ ID NO:	7798 2	8610 2	8610 2	9565 2	Ľ			L	l	J	ı	8100	8109	L				ł		ł			1	9303

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Detabase Source	Top Hit Descriptor
8388	22050		1.42		3.0E-35 AF223301.1	, L	Homo sapiens calctum channel alpha1E subunit (CACNA1E) gene, exons 7-49, and pertial cds, attemetively spliced
10074	22722	35930	1.12		3.0E-35 AW 003083.1	EST_HUMAN	wr03e05.x1 NCI_CGAP_GC6 Homo sepiens cDNA done IMAGE:2480432.3' similer to SW:POL1_HUMAN P10296 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE;
50	15535	25567	1.88		2.0E-35 N88965.1	EST HUMAN	K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 6' similar to REPETITIVE ELEMENT
1165	13010				2.0E-35 T11909.1	EST_HUMAN	A971F Heart Homo septens cDNA clone A971
2215	14943	27683	5.73	2.0E-35	2.0E-35 AB018413.1	F	Homo sapiens mRNA for Gab2, complete cds
3306	16096	28714	1.12	2.0E-35	0912459 NT	Į.	Homo sepiens Grb2-essociated binder 2 (KIAA0671), mRNA
3308	16066	28715			2.0E-36 6912459 NT	TN	Homo sapiens Grb2-essociated binder 2 (KIAA0571), mRNA
3545	16300		76 '0	2.0E-35	AB020702.1	۲N	Homo sepiens mRNA for KIAA0995 protein, pertial cds
3800	16640	28279	0.78		2.0E-35 BE247575.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute tymphoblastic leukemia Baylor-HGSC project≔TCBA Homo sapiens cDNA clone TCBAP4328
1							TCBAP2E4328 Pediatric pre-B cell acute lymphobiastic leukernia Baykor-HGSC project=TCBA Homo sapiens
0888	19845	28280	0.78	2.0E-35	2.0E-35 BE247575.1	EST HUMAN	CONA CICUS TCBAP4528
100	82/	1		2.05-30	F148239.1	ESI HOMAN	MINERALLY SOME OF THE BORNEY IN THE HOURS SECTION OF THE STATE OF THE
8	18294	31182			2.0E-35 BF332417.1	EST HUMAN	QV0-BT0701-210400-198-604 BT0701 Hamo septems cDNA
ğ	19998	32749		1	2.0E-35 BEB32636.1	EST HUMAN	CM2-MT0125-280700-297-502 MT0125 Homo sepiens cDNA
7007	9896	32750			2.0E-35 BE832636.1	EST HUMAN	CM2-MT0125-280700-297-G02 MT0125 Hamo sepiens cDNA
118	8	33503		╻┃	2.0E-35 AV723718.1	EST HUMAN	AV723718 HTB Hano saplens aDNA done HTBAYA10 5
7178	20471	33594			2.0E-36 AV723718.1	EST HUMAN	AV723718 HTB Hamo sepiens cDNA clone HTBAYA10 5
10897	23388	36626			2.0E-35 X59417.1	F	H.septens PROS-27 mRNA
11817	18294	31102			BF33241	EST HUMAN	QV0-BT0701-210400-189-504 BT0701 Hamo sapiens cDNA
11889	16066	28714			6912459 NT	NT	Homo saplens Grb2-associated binder 2 (KIAA0571), mRNA
11880	16066	28715			6912459 NT	NT	Homo seplens Gh2-associated binder 2 (KIAA0571), mRNA
12062	24577	31120	1.38		2.0E-35 BE904978.1	EST_HUMAN	601496774F1 NIH_MGC_70 Homo septems cDNA clams IMAGE:3898699 51
12062	24577	31121	1.36		2.0E-35 BE904978.1	EST HUMAN	801496774F1 NIH_MGC_70 Homo septems cDNA clone IMAGE:3898899 5'
12572	24900		5.96	2.0E-35	2.0E-35 AL163210.2	IN	Hamo saplens chranosame 21 segment HS21C010
			,				K6632F Human fetal heart, Lambda ZAP Express Homo expiens cDNA clone K6632 5' similar to
12000	19830	28687	£.	20E-35	2.0E-35 NB6965.1	EST HUMAN	REPETITIVE ELEMENT
€ €	128/4	25496	6.81	1.0E-35	1.0E-35 AA631949.1	EST HOMAN	firmfold Regional genomic DNA specific cDNA library Homo saplens cDNA clone CR12-1
₹ 2	12874	25497	. 6.81		1.0E-35 AA631949.1	EST HUMAN	fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
735	13500	26165	19.5		1.0E-35 AW389473.1	EST HUMAN	IL2-ST0162-131099-006-412 ST0162 Hamo seplens cDNA

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7952	20647	33770	1.34	1.0E-36 AA4204	AA420467.1	EST_HUMAN	nc60e08.rt NCI_CGAP_Pr1 Homo sepiens cDNA clone IMAGE:745670
7962	20647	33771	1.34	1.0E-36 AA4204	AA420467.1	EST HUMAN	nc80e08.r1 NCI_CGAP_Pr1 Hamo septens cDNA clane IMAGE:745670
6208	20773	33902	19'0	1.0E-36	1.0E-36 AU141688.1	EST_HUMAN	AU141688 THYRO1 Hamo septens cDNA alone THYRO1001033 6'
8079	20773	33903	19.0	1.0E-38	1.0E-36 AU141688.1	EST_HUMAN	AU141688 THYRO1 Hamo septens dNNA dane THYRO1001033 5'
8927	21618	34782			1.0E-36 AW103658.1	EST HUMAN	xe82b07.x1 NCI_CGAP_Brn35 Homo septems cDNA clone IMAGE:2614357 3'
10014					1.0E-36 BF364169.1	EST HUMAN	QV3-NN1023-010000-199-h01 NN1023 Homo sepiens cDNA
10226		36086	95'0		1.0E-36 AW855868.1	EST_HUMAN	RC3-CT0279-040500-017-e10 GT0279 Homo septens cDNA
10226	22874	39087	0.56		1.0E-36 AW855868.1	EST_HUMAN	RC3-CT0279-040500-017-a10 CT0279 Homo saplens cDNA
10867	23547		3.3		AW897636.1	EST_HUMAN	CM3-NN0061-140400-147-h12 NN0061 Hamo sepiens cDNA
11354	24044	37347	4.17	1.0E-36 AW504	AW 504143.1	EST_HUMAN	UI-HF-BNO-ele-c-03-0-UI.r1 NIH_MGC_50 Hamo saplens cDNA clane IMAGE:3079277 5
11393	23990	37302	1.45	1.0E-36 AI9055	AI905536.1	EST_HUMAN	RC-BT091-210199-110 BT091 Homo septems cDNA
11393	<u> </u>			1	AIB05536.1	EST_HUMAN	RC-BT091-210199-110 BT091 Homo sepiens cDNA
12060			3.81	1.0E-36	11418177 NT	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12501	24855		3.03		1.0E-36 AL163213.2	LN	Homo saplens chromosome 21 segment HS21C013
12747	25011		3.23		AF202723.1	NT	Homo sapiens Sad1 uno-84 domain protein 2 (SUN2) mRNA, partial cds
7281	19965	33042			9.0E-37 AW009277.1	EST_HUMAN	ws80b07.x1 NCL CGAP_Cc3 Hamo sapiens cDNA clone IMAGE:2504245 3'
7281	19985	33043	212		9.0E-37 AW009277.1	EST_HUMAN	ws80b07.x1 NCI_CGAP_Co3 Hamo sapiens cDNA clane IMAGE:25042453'
12309	24733				W22618.1	EST_HUMAN	73D4 Human retina cDNA Tep509I-cleaved sublibrary Homo sapiens cDNA not directional
3350		28765			TN 87878	N _T	Homo saplens chimerin (chimaerin) 2 (CHN2) mRNA
5168	17971		1.58		8.0E-37 BE608077.1	EST_HUMAN	CM0-UT0003-050800-503-d09 UT0003 Homo seplens cDNA
							ht09g01.x1 NCI_CGAP_Kd13 Homo sepiens cDNA done IMAGE:3146256 3' similar to contains MER29.b3
5738	18530	31451	3.75	8.0E-37 BE350	BE350127.1	EST HUMAN	WEXZA repeative General II.
82.19	18530	31452	375	8.0E-37 BE350	BE350127.1	EST HUMAN	ht09g01x1 NCI_CGAP_Kid13 Homo sepiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER20 repetitive element :
24.6						EST HUMAN	RC1-CN0008-210100-012-409_1 CN0008 Homo sapiens cDNA
	L.	L.					H. sepiens DMA, DMB, HLA-21, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RINO8, 9, 13 and 14
7384	20479	33604	622	8.0E-37	XB7344.1	뉟	genes
1282	<u> </u>		3.03	7.0E-37	7.0E-37 AL042800.1	EST HUMAN	DKFZp434E0422_r1 434 (synonym: htes3) Homo sepiens cDNA clone DKFZp434E0422 5
1738	14480	27179	26'0	7.0E-37 AF1111	AF111167.2	¥	Homo sapiens fun dimertzation protein gene, pertial ods; cfos gene, complete ods; and unknown gene
į	J			100			and a second to the shall and a second second to the second secon
1/30	14400	27.190	JAYO	1.UE-5/ AF1111	7./011/11/A	Z	G 120 - 17 FOR THE PROPERTY OF
10657	23348	36585	8.69	7.0E-37 AI81770	AI817700.1	EST_HUMAN	wk25511.x1 NCI_CGAP_Bm25 Homo sapiens cDNA done IMAGE:2413341 3' simitar to contains P1K3.t2. PTR5 repetitive element;

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Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Detabase Source	Top Hit Descriptor
10811	23494	36729	2.25	7.0E-37	Al536702.1	EST_HUMAN	tm87g03.x1 NCL_CGAP_Bm25 Homo sepiens cDNA clone IMACE:2165140.3' similar to contains L1.b3 L1 repetitive element;
8888	21031	34168	1.34		6.0E-37 AF169689.1	TK.	Homo sapiens protocadherin siphe 10 alternate isoform (PCDH-siphe10) mRNA, complete cds
12624	24929		2.94	6.0E-37	6.0E-37 AF202723.1	뉟	Homo sapiens Sad1 uno-84 domain protein 2 (SUN2) mRNA, partial cds
6002	18783	31744	3.9		5.0E-37 AA307123.1	EST_HUMAN	EST178035 Colon carchroma (HCC) cell line Homo saplena cDNA 5 end
6002	18783	31746	3.9		6.0E-37 AA307123.1	EST_HUMAN	EST178035 Colon cardinoma (HCC) cell line Homo seplens cDNA 5' end
8654	21346	34490	6.0		5.0E-37 AV750211.1	EST_HUMAN	AV760211 NPC Hamo sepiens aDNA done NPCBGH09 5
10837			4	5.0E-37	TN 2117897	INT	Homo saplens glycine C-ecetyltransferase (2-emino-3-ketobutyrata-CoA ligase) (GCAT), mRNA
12066			6.86		5.0E-37 AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, excrs 1, 2, and 3
2423	15144	27877	2.12		4.0E-37 AA702794.1	EST_HUMAN	z/90b04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448015 3'
6194			19.0	4.0E-37	4.0E-37 AW 794502.1	EST_HUMAN	RC8-UM0014-210200-021-H05 UM0014 Homo sapiens cDNA
8228	21835	35109	0.74		4.0E-37 AA843806.1	EST_HUMAN	ak09c02.s1 Soares_parathyrold_turnor_NbHPA Homo sapiens cDNA clone IMAGE:1405442.3'
2010	14745		3.2	3.0E-37	3.0E-37 AL048956.1	EST_HUMAN	DKFZp434L2418_71 434 (synonym: https:// Homo sapiens cDNA clone DKFZp434L2418
2010		27473	3.2		3.0E-37 AL048956.1	EST_HUMAN	DKFZp434L2418_r1 434 (synanym: https://domo.sapiens.cDNA.clane.DKFZp434L2418
2965			3.15		3.0E-37 AW961150.1	EST_HUMAN	EST373222 MAGE resequences, MAGF Homo seplens cDNA
6774	18565	31494	0.92	•	3.0E-37 AL138274.1	EST_HUMAN	DKFZp547G087_r1 547 (synonym: hfbrt) Homo septens cDNA clone DKFZp547G087 5'
							at34c05.x1 Barsteed colon HPLRB7 Homo sapiens cDNA clone IMAGE:2373896 3' similar to TR:Q13537
7455			0.71	3.0E-37	3.0E-37 AI740052.1	EST_HUMAN	Q13537 SIMILAR TO POGO ELEMENT.;
372			0.68	2.0E-37	2.0E-37 D89790.1	Ę	Homo sapiens mRNA for AML1, complete cds
372	13197	25843	0.68	2.0E-37	2.0E-37 D89790.1	NT	Homo sepiens mRNA for AML1, complete cds
1058			2.64	2.0E-37	2.0E-37 AU131202.1	EST_HUMAN	AU131202 NT2RP3 Hamo septens cDNA clone NT2RP3002166 5
1058			2.64	2.0E-37	2.0E-37 AU131202.1	EST_HUMAN	AU131202 NT2RP3 Homo sepiens cDNA clone NT2RP3002166 5
1956	14682	27405	1.67	2.0E-37	2.0E-37 AL163247.2	NT	Homo saplens chromosome 21 segment HS21C047
Ş		3	į	1		ļ	Hamo septens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylese, cerebrotendinous
2/8		L0787	4./8	2.0E-3/		Ž	centrionidates, polypeptide 1 (CYYZ/A1b) mKNA
4908			0.83	2.0E-37	2.0E-37 AL163284.2	Z.	Hamo sepiens chramosome 21 segment HS21C084
38			0.56	2.0E-37	2.0E-37 BF035327.1	EST HUMAN	601458531F1 NIH_MGC_86 Hamo sapiens cDNA clane IMAGE:3862086 5'
6561	19326		3.46	2.0E-37	2.0E-37 AA348720.1	EST_HUMAN	EST52831 Fetal heart II Homo sepiens cDNA 5' end
7886	20590	33720	0.48	2.0E-37	2.0E-37 BE537764.1	EST_HUMAN	601067534F1 NIH_MGC_10 Homo saplens cDNA clone IMAGE:3453657 5'
7885	20590	33721	0.46	2.0E-37	2.0E-37 BE537764.1	EST_HUMAN	601067534F1 NIH_MGC_10 Hamo sapiens cDNA clane IMAGE:3453657 5'
7837		33769	2.88	2.0E-37	2.0E-37 BF204032.1	EST_HUMAN	601809157F1 NIH_MGC_17 Homo saplens cDNA clone IMAGE:4111406 5'
11549		37459	11.22	2.0E-37	2.0E-37 AF176013.1	NT	Homo sapiens J domain containing protein 1 isoform b (JDP1) mRNA, complete cds
12784	25037		3.54	2.0E-37		F	Homo sapiens pescedillo (zebrefish) homolog 1, containing BRCT domain (PES1), mRNA
2081	14813	27548	4.93	1.0E-37	1.0E-37 AL163281.2	NT.	Homo sepiens chromosome 21 segment HS21C081

Page 274 of 536 Table 4 Single Exon Probes Expressed in Brain

	T	1	丁		П		٦	-1	\neg	7	٦	乛	٦		· -	7	٦	1	7	٦	7	\neg		7	7		Т		Τ	Γ	Π	П	П
RC3-CT0347-210400-016-h03 CT0347 Homo sapiens cDNA		Homo sapiens ribonucleese III (KN3) mKNA, complete cas	QV0-FN0180-280700-318-c10 FN0180 Homo saplens cDNA	Mus musculus otogelin (Otog), mRNA	601072419F1 NIH MGC_12 Homo saplens cDNA clone IMAGE:3458308 5	zp21b02.rt Stratagene neuroopitheitum (#637231) Homo sapiens ciDNA clone IMAGE:610059 5' similar to	contains L1.t2 L1 repetitive element;	Human somatic cytochrome c (HC1) processed pseudogene, complete cds	CM3-FT0096-140700-243-d07 FT0096 Homo sapiens cDNA	Rattus norvegicus multidometri presynaptic cytomatrix protein Piccolo (LOC56768), mRNA	Homo sepiens Grb2-associated binder 2 (KIAA0571), mRNA	602018401F1 NCI_CGAP_Bm67 Hamo sapiens cDNA clane IMAGE:4153992 5'	Homo septems Grb2-associated binder 2 (KIAA0571), mRNA	yn51f07,r1 Soares adult brain N2b5HB55Y Homo saplens cDNA clone IMAGE:171973 5	Mus musculus ATP-binding cassette 1, sub-family A, member 1 (Abca1) gene, complete cds	601455722F1 NIH_MGC_66 Homo sepiens cDNA clone IMAGE:385s348 5	Hamo sepiens zinc finger protein ZNF287 (ZNF287), mRNA	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA	Homo sepiens hypothetical protein FLJ20128 (FLJ20128), mRNA	Homo septens chromosome 12 open reading frame 3 (C12ORF3), mRNA	Homo sepiens DNA for Human P2XM, complete cds	Homo sepiens adenylosuccinate lyase (ADSL), mRNA	EST383908 MAGE resequences, MAGL Homo sapiens cDNA	Homo sapiens RIBIIR gene (partial), excn 8	Homo sapiens deiodinase, iodoffryronine, type II (DIO2), transcript verlant 2, mRNA	yd40N07.r1 Sogres fetal liver spleen 1NFLS Home sapiens cDNA clone IMAGE:110749 5' similar to	SPOCKS_MOUSE POSZS OLFACTORY RECEPTOR;	MANUAL COMES FOR INC. SPECIAL LIVERS INC. SPECIAL COMES CANDE INVOLVED IN TACK TO SERVER TO SPECIAL COMES PS2275 OF FACTORY RECEPTOR:	801450148F1 NIH_MGC_85 Hamo septens aDNA done IMAGE:3854074 5'	B. taurus mitochondrial espertate aminotransferase mRNA, complete CDS	B.taurus mitochondrial aspartate aminotransferase mRNA, complete CDS	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions	Homo sepiens HIRA interacting protein 4 (dnaJ-like) (HIRIP4), mRNA
FST HIMAN	NO LICENSE			NT	EST_HUMAN		EST_HUMAN	H	EST HUMAN	MT	LN.	EST HUMAN	NT	EST_HUMAN	NT	EST HUMAN	NT	뒫	Į.	TN	N-	NT	EST_HUMAN	LΝ	NT.		EST HOMAN	EST HIMAN	EST HUMAN		Z	TN	H
W PSC 20R2 1	W 002002.1	-	1		3E546032.1		1		.1	10048482	11436955		11436955	119092.1	1	3F033033.1	11425114	11425114	8923130	11435947	1	11418164	W971819.1	J237740.1	7549804	, = 0, 0,	83107.1	[83407.4	3E871610.1	25468.1	25466.1	\F003630.1	7549807 NT
Varue 1 0F-37	1.00.1	1.05-37/	1.0E-37	1.0E-37	1.0E-37		1.0E-37	1.0E-37	1.0E-37	9.0E-38	8.0E-38	8.0E-38	8.0E-38	7.05-38	7.05-38	8.0E-38	8.0E-38	86-30.8	8.0E-38	8.0E-38	6.0E-38	8.0E-38	5.0E-38	5.0E-38/	5.0E-38		5.0E-38	A 0E-38	5.0E-38	4.0E-38	4.0E-38	3.0E-38	3.0E-38
180	3	0.72	2.35	0.94	1.25		2.57	2.98	2.81	2	2.02	1.8	1.8	0.73	1.31	1.2	1.8	1.6	0.57	2.57	12.79	1.7	1.38	0.99	0.85	,	0.92	8	1.48	4.59	4.50	5.25	2.19
1		28332	30234		33940	 -	34468	36529		31402	26816	27962	26616	29563		28450	31189	31200	32986		31038	30900	26133	27912	20086	-	238307	20308	32712	25675	25578		
790	2	1	17615	18699	20807		21326	23291	24786	18483	13952	15219	13952	16938	17758	15803	18300	18300	19913	24480	24783	25161	13484	15173	16446		1000/	10007	88	12836	12836	14824	16437
3102 1506		3943	-		~	1	.,	``	``								L	5502	L., I	11918	12395	Li	L	2455			J		┸	199	116	2083	3684
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1.0E-37 BE546032.1 EST_HUMAN 34468 2.57 1.0E-37 AA171406.1 EST_HUMAN 36529 2.96 1.0E-37 M22878.1 NT	29332 1.06 1.06-37 AW862082.1 EST HUMAN 30234 2.35 1.06-37 BF371719.1 EST HUMAN 0.94 1.06-37 BF371719.1 EST HUMAN 33940 1.25 1.06-37 BE546032.1 EST HUMAN 34468 2.57 1.06-37 AA171408.1 EST HUMAN 36529 2.96 1.06-37 M22878.1 NT EST HUMAN 2.51 1.06-37 BE771814.1 EST HUMAN	1.06 1.0E-37 AW862082.1 EST HUMAN 30234 2.35 1.0E-37 BF371719.1 EST HUMAN 0.04 1.0E-37 BF371719.1 EST HUMAN 33940 1.25 1.0E-37 BE546032.1 EST HUMAN 34468 2.57 1.0E-37 AA171406.1 EST HUMAN 36529 2.96 1.0E-37 M22878.1 NT 31402 2.81 1.0E-37 BE771814.1 EST HUMAN 31402 2.81 1.0E-37 BE771814	29332 1.06 1.06-37 AV862082.1 EST HUMAN 30234 2.35 1.06-37 BF371719.1 EST HUMAN 0.04 1.06-37 BF371719.1 EST HUMAN 33940 1.25 1.06-37 BE546032.1 EST HUMAN 36529 2.96 1.06-37 AA171406.1 EST HUMAN 36529 2.96 1.06-37 BE771814.1 EST HUMAN 31402 2.81 1.06-37 BE771814.1 EST HUMAN 31402 2.81 1.06-37 BE771814.1 EST HUMAN 31402 2.81 1.06-37 BE771814.1 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0.57 8.06-38 11435947 NT 25647 NT 2567 8.06-38 11435947 NT 2567 8.06-38 11443647 NT 2567 8.06-38 11435947 NT 2567 8.06-38 11443647 NT 2567 8.06-38 11443647 NT 2567 8.06-38 11443647 NT 2567 8.06-38 1144	29332 1.06 1.06-37 AF189011.1 NT 30234 2.35 1.06-37 AF189011.1 NT 30234 2.35 1.06-37 AF189011.1 NT 303340 1.25 1.06-37 BF371719.1 EST_HUMAN 36529 2.96 1.06-37 MZ2878.1 NT 36529 2.96 1.06-37 BF771814.1 EST_HUMAN 31402 2.57 1.06-37 BF771814.1 EST_HUMAN 28616 2.02 8.06-38 11436956 NT 28616 1.8 8.06-38 BF346221.1 EST_HUMAN 1.31 7.06-38 BF33333.1 EST_HUMAN 1.32986 0.57 8.06-38 11435947 NT 28638 11200 1.6 6.06-38 11435947 NT 28638 112038 12279 8.06-38 AB002059.1 NT	29332 1.06 1.06-37 AF189011.1 NT 30234 2.35 1.06-37 AF189011.1 NT 30234 2.35 1.06-37 AF189011.1 NT 303340 1.25 1.06-37 BF371719.1 EST_HUMAN 31468 2.57 1.06-37 BF371719.1 EST_HUMAN 31402 2.98 1.06-37 BF371714.1 EST_HUMAN 31402 2.98 1.06-37 BF371714.1 EST_HUMAN 22956 1.06-38 11438955 NT 229563 0.73 7.06-38 BF346221.1 EST_HUMAN 1.31 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8.0E-38 BF346221.1 EST_HUMAN 31189 1.8 8.0E-38 BF346221.1 EST_HUMAN 31189 1.8 8.0E-38 BF346221.1 EST_HUMAN 31189 1.8 8.0E-38 BF033033.1 EST_HUMAN 31200 1.8 6.0E-38 T1425114 NT 2986 0.57 8.0E-38 T1425114 NT 32986 0.57 8.0E-38 T1435947 NT 30900 1.7 6.0E-38 T1418164 NT 298133 1.38 6.0E-38 AW971819.1 EST_HUMAN	29332 1.06 1.06-37 AF189011.1 NT 30234 2.35 1.06-37 AF189011.1 NT 30234 2.35 1.06-37 AF189011.1 NT 303340 1.25 1.06-37 BF371719.1 EST_HUMAN 31408 2.57 1.06-37 BF371719.1 EST_HUMAN 31402 2.59 1.06-37 BF371719.1 EST_HUMAN 31402 2.59 1.06-37 BF37171406.1 EST_HUMAN 31402 2.59 1.06-39 BF346221.1 EST_HUMAN 229563 0.73 7.06-39 BF346221.1 EST_HUMAN 31189 0.73 7.06-39 BF346221.1 EST_HUMAN 31189 0.73 7.06-39 BF346221.1 EST_HUMAN 31189 0.57 8.06-39 BF346221.1 EST_HUMAN 31189 0.57 8.06-39 BF346221.1 EST_HUMAN 31189 0.57 8.06-39 H19092.1 EST_HUMAN 31200 1.8 6.06-39 AB002059.1 NT 806-39 E.06-39 AB0020740.1 NT 806-39 E.06-39 AB0020740.1 NT 806-39 AB0020740.1 NT 8	29332 0.72 1.0E-37 AF189011.1 NT 30234 2.35 1.0E-37 BF371719.1 EST_HUMAN 0.94 1.0E-37 BF371719.1 EST_HUMAN 1.25 1.0E-37 BF371719.1 EST_HUMAN 1.25 1.0E-37 BF371719.1 EST_HUMAN 1.25 1.0E-37 BF371719.1 EST_HUMAN 1.25 1.0E-37 BF371719.1 EST_HUMAN 1.25 1.0E-37 BF371714.1 EST_HUMAN 1.29563 0.73 1.0E-38 11436955 NT 1.29563 0.73 7.0E-38 BF346221.1 EST_HUMAN 1.31 7.0E-38 BF346221.1 EST_HUMAN 1.31 7.0E-38 BF346221.1 EST_HUMAN 1.31 7.0E-38 BF346221.1 EST_HUMAN 1.31 7.0E-38 BF33333.1 EST_HUMAN 1.3199 0.57 6.0E-38 BF346201.1 EST_HUMAN 1.29563 0.57 6.0E-38 BF33313.0 NT 11425114 NT 6.0E-38 11436947 NT 1143694 NT 29133 1.38 6.0E-38 AN9971819.1 EST_HUMAN 1.29583 0.50 0.99 6.0E-38 AN9371819.1 EST_HUMAN 1.29086 0.85 6.0E-38 AN9371819.1 EST_HUMAN 1.29086 0.89 6.0E-38 AN337740.1 NT 1.29086 0.89 6	1.06 1.0E-37 AF18901.1 NT 29332 0.72 1.0E-37 AF18901.1 NT 7305360 NT 7305361	28332 0.72 1.0E-37 AF186011.1 NT 28332 0.72 1.0E-37 AF186011.1 NT 30234 2.35 1.0E-37 AF186011.1 NT 33940 1.25 1.0E-37 BF371719.1 EST HUMAN 34488 2.57 1.0E-37 BE546032.1 EST HUMAN 31402 2.81 1.0E-37 BE771814.1 EST HUMAN 28616 2.02 8.0E-38 10048482 NT 2865 0.73 7.0E-38 BF346221.1 EST HUMAN 28450 1.31 7.0E-38 BF346221.1 EST HUMAN 31189 1.31 7.0E-38 BF346221.1 EST HUMAN 31189 1.31 7.0E-38 BF336321.1 EST HUMAN 31200 1.3 6.0E-38 BF033033.1 EST HUMAN 31200 1.3 6.0E-38 BF033033.1 EST HUMAN 31038 1.2 6.0E-38 BF032033.1 EST HUMAN 28616 2.05 8.0E-38 BF032033.1 EST HUMAN 31038 1.2 6.0E-38 BF032033.1 EST HUMAN 28618 0.57 8.0E-38 AB002089.1 NT 28000 1.7 6.0E-38 AB002089.1 NT 28000 0.73 7.0E-38 AB002089.1 NT 28000 1.7 6.0E-38 AB002089.1 NT	28332 0.72 1.0E-37 AF186011.1 NT 30234 2.35 1.0E-37 AF186011.1 NT 30234 2.35 1.0E-37 AF186011.1 NT 3040 1.25 1.0E-37 BF371719.1 EST HUMAN 36529 2.99 1.0E-37 BE771814.1 EST HUMAN 31402 2.00 1.0E-37 BF771814.1 EST HUMAN 28616 2.02 8.0E-38 BF346221.1 EST HUMAN 28650 0.73 7.0E-38 BF346221.1 EST HUMAN 28650 0.73 7.0E-38 BF346221.1 EST HUMAN 28450 1.2 8.0E-38 BF346221.1 EST HUMAN 28450 1.2 8.0E-38 BF346221.1 EST HUMAN 31200 1.2 6.0E-38 BF03303.1 EST HUMAN 31200 1.0 8.0E-38 BF03303.1 EST HUMAN 32860 0.57 8.0E-38 BF03303.1 EST HUMAN 32890 0.57 8.0E-38 BF03303.1 EST HUMAN 28450 1.2 6.0E-38 BF03303.1 EST HUMAN 28500 0.57 8.0E-38 AB002059.1 NT 28600 0.57 8.0E-38 AB002059.1 NT 28600 0.57 8.0E-38 AB002059.1 NT 28600 0.57 8.0E-38 AB002059.1 NT 28600 0.58 5.0E-38 AB3107.1 EST HUMAN 28600 0.82 5.0E-38 TR3107.1	1.06 1.0E-37 AW86Z082.1 EST HUMAN 28332 0.72 1.0E-37 AF189011.1 NT 30234 2.35 1.0E-37 BF371719.1 EST HUMAN 33940 1.25 1.0E-37 BE546032.1 EST HUMAN 34468 2.57 1.0E-37 BE546032.1 EST HUMAN 31402 2.81 1.0E-37 BF771406.1 EST HUMAN 28616 2.02 8.0E-38 1143895.8 NT 28450 1.2 8.0E-38 H19062.1 EST HUMAN 28450 1.31 7.0E-38 BF033033.1 EST HUMAN 31200 1.6 8.0E-38 BF033033.1 EST HUMAN 31200 1.6 8.0E-38 H1435947 NT 32000 1.7 6.0E-38 BF033033.1 EST HUMAN 31038 12.79 8.0E-38 H1435947 NT 30000 1.7 6.0E-38 AF287289.1 NT 30000 1.7 6.0E-38 AF38729.1 NT 30000 1.7 6.0E-38 AW971819.1 EST HUMAN 28133 1.38 6.0E-38 AW971819.1 EST HUMAN 28030 0.92 5.0E-38 R83107.1 EST HUMAN 22721 0.89 5.0E-38 R83107.1 EST HUMAN 22721 EST HUMAN 226308 0.92 5.0E-38 R83107.1 EST HUMAN 32771 EST HUMAN 32711 EST HUMAN 32711 E	1.06 1.0E-37 AF186011.1 NT 30234 2.35 1.0E-37 AF186011.1 NT 30234 2.35 1.0E-37 BF371719.1 EST_HUMAN 33940 1.25 1.0E-37 BF371719.1 EST_HUMAN 3468 2.57 1.0E-37 BF7187.1 EST_HUMAN 31402 2.81 1.0E-37 BF7187.1 EST_HUMAN 31402 2.81 1.0E-37 BF7187.1 EST_HUMAN 28616 1.6 8.0E-38 BF346221.1 EST_HUMAN 28650 0.73 7.0E-38 BF346221.1 EST_HUMAN 28650 0.73 7.0E-38 BF346221.1 EST_HUMAN 31402 1.2 6.0E-38 BF346221.1 EST_HUMAN 31409 1.1 6.0E-38 BF346221.1 EST_HUMAN 31409 1.1 6.0E-38 BF346221.1 EST_HUMAN 31500 1.1 6.0E-38 BF03303.1 EST_HUMAN 31600 1.1 6.0E-38 BF03303.1 EST_HUMAN 31600 1.1 6.0E-38 BF032033.1 EST_HUMAN 32000 1.7 6.0E-38 BF032033.1 EST_HUMAN 28133 1.38 6.0E-38 AM971810.1 EST_HUMAN 28030 0.92 6.0E-38 BF31760.1 EST_HUMAN 220308 0.92 6.0E-38 BF31760.1 EST_HUMAN 22712 1.48 6.0E-38 BF31760.1 EST_HUMAN 227212 1.48 6.0E-38 BF31760.1 EST_HUMAN 227312 1.48 6.0E-38 327312	1.06 1.06-37 AF180011.1 NT 30234 2.35 1.06-37 AF180011.1 NT 30234 2.35 1.06-37 BF371719.1 EST_HUMAN 33940 1.25 1.06-37 BE546032.1 EST_HUMAN 34468 2.57 1.06-37 BE576032.1 EST_HUMAN 31402 2.96 1.06-37 BE771414.1 EST_HUMAN 31529 2.96 1.06-37 BE771414.1 EST_HUMAN 31520 2.96 1.06-38 BF736231.1 EST_HUMAN 28550 0.73 7.06-38 BF73633.1 EST_HUMAN 31189 1.1 8.06-38 BF73633.1 EST_HUMAN 31200 1.0 6.06-38 BF73633.1 NT 31038 12.79 6.06-38 BF73633.1 NT 31038 12.79 6.06-38 BF736374.0 NT 32090 1.7 6.06-38 BF736374.0 NT 32090 1.7 6.06-38 AM971810.1 EST_HUMAN 28133 1.38 6.06-38 AM971810.1 EST_HUMAN 28207 0.92 5.06-38 BF874610.1 EST_HUMAN 282712 1.48 5.06-38 BF874610.1 EST_HUMAN 32712 1.48 5.06-38 BF874610.1 EST_HUMAN 32712 1.48 5.06-38 BF874610.1 EST_HUMAN 28578 4.96-38 Z55468.1 NT 28578 4.66-38 Z55468.1 NT 325460 325468.1 NT 325461 NT 3254621 NT 32	1.06

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Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3836	16587	L	1.78	3.0E-38 P53538	P53538	SWISSPROT	SSU72 PROTEIN
3836	16587	29225	1.76		P53538	SWISSPROT	SSU72 PROTEIN
4574	17309		1.47	3.0E-38	3.0E-38 BE279301.1	EST_HUMAN	801157633F1 NIH_MGC_21 Homo saplens cDNA clone IMAGE:3504272 5
6855	25097	32430			3.0E-38 AL163300.2	IN	Homo saplens chronosome 21 segment HS21C100
7144	19831	32900	0.56		3.0E-38 AW302461.1	EST_HUMAN	xw04d01x1 NCI_CGAP_Bm53 Hamo sapiens dDNA clane IMAGE:2827009 3'
7488	20160		8.26		3.0E-38 BF373664.1	EST_HUMAN	CM3-FT0181-140700-241-f07 FT0181 Homo sapiens cDNA
8548	21240	34383	21		3.0E-38 H85494.1	EST_HUMAN	yw88b04,71 Sogres melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:249775 5
8548	21240				3.0E-38 H85494.1	EST_HUMAN	w88b04,r1 Soares melanocyte 2NbHM Homo sapiens cDNA done IMAGE:249775 5
9872	77527		2.24	L	3.0E-38 AL163248.2	NT	Homo saplens chromosome 21 segment HS210048
12630	17896	30488	1.65	3.0E-38	11435947 NT	ĮN.	Homo saplens chromosome 12 open reading frame 3 (C12ORF3), mRNA
49	12878	25504	4.4		2.0E-38 AL163248.2	N	Homo sapiens chromosome 21 segment HS21CO48
1358	14106	26781	2.89	_	5902097 NT	¥	Homo sepiens SMT3 (suppressor of mif two 3, yeast) homolog 2 (SMT3H2), mRNA
126	14387	27075	221	2.05-38	2.0E-38 AA437353.1	EST HUMAN	2w30d01.r1 Soares overy tumor NbHOT Homo septens dDNA dane IMAGE:770785 5' strailer to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE;
							zw30d01,r1 Sogres overy tumor NbHOT Homo sepiens cDNA done IMAGE:770785 5 similar to
1641	14387	27076	2.21	2.0E-38	2.0E-38[AA437353.1	EST_HUMAN	SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE;
2408	15129		1.45		2.0E-38 W78571.1	EST_HUMAN	zd86g09.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:345684 51
5632	18427	31339	0.69		2.0E-38 Z28634.2	NT	Homo saplens mRNA for ankyrin B (440 kDa)
5632	18427	31340	0.69		2.0E-38 Z26634.2	NT	Homo saplens mRNA for ankyrin B (440 kDa)
7619	20285	33395	1.46		2.0E-38 AV721103.1	EST_HUMAN	AV721103 HTB Homo sapiens cDNA clone HTBARH11 5
8382	21075		4.38		2.0E-38 BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo septens cDNA
8793		34631	0.56		2.0E-38 F06450.1	EST_HUMAN	HSC18F031 normalized infant brain aDNA Homo sapiens aDNA clone c-18f03
8864	21555	34700	2.04		2.0E-38 AF069755.1	NT	Homo sapiens orphan G protein-coupled receptor HG20 (HG20) mRNA, complete cds
9121	21809		100		2 0F-38 BF222258.1	EST HUMAN	hu08g02x1 NCL_CGAP_Lu24 Homo sepiens cDNA clone IMAGE:3166130 3' similiar to TR:002710 002710 GAG POLYPROTEIN .
10346	L	36212			2.0E-38 D63479.2	Ę	Homo sapiens mRNA for KIAA0145 protein, partial ods
130	L.			90 100	2005 200 4 4 50 54 50 4	NAM: IL FOR	no34g03.st NCI_CCAP_Pr23 Home sapiens cDNA done IMAGE:1102812.3 samilar to TR:E212316
	1			2:00			
11200	23865	37152	1.37	2.0E-38	2.0E-38 AA595480.1	EST_HUMAN	IROSABUS STINCI CICAR PTZS Homo septems CDNA GONE IMAGE: T10Z812 S smilet to 1 K:EZ1Z318 EZ1Z316 NADP DEPENDENT LEUKOTREINE B4 12-HYDROXYDEHYDROGENASE;
11472	24073	37382	5.79		2.0E-38 BE712790.1	EST_HUMAN	QV2-HT0698-080800-293-405 HT0698 Homo sapiens cDNA
11638	24235	37567	3.52		2.0E-38 AF190501.1	5	Homo septens feucine-rich repeat-contenting G protein-coupled receptor 6 (LGR6) mRNA, pertial cds
	ı	l					

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Table 4
Single Exon Probes Expressed in Brain

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Top Hit Descriptor	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR8) mRNA, pertial cds	AV726988 HTC Homo sepiens cDNA clone HTCAXH07 5	Homo sapiens gene for kinesin-like protein, complete cds	CHR220580 Chromosome 22 exon Homo sapiens cDNA clone C22_788 5	E1 beta=pyruvate dehydrogenase beta (promoter) [human, placenta, Genomic, 1280 nt]	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA	zu62b02.r1 Soares_testis_NHT Homo septens cONA clone IMAGE:742539 5' similar to contains element. MER19 repetitive element;	Homo sapiens guenine nucleotide binding protein-like 1 (GNL1), mRNA	Hamo sapiens KIAA0173 gene product (KIAA0173), mRNA	Homo sapiens cyclin K (CCNIK) gene, excn 7	Homo sapiens chromosome 21 segment HS21C003	Homo sapiens chromosome 21 segment HS21C003	Homo sapiens hypothetical protein FLJ10600 (FLJ10600), mRNA	Mus musculus otogelin (Otog), mRNA	Mus musculus otogetin (Otog), mRNA	Homo sapiens mRNA for KIAA0612 protein, partial cds	Homo sepiens hypothetical protein FLJ10600 (FLJ10600), mRNA	ht09g01.x1 NCI_CGAP_Kid13 Homo septens cDNA done IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element;	y/96b08.r1 Sognes Infant brain 1NIB Homo sapiens cDNA clone IMAGE:30486 5	Homo sepiens KIAA0426 gene product (KIAA0426), mRNA	Homo sapiens chromosome 21 segment HS210084	Homo sepiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) 1640 (ATP6C) mRNA	Homo sapiens estrogen receptor-binding fragment-associated gene 9 (EBAG9) mPNA	wh53f10.xf NG_CGAP_Kld11 Homo sepiens cDNA clone IMAGE:2384491 3' similiar to TR:P87890 P87890 POL PROTEIN ;	Homo seplens chromosome 21 segment HS21C027	QV1-BT0631-040800-357-f02 BT0631 Homo sapiens oDNA	7e34c03.x1 NCI_CGAP_Lu24 Homo sepiens cDNA done iMAGE:3284356 3' similar to WP:R151.6 CE00828	Homo septens X-linked antitidrotito ectodermal dysplasia protein gene (EDA), excn 2 and flanking repeat	a ryfa i
 Top Hit Database Source	¥	EST_HUMAN	NT	EST_HUMAN	NT	TN	EST HUMAN	LN LN	Z	Ę	뒫	NT	۲	LN	TN	IN	M	EST HUMAN	EST HUMAN	NT	TN	NT	ᅜ	EST_HUMAN	E	EST_HUMAN	EST HUMAN	Ę	-
Top Hit Acession No.	\F190501.1	2.0E-38 AV726988.1	2.0E-38 AB012723.1		1	11418248 NT	1,0401570.1	4885288 NT	7661969 NT	1.0E-38 AFZ70831.1	AL163203.2	1.0E-38 AL163203.2	8922543 NT	7305360 NT	7305360 NT		11422250 NT	3E350127.1	318512.1	7662109 NT	1.0E-38 AL163284.2	4502312 NT	4758229 NT	1823404.1	7.0E-39 AL 163227.2	6.0E-39 BF331829.1	3E670394.1	E OC 30 A EOMOR 28 4	1,000000
Most Similar (Top) Hit BLAST E Value	2.0E-38 AF19050	2.0E-38	2.0E-38	2.0E-38 H55641.	2.0E-38 S74906.	2.0E-38	1.0E-38 AA40157	1.0E-38	1.0E-38	1.0E-38	1.0E-38 AL16320	1.0E-38	1.0E-38	1.0E-38	1.0E-38	1.0E-38 AB0145	1.0E-38	1.0E-38 BE35012	1.0E-38 R18512.	1.0E-38	1.05-38	8.0E-39	8.0E-39	8.0E-39 AI823404	7.0E-39	6.0E-39	6.0E-39 BE67039	00 00).ec⊐0.c
Expression Signal	3.52	3.05	2.06	6,45	1.43	3.76	2.55	2.53	1.11	2.34	123	1.23	F	4.71	4.71	3.15	0.71	5.13	0.58	1.28	22	15.3	1.45	1.27	5.79	2.24	-		/C.T
ORF SEQ ID NO:	37558			31081				27450	27475	27960		29656		31677	31678	23062	34898	35150	36163	37503			26796			36639			20412
Exan SEQ ID NO:	24236	24517	24518	24705	24742	25031	13829	14728	14747	15216	17029	17029	17283	18719	18719	19887	21740	21977	22948	24187	25140	12882	14121	14580	14819	23400	24979	40750	3/2
Probe SEQ ID NO:	11638	11971	11973	12280	12323	12777	1071	1992	2012	2489	4290	4290	4558	5937	5937	7304	9051	9310	10301	11588	12118	83	1373	1821	2087	10711	12605	201	792
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					5		
Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
88	15750	28397	8.62	5.05-39	5.0E-39 AI750154.1	EST_HUMAN	at36b04.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2374063 3' similar to TR:Q15408 Q15408 NEUTRAL PROTEASE LARGE SUBUNIT ;contains LTR7.tt LTR7 repetitive element;
12410	24793		2.04	5.0E-39	11420289 NT	NT	Hamo septens hypothetical protein FLJ10803 (FLJ10803), mRNA
537	13320	72964	87.8	4.0E-39 AB0156	10.1	NT	Chlorocebus aethiops mRNA for ribosomal protein S4X, complete cds
3559	16314	28961	0.97	4.0E-39	4.0E-39 AL163210.2	NT	Homo sepiens chromosome 21 segment HS21C010
7974	20669	33791	12.1	4.0E-30	4.0E-30 AA682949.1	EST_HUMAN	ae92g04.s1 Stratagene schizo brain S11 Homo sapiens cDNA done IMAGE:1020438 3' similar to contains OFR.b1 OFR repetitive element;
828			0.56	4.0E-39 D84116.	1	Į,	Homo sapiens DNA for prostacyclin synthese, exon 2
8778			0.56	4.0E-39 D84116.	1	Ŋ	Homo sapiens DNA for prostacyclin synthese, excn 2
12427	24802		4.47	4.0E-30	11418177 NT	L	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12534	24878		2.71	4.0E-39 BE8364	BE836452.1	EST_HUMAN	QV0-FN0063-260600-278-c06 FN0063 Hamo sepiens cDNA
8	12875		14.86	3.0E-39	3.0E-39 AA631949.1	EST_HUMAN	firstones genomic DNA specific cDNA library Homo sepiens cDNA clone CR12-1
\$	12875		14.86	3.0E-39	3.0E-39 AAB31949.1	EST_HUMAN	frinfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
\$			14.98	3.0€-39	3.0E-39 AA531949.1	EST_HUMAN	finifo16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
	<u>l _</u>	<u> </u>					ad3a10.s1 Soares N#HMPu_S1 Home septens cDNA clone IMAGE:1660996 3' similar to SW:GTR5_RAT
11963	24511	37257	4.35	3.0E-30	3.0E-30 AI084557.1	EST HUMAN	P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE;
1,000	24844	2772	YE 7		3 0E-30 A M94657 4	EST HIMAN	অ63a10.s1 Soarse_NiHMPu_S1 Homo sapiens cDNA clone IMAGE:1680986 3' similar to SW:GTR5_RAT P43427 যে UCOSE TRANSPORTER TYPE 5. SMALL INTESTINE :
200	1_	L	5.82			EST HUMAN	yp51c06.s1 Soeres retina N2b4HR Homo septems cDNA clone IMAGE:1909543'
877	L.		6.8	2.0E-30	2.0E-30 BE409203.1	EST HUMAN	601301607F1 NIH_MGC_21 Homo saplens cONA clone IMAGE:3636289 5'
88	L		14.08	2.0E-39	2.0E-39 AI525119.1	EST HUMAN	promme-7,D01,r bytumor Homo sapiens cDNA 5'
8	13760		4.2	2.0E-39	2.0E-39 AF000573.1	IN	Homo sapiens homogentisate 1,2-dioxygenase gene, complete cds
1520	14287		11.91	2.0E-30	2.0E-39 AW372318.1	EST_HUMAN	PM0-BT0340-211289-003-d02 BT0340 Hamo sapiens cDNA
	İ		·				nw21g02.s1 NCI_CGAP_GCB0 Homo sepiens cDNA clone IMAGE:1241138 3' similar to contains THR.t3
200					2.0E-39 AA720574.1	EST_HUMAN	I FIX repoutive element;
2834				2.0E-30	2.0E-39 AL163248.2	¥	Homo septens chromosome 21 segment HS21C048
4370	17108	29743	1.48	2.0E-39	2.0E-39 BF370207.1	EST_HUMAN	RC4-FN0037-290700-011-#10 FN0037 Homo sepiens cDNA
5403	18203	20602	124	2.0E-39	2.0E-39 AA508880.11	EST_HUMAN	ng88ft3.s1 NCI_CGAP_Pr6 Hamo sepiens aDNA clane IMAGE:941693
7260	10063	33020	238	2.0E-39	2.0E-39 AA080867.1	EST HUMAN	znötfüzirt Stratagene hNT neuron (#837233) Homo saplens cDNA clone IMAGE:540651 5
7431	20108	33195		2.0E-39	2.0E-39 AL163202.2	NT	Hamo sapiens chromosame 21 segment HS21 C002
7431			0.72	2.0E-39	2.0E-39 AL163202.2	NT	Hamo sapiens chromosame 21 segment HS21 C002
8209		34038		2.0E-39	2.0E-39 AF078779.1	NT	Rattus norvegicus putative four repeat kon channel mRNA, complete cots
88	22056		0.55	2.0E-39	2.0E-39 AA984531.1	EST_HUMAN	am88c11.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1630196 3'

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						A	
Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9526	22179		0.73	2.0E-39	2.0E-39 AIG86660.1	EST_HUMAN	tu35e03.x1 NCI_CGAP_Pr28 Homo sepiens cDNA clone IMAGE:22553052.3'
11400	24058	37365	2.97	2.0E-39	2.0E-39 D86964.1	NT	Human mRNA for KIAA0209 gene, pertial cds
1503	14249	26936	3.71	1.0E-39	1.0E-39 AJ006345.1	NT	Homo saplens KVLQT1 gene
1503	14249	26937	3.71	1.0E-39	1.0E-39 AJ006345.1	INT	Homo sapiens KVLQT1 gene
1521	14268	28952	424	1.0E-39	7657020 NT	N	Homo saplens DKFZp434P211 protein (DKFZP434P211), mRNA
860*	16841	29467	2.0	1.0E-30	11430303 NT	۲	Homo sapiens catenin (cadherin-associated protein), apha 2 (CTNNA2), mRNA
4096	16841	29468	2.0	1.0E-39	11430303 NT	NT	Homo saplens caterin (cadherin-associated protein), alpha 2 (CTNNA2), mRNA
4812	17347	29980	2.5		1.0E-39 AW951995.1	EST_HUMAN	EST364065 MAGE resequences, MAGB Homo sepiens cDNA
4812	17347	29981	2.5		1.0E-39 AW951996.1	EST_HUMAN	EST364085 MAGE resequences, MAGB Homo sapiens cDNA
4054	17388	30021	8.86	1.0E-39	7857020 NT	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
الانباء		7.00			•	<u>!</u>	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain
97/4	180/3	30736	1.02	1.0E-39	11417342 NI	N.	(1M) and short cytoplasmic domain, (semaphorin) b4 (SEMADA), mXNA
5274	18079	30736	1.02	1.05-39	11417342 NT	F	Homo sepiens seme domein, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
							yd28g08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:109402 5' sknilar to contains
5542	18339	31246	1.97	1.0E-39	1.0E-39 T80876.1	EST_HUMAN	Alu repetitive element,contains LTR1 repetitive element;
5578	18375	31287	4.84	1.0E-39	1.0E-39 AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X 1 (NIX1) (Nix1 gene)
5578	18375	31288	4.84	1.0E-30	1.0E-30 AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X 1 (NIX1) (Nix1 gene)
6727	19561		1.57	1.0E-39	1143 <i>67</i> 38 NT	N	Homo septens tubby like protein 3 (TULP3), mRNA
7264	19948	33025	1.8		1.0E-39 D78132.1	TN	Homo sapiens mRNA for ras-related GTP-binding protein, complete cds
8462	21154	34207	1.03	1.0E-30	1.0E-39 046530	SWISSPROT	RIBONUCLEASE K6 PRECURSOR (RNASE K6)
12357	24781		1.34	1.0E-39	1.0E-39 U07000.1	NT	Human breakpoint duster region (BCR) gene, complete cds
542	. 1	25957	1.68	9.0E-40	IN 0125083	NT	Homo saplens UDP-glucose pyrophosphorylase 2 (UGP2), mRNA
1213		26820	15.14	9.0E-40	1N 9755145	IN	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1213	13963	20630	15.14	9.0E-40	TN 55145 NT	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1432	14179	26865	6.54	9.0E-40	4507512 NT	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Soraby fundus dystrophy, pseudoinflammatory) (TIMP3) mRNA
3766	16617	29165	26.0	9.0E-40	1N[4925034	NT	Homo sapiens fragile X mental retardation 1 (FMR1) mRNA
3956	17878	28343	3.99	9.0E-40	9.0E-40 AB033070.1	NT	Hamo sapiens mRNA for KIAA1244 proben, pertial cds
3036	15802	28440	0.84	8.0E-40	8.0E-40 AA078165.1	EST_HUMAN	7H15A04 Chromosome 7 HeLa cONA Library Homo septens cDNA clone 7H15A04
3903	10653		3.35	8.0E-40	8.0E-40 BE398641.1	EST_HUMAN	601288958F1 NIH_MGC_8 Hamo sapiens cDNA clane IMAGE:3619168 5
7818	20282	33300	2	7.05.40	7 OF ADI IRO32K 1	<u> </u>	Himse DNA reference commo mRNA suches name enverten mitechandral protein complete ode
	ı	22220	7.50	10:1	000050.1		rement over populations gaining the contract gains at remaining the contract and proventy continued con-

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Table 4
Single Exon Probes Expressed in Brain

					ř	ייין זיייש פולי	Single Extended Expressed in Digit
Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similer (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7818	20282	18888	2.03	7.0E-40	7.0E-40 U60325.1	¥	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
10813	L	36732	227	7.0E-40	7.0E-40 AL163246.2	Ę	Homo sepiens chromosome 21 segment HS210048
2730	15437	28174	8.41	6.0E-40	6.0E-40 AA361275.1	EST_HUMAN	EST70527 T-cell lymphome Homo sepiens cDNA 5' end similar to similar to zinc finger protein family
2730	15437	28175	8.41	6.0E-40	6.0E-40 AA361275.1	EST HUMAN	EST70527 T-cell lymphoma Homo saplens cDNA 5' end similar to similar to zinc finger protein family
5849	18636		2.24	8.0E-40	6.0E-40 BE504766.1	EST_HUMAN	hz40g01.x1 NCI_CGAP_GC8 Homo septens cDNA clone IMAGE;3210480 3'
6055			1.11	6.0E-40		N F	Homo sapiens KIAA0211 gene product (KIAA0211), mRNA
6836	19498	32522	3.56	6.0E-40	11439783 NT	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
6836	19498	32523	3.58	6.0E-40	TN 887883 NT	Į.	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
9877	22527	35722	10.25	6.0E-40 AV6530	AV653028.1	EST_HUMAN	AV653028 GLC Hamo sapiens aDNA clane GLCDGF04 3'
7288	22527	35723	10.25	6.0E-40	6.0E-40 AV653028.1	EST_HUMAN	AV653028 GLC Hamo septens aDNA clane GLCDGF043'
1869	14607	27318	1.78	4.0E-40	4 DE-40 A 168 8005.1	EST HUMAN	1891b01.x1 NCI_CGAP_Pr28 Homo septens cDNA clone IMAGE:2248873 3' similar to TR:073505 073505 POL PROTEIN.
		İ				ı	Homo sepiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat
2101	14832		227	4.0E-40	4.0E-40 AF003528.1	۲	regions
4356		29729	80.6	4.0E-40	1982117 NT	NT	Homo septens KIAA0433 protein (KIAA0433), mRNA
7786		33606	0.5	4.0E-40	4.0E-40 AU127831.1	EST_HUMAN	AU127831 NT2RP2 Homo sepierts cDNA clone NT2RP 2002/172 61
7890	20585	33714	6.22	4.0E-40	4.0E-40 AA742809.1	EST_HUMAN	m34e10.r1 NCI_CGAP_Br4 Hamo septens aDNA clane IMAGE:1222122
8953	21644	34793	6.17	4.0E-40	4.0E-40 BE009416.1	EST_HUMAN	PMO-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA
8963	21644	34794	5.17	4.0E-40	4.0E-40 BE009416.1	EST_HUMAN	PMO-BN0167-070600-002-h12 BN0167 Homo septens cDNA
10616	53308	36548	3.03	4.0E-40	4.0E-40 AW841585.1	EST_HUMAN	RC1-CN0017-120200-012-e04 CN0017 Homo septiens cDNA
4111	16854	29481	1.02	3.0E-40	3.0E-40 Al925949.1	EST_HUMAN	wh12/07.x1 NCI_CGAP_Kid11 Homo saplens cDNA clone IMAGE:2380549 31
6543	19308	32313	7.02	3.05-40	TN 242/1417	Į.	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short evtoplasmic domain, (semachorin) SA (SEMASA), mRNA
8280	_	34115	3.62	3.0E-40		LX.	Homo sapiens HBV associated factor (XAP4) mRNA
8888		34704	1.25	3.0E-40 AF0787	AF078779.1	Į.	Rattus nonegicus putative four repeat ion channel mRNA, complete cds
9111	21799	34963	1.42	3.0E-40	9.1	LN	Rattus norvegicus putative four repeat ion channel mRNA, complete ods
11232	23805	37182	8.38	3.0E-40	6005813 NT	NT	Homo sapiens serine threonine protein kinase (NDR), mRNA
11563	24162	37478	2.23	3.06.40	3.0E-40 AW118799.1	EST HUMAN	x496h02.x1 Sogree_NFL_T_GBC_S1 Homo septens cDNA clone IMAGE:2905491 3' similar to TR:Q15804 Q15804 SIMILAR TO ENV OF TYPE A AND TYPE B RETROVIRUSES AND TO CLASS II HERVS :
317			8.53	2.0E-40		EST HUMAN	qg52h08.x1 Soares_bests_NHT Homo saplens cDNA clone IMAGE:1838847 3'

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Detabase Source	Top Hit Descriptor
111	13549		1.01	2.0E-40	2.0E-40 AW303868.1	EST_HUMAN	x24e10.x1 NCI_CGAP_Ut4 Homo septens cDNA clone IMAGE:2761088 3' similar to SW:RS5_MOUSE P97461 40S RIBOSOMAL PROTEIN S5;
1818	14557		0.92		2.0E-40 AV731601.1	EST_HUMAN	AV731601 HTF Homo saplens cDNA clone HTFAZE05 5"
1927	14683	27375	85.1	2.0E-40	4508188 NT	Ę	Homo sapiens protessome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products.
1927	14663	27376	1.38			Ę	Homo sapiens protessome (prosome, mecropein) subunit, alpha type, 7 (PSMA7) mRNA, and translated products.
288	14796	27522	121		Alpesse	EST HUMAN	w80a11.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2514716 3' stmiler to TR:Q81929 Q81929 ZINC FINGER PROTEIN.;
2166		27630	2.48		5453592 NT	Į.	Homo sepiens adentylyl cyclesse associated protein 2 (CAP2) mRNA
2695			1.44	2.0E-40	BE27590	EST HUMAN	601121567F1 NIH_MGC_20 Homo sepiens cDNA clone iMAGE:3345784 5
3123	15888	28529	4.28		6463592 NT	TN	Homo sapiens adenylyl cyclase-essociated protein 2 (CAP2) mRNA
4843	17573	30197	1.08		2.0E-40 AL163280.2	NT	Homo saplens chromosome 21 segment HS21C080
4843	17573	30198	1.68		2.0E-40 AL163280.2	TN.	Homo septens chromosome 21 segment HS21C080
863	13632		1.78		1.0E-40 AA225989.1	EST_HUMAN	nc09e09.s1 NCI_CGAP_Pr1 Homo septens cDNA done IMAGE:1007608
2627	15339	28083	0.83		1.0E-40 BF036881.1	EST_HUMAN	601460375F1 NIH_MGC_66 Hamo saplans cDNA clane IMAGE:3863803 5
2602			1.34			EST_HUMAN	bb79e10.y1 NIH_MGC_10 Homo sepiens cDNA clone IMAGE:3048570 5' similar to TR:Q8Z158 Q8Z158 SYNTAXIN 17.;
2741	15447	28185	1.18		1.0E-40 BF541030.1	EST_HUMAN	602068604F1 NIH_MGC_58 Homo saplems cDNA clone IMAGE:4067738 5
2741	15447	28186	1.18		1.0E-40 BF541030.1	EST_HUMAN	602088604F1 NIH_MGC_58 Homo suplems cDNA clone IMAGE:4087736 5
3282	16053		1.27	1.0E-40		NT	Homo saplens sorting nextn 3 (SNX3) mRNA
4571	17306	28834	4.52	1.0E-40	4508012 NT	NT TA	Homo eaplens zinc finger protein 200 (ZNF200) mRNA, and translated products
6161	18938	31907	0.75		1.0E-40 W92708.1	EST_HUMAN	zh79f11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sepiens cDNA clone IMAGE:418317.3'
6161	18938	31908	0.75		1.0E-40 W92708.1	EST_HUMAN	zh79f11.s1 Soares_fetal_Iver_spicen_1NFLS_S1 Homo sapiens cDNA done IMAGE:418317.31
6987	19690	32727	1.77	1.0E-40	1.0E-40 AA573201.1	EST_HUMAN	nj42704.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:995167 3'
6987	19680	32728	1.77	1.0E-40	1.0E-40 AA573201.1	EST_HUMAN	nj42f04.s1 NCI_CGAP_AA1 Hamo sepiens cDNA clane IMAGE:995167 3'
7133	19820	32886	0.69		1.0E-40 P26808	SWISSPROT	POL POLYPROTEIN (CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
10834	23516	36758	8.34		1.0E-40 AU149345.1	EST_HUMAN	AU149345 NT2RM4 Homo seplens cDNA clone NT2RM4002122 3'
11694	24289	37612	1.89		1.0E-40 AA614255.1	EST_HUMAN	nposh03.s1 NCI_CGAP_Pr3 Homo septens oDNA clone IMAGE:1115861 similar to TR:G1136406 G1136406 KIAA0173 PROTEIN.;
11694		37613	1.89		1.0E-40 AA614255.1	EST HUMAN	np09h03.s1 NCL_CGAP_Pr3 Homo sapiens cDNA clone IMAGE:1115861 similar to TR:G1136406 G1136406 KIAA0173 PROTEIN.;
12376			10.09		1.0E-40 BF334112.1	EST_HUMAN	MR2-CT0222-211089-002-e10 CT0222 Homo espiens dDNA
7822	20517	33643	1.62		3.2	MT	Homo saplens chromosome 21 segment HS21C003

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Expression (Top) Hit Acession (Top) Hit Acession Signel BLASTE No. Source	EST_HUMAN	7.24 4.0E-41 BF304683.1 EST_HUMAN 601888098F1 NIH_MGC_17 Hamo saplens cDNA clane IMAGE:4122119 5'	11.07 4.0E-41/AV710480.1 EST_HUMAN AV710480 Cu Homo septens cDNA clane CuAACC07.5'	1.63 4.0E-41 AV708431.1 EST_HUMAN (AV708431 ADC Hamo sapiens cDNA clone ADCARE02.5	EST_HUMAN	IN	7 0000000000000000000000000000000000000	2.40 3.0E-41 (ABUZ0898.) N1 (Continue Cas) 2.72 3.0E-41 (ABUZ0898.) NT (H sextens mRNA for putative D84 CL CP profess	3.0E-41 AB037808 1 NT	3.0E-41 AA356168.1 EST HUMAN	3.0E-41 AJ229041.1 NT	3.0E-41 AA609768.1 EST_HUMAN	3.0E-41 BF125922.1 EST_HUMAN	2.0E-41 U43701.1 NT	HUMAN	TN	2.0E-41 X89831.1 NT		.1 EST_HUMAN	NT	2 NT	DATE AND ASSECT A SET HISTORY COACTIVATOR 1:	2.0E-41 4504778 NT	2.0E-41 AF03840	1.45 2.0E-41 M99944.1 NT Human B-cell specific transcription factor (BSAP) mRNA, complete cds	2.0E-41 M96944.1 NT	1.12 2.0E-41 AA328265.1 EST_HUMAN EST31723 Embryo, 12 week I Homo septens cDNA 5' end	SWISSPROT		7118NT	2.0E-41 AA372637.1 EST_HUMAN	1.05 1.0E-41 BE898735.1 EST_HUMAN 601445647F1 NIH_MGC_65 Homo sepiens CDNA clone IMAGE:3849803 5
															L	L					L							L				
ORF SEQ	19184	22246 35430	L	25184	24998 30971			1/040 2900/					24825		14686 27399	14944 27684	14990 27730	14299 26987	16081 28731	17314 29942	17314 29943	178°FD 30475		20241 33346	20662 33786		20690 33818	21585 34710	21984 35155	21984 35156		15964 28616
Probe Econ SEQ ID SEQ ID NO: NO:	6416 19					<u> </u>		5404 49	1					L	1051 14	<u></u>	L	L			L	Z+ +7-	1	ı	7967	ı	7996 20	l		12 21	11468 24	3201 15

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SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Detrabese Source	Top Hit Descriptor
3201 15984	1 28617	1.05		1.0E-41 BE869735.1	THUMAN	601445647F1 NIH_MGC_65 Hamo seplens aDNA clane IMAGE:3849803 51
4529 17284	29897	14.08	1.0E-41	6678468 NT		Mus musculus tubulin elpha 6 (Tubad), mRNA
6749 17918	30582	99.0		1.0E-41 H99079.1	EST_HUMAN	yx18b03.s1 Soeres melanocyte ZNbHM Homo sapiens cDNA done IMAGE::282081 3'
9318 21985	35157	1.69		1.0E-41 A1217868.1	EST_HUMAN	q775c10.x1 Soares_testis_NHT Homo saplens cDNA done MAGE:1755868 3'
11111 23781	37056	1.66	1.0E-41	1.0E-41 AW847812.1	EST HUMAN	II.3-CT0213-190200-040-F09 CT0213 Homo septens cDNA
12054 24571		2.81	1,05-41	526291	NT	Homo sepiens hypothetical protein PLJ20464 (PLJ20464), mRNA
		1.14		BE17919	T_HUMAN	RC0-HT0613-210300-032-g01 HT0613 Hamo sapiens cDNA
9072 21761	34922	3.49	9.0E-42	11560161 NT		Homo saplens hypothetical CZH2 zinc finger protein FLJ22504 (FLJ22504), mRNA
9072 21761		3.49		11560151 NT	NT _	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
450 13236	35875	17.7	8.0E-42	8.0E-42 AF003530.1	LN	Hamo sapiens hameabax protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
2102 14833	77267	0.92	8.0E-42	8.0E-42 AB026898.1	Ę	Hamo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
ł		4.4		8.0E-42 AA493898.1	EST_HUMAN	nh07c02.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943586 similar to TR:0434304 0434304 3678P EXPRESSED SEQUENCE TAG MRNA;
L.,						xx97a04.x1 NCI_CGAP_Brn35 Homo sepiers cDNA clone IMAGE:2592174 3' skniler to contakts OFR.t2.
_		1.56		8.0E-42 AW088062.1	HOMAN	OFR repetitive element;
				7.0E-42 AL163285.2	Т	Homo saprens chromosome 21 segment nozhous
			7.0E-42	7.0E-42 AI204358.1	П	qf68g12xf Sogres_tests_NHT Hamo sapiens cDNA clane IMAGE:17542783
					HUMAN	nf23g07.s1 NCI_CGAP_PT1 Hamo septens cDNA clane IMAGE:914662
11128 23795	37072	1.3			EST HUMAN	nf23g07.s1 NCL_CGAP_Pr1 Hamo sepiens cDNA clone IMAGE:914652
1848 14588		3.21	6.0E-42	6.0E-42 AF012872.1	NT	Hamo espiens phosphetidylinosital 4-kinase 230 (pi4K230) mRNA, complete cds
1848 14596	5 27300		6.0E-42		LN	Hamo sepiens phosphetidylinosital 4-lánese 230 (pi4K230) mRNA, complete cds
						xp29f08.x1 NCI_CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741789 3' similar to contains L1.t1 L1
5287 16012 5381 18181	30871	3.30		6.0E-42 AW 286050.1	ES L' FICIMAN	repositive marries r., Homo septems mRNA for KJAA1087 protein, partial cds
1		1.45	1		L	Hamo septens mRNA for KIAA 1067 protein, partial cds
	L	7.53	L	2		Homo sepiens Xq peeudoeutoscmal region; segment 1/2
	25859	1.41	5.0E-42		T HUMAN	hk31e11.x1 NCI_CGAP_Lu24 Homo septems cDNA clone IMAGE:3175052 3'
474 13280		2.67	5.0E-42	5730038 NT	TN	Homo sapiens SET domain and martner transposase fusion gene (SETMAR) mRNA
476 13281		2.74	5.0E-42	5730038 NT	TN	Homo sepiens SET domain and martner transposase fusion gene (SETMAR) mRNA
6587 19350	32363	1.04	5.0E-42	1143306S NT	TN	Homo sepiens ubiquitin protein ligase E3A (furnan papiliona virus E5-associated protein, Angelman syndrone) (UBE3A), mRNA
A587 40350	93364	70,7	5 OF 40	11/33083 NT	5	Homo septens ubiquitin protein Itgase E3A (fruman papilloma virus E6-associated protein, Angelman sendoman) (HRE3A) mRNA
1		12:	200	SANCE I		the second secon

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Single Exon Probes Expressed in Drain	Top Hit Descriptor	Homo sepiens myotubularin related protein 3 (MTMR3), mRNA	Homo sapiens multifunctional calcum/calmodulin-dependent protein kinase II delta2 isoform mRNA, complete ods	Homo sapiens reelin (RELN) mRNA	Homo sapiens mRNA for KIAA1294 protein, pertial cds	Homo eapiens hypothetical protein FLJ20163 (FLJ20163), mRNA	Homo sapiens MHC class 1 region	Homo saplens MHC class 1 region	Homo seplens ribonucleese III (RN3) mRNA, complete cds	H.sepiens PROS-27 mRNA	Homo saplens SNARE protein kinase SNAK mRNA, complete cds	Homo seplens regulatory factor X, 4 (influences HLA class II expression) (RFX4) mRNA	Homo seplens zino finger probein 177 (ZNF177) mRNA	RC1-ST0278-040400-018-h11 ST0278 Homo septens cDNA	RC1-ST0278-040400-018-h11 ST0278 Homo septens cDNA	601468631F1 NIH_MGC_66 Homo sepiens cDNA clone IMAGE:3862086 5	RC0-TN0079-110900-024-g07 TN0079 Homo septems cDNA	RC3-NN0070-270400-011-h10 NN0070 Homo septems cDNA	2819283.3prime NIH_MGC_7 Homo septens cDNA clone IMAGE:2819293 3'	EST367438 MAGE resequences, MAGC Homo sepiens oDNA	EST367438 MÄGE resequences, MAGC Homo seplens oDNA	ow83d05.x1 Source fetal liver_epteen_1NFLS_S1 Homo septens cDNA clone IMAGE:1663417 3'	601061284F1 NIH_MGC_10 Hamo septems aDNA done IMAGE:3447620 5	RIBONUCLEASE K3 (RNASE K3)	RIBONUCLEASE K3 (RNASE K3)	Homo septens chromosome 21 segment HS21C048	Human endogenous retrovirus pHE.1 (ERV9)	UI-H-BI1-4th-6-04-0-UI:s1 NGL CGAP Sub3 Homo sapiens cDNA clone IMAGE:2721871 3'	Homo saplens partial C9 gene for complement component C9, exon 1	Homo saplens partial C9 gene for complement component C9, exon 1	Homo sapiens NADH-ubiquinone addoreductass AGGG subunit precursor homolog mRNA, nuclear gene	encoding mitochandrial problem, complete cds	Homo septens NADH-ubiquinane addoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds	
gie Exon Proc	Top Hit Detabase Source	NT	Ę	Į.	F	N FN	FN	TN	TN	¥	F	F	Ę	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	SWISSPROT	SWISSPROT	LΝ	TN	EST_HUMAN	IN.	LN		NT	_ LZ	
מוס	Top Hit Acession No.	11417957 NT	NE0745/90 4		۱Ŀ	8923162 NT	4.0E-42 AF055086.1	4.0E-42 AF065088.1	4.0E-42 AF189011.1	(59417.1	4.0E-42 AF246219.1	4506496 NT	4508008 NT	18	AW818630.1	4.0E-42 BF035327.1	2.0E-42 BF376834.1	2.0E-42 AW898344.1	2.0E-42 AW 250059.1	2.0E-42 AW955368.1	20E-42 AW055368.1	2.0E-42 A1052588.1	2.0E-42 BE538919.1	281649	981649	4L163246.2	1.0E-42 X57147.1	4W295809.1	4,1251818.1	4,1251818.1		AF067166.1	4.F067166.1	
	Most Similar (Top) Hit BLAST E Value	5.0E-42	A DE 40 AFD?	5.0E-42	6.0E-42 AB037	5.0E-42	4.0E-42	4.0E-42	4.0E-42	4.0E-42 X5941	4.0E-42	4.0E-42	4.0E-42	4.0E-42 AW81	4.0E-42 AW81	4.0E-42	2.0E-42	2.0E-42	2.0E-42	2.0€-42	20E-42	2.0E-42	2.0€-42	2.0E-42 P81649	2.0E-42 P8164	2.0E-42 AL163	1.0E-42	1.0E-42 AW29	1.0E-42 AJ251	1.0E-42 AJ251		1.0E-42 AF067	1.0E-42 AF067	
	Expression Signal	3.12	\$	0.57	3.65	2.44	5,09	5.09	3.46	122	1.07	4.15	15.12	1.58	1.58	1.5	2.81	2.92	222	7.8	7.8	1.46	1.32	89.0	0.08	1.37	1.21	=	1.18	1.18		16.49	16.49	
	ORF SEQ ID NO:	32662	27864			36849		26168		29541	29670	29589	29809	36475	36476	37297	26902		27879	31379	31380	32429	35596	20898	32808	37880	26143	20441	26495	26496		28841	28842	
	Exen SEQ ID NO:	19619	10780	20375	21369	23600	13510	13510	13803	16911	16943	16964	17278	23241	23241	23895	14213	15134	15146	18465	18465	19416	22302	22603	22603	24334	13490	13778	13837	13837		15583	15563	
	Probe SEQ ID NO:	6704	70	7117	242	10920	738	736	104 4401	4171	4202	4223	4543	10545	10545	11389	1488	2413	2425	929	5670	9864	0741	9955	9955	11742	717	1019	1079	1079		1220	1220	

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Charles and the control of the contr	Signal ORF SEQ Expression (Top) Hit Accession	14439 27137 1.13 1.0E-42 11423218[NT Homo septens rec (LOC51201), mRNA	15291 27998 1.0E-42 6174458 NT Homo sapiens major histocompetibility complex, class II, DM alpha (HLA-DMA) mRNA	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORCSL) mRNA, and translated	28380 10.28 1.0E-42 4505524 NT	29088 2.6 1.0E-42 7662027 NT	1.17 1.0E-42 AL163267.2 NT Homo sepiens chromosome 21 segment HS21C067	16962 29587 1.92 1.0E-42 AL163280.2 NT Homo sepiens chromosome 21 segment HS210080	29918 0.75	30062 1.88 1.0E-42 6803122 NT	17431 30063 1.88 1.0E-42 5803122 NT Homo expiens probesome inhibitor (PI31), mRNA	30097 6.02 1.0E-42 4506758 NT	30378 1.08 1.0E-42 4501912 NT	17763 90379 1.08 1.0E-42 4501912 NT Homo sapiens a disintagrin and metalloproteinase domain 23 (ADAM23) mRNA	22634 35844 4.03 9.0E-43 4757966 NT Homo sepiens chromodomain protein, Y chromosome-like (CDYL) mRNA	26052 19.69 8.0E-43 AV736824.1 EST_HUMAN	28053 19.69 8.0E-43 AV738824.1 EST_HUMAN	26104 5.03 8.0E-43 8823276 NT	28105 6.03 8.0E-43 8923276 NT	13459 26106 6.03 8.0E-43 8923276 Homo sapiens hypothetical protein FL/20297 (FL/20297), mRNA	18408 31321 0.76 8.0E-43 H13952.1 EST_HUMAN 1909e11.11 Sources placenta Nb24P Homo saplens cDNA clone IMAGE:148172 6	29025	wp89b01x1 NCI_CGAP_Bri25 Homo sepiens cDNA clone MAGE:24063985 3' shnifer to TR:O15475 4.09 7.0E-43 Al936748.1 EST_HUMAN O15475 UNNAMED HERV-H PROTEIN ;contains LTR7.b1 LTR7 repetitive element;	20.1 EST_HUMAN	2.25 6.0E-43 AV708201.1 EST_HUMAN	31969		32492 2.09 8.0E-43 AW 488897.1 EST_HUMAN		35607 2.16 6.0E-43 AA195154.1 EST HUMAN	2.55 6.0E-43 AL119158.1 EST HUMAN	•
							i										L						:				L					
	B Exem ID SEQ ID : NO:	1696 14439	2546 15261		2964 15730	3695 16449	3905 16655	4221 16962	4554 17289	4697 17431	4697 17431	4728 17460	44 17763	44 17763	9986 22634	637 13416	637 13416	684 13459	684 13459	684 13459	5612 18408	3632 16385	8067 21359	1321 14070	2600 15314	6219 18923		6808 19469	L	J		138 12953
	Probe SEQ ID NO:	16	%		8	36	88	42	₹	46	46	47.	11 09	5044	8	۳	8	9	8	စ	88	8	8	13	28	8		8		9751	11044	•

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Top Hit Descriptor Source	NT Human TBXAS1 gene for thromboxene synthasa, promoter region and exon 1			NT Human ribosomel RNA upstream binding transcription factor (UBTF) gene, partial ode	ea88f11.s1 Stratagene fetal retina 937202 Homo sepiens cDNA clone IMAGE:838413 3' strillar to contains EST HUMAN THR.t2 THR repetitive element;			ed01c09.xt Scares_testis_NHT Homo sepiens cDNA clone IMAGE:1733968 3' similar to contains PTR7.t3 EST_HUMAN PTR7 PTR7 repetitive element;	hubbapart NCI_CGAP_Bm41 Homo sapiens cDNA clone IMAGE:3173750 3' similer to contains element EST_HUMAN MER40 repetitive element;	hu53e08.x1 NCI_CGAP_Bm41 Homo septens cDNA clone IMAGE:3173750 3' similar to contains element is yet the IMAN MERAD receitive element:	1		EST_HUMAN FB1G5 Fetal brain, Stratagene Homo sapiene cONA done FB1G5 3'end similar to LINE-1			INT Hamo septents phromosome 21 aegment HSZTCU84 Ect. La MAN FROMOSSARFI NCI. CGAP Bringt Homo seniors cDNA clone IMAGE 4157868 5				19940e01.1 Sourse infart brain 1NIB Homo sapiens cDNA clone IMAGE:34732 5' similar to EST HUMAN SP-BD38_MOUSE P29666 BRAIN PROTEIN DN38;	Ī		EST HUMAN EST376749 MAGE resequences, MAGH Homo septens cDNA	EST_HUMAN EST396299 MAGE resequences, MAGB Homo septems oDNA	r		T_HUMAN	EST_HUMAN wb69b04x1 NCL_CGAP_P728 Homo septems GDNA done IMAGE:2313775 3'
Most Similar Top Hit Acession RLASTE No.	72 3.0E-43 D34613.1	24 3.0E-43 7305360 NT	24 3.0E-43 7305360 NT	29 3.0E-43 U65487.1	3.0E-43 AA458824.1	3.0E-43	3.0E-43	77 2.0E-43 Al190784.1	2 0F-43 BF22277	7 OE 43 BE2227	2.0E-43 AW 2073]_			57 1.0E-43 AL163284.2		1.0E-43	1.0E-43	1.0E-43 R19751.		Ŀ		L		1.05-43	1.0E-43 AL13790	39 1.0E-43 AI675416.1
65 ₹ 2	0.72	2.24 3.0E-43	2.24 3.0E-43	4.29		1.87 3.0E-43	0.56 3.0E-43		1.13 2.0E-43 BE22277	1600 BE 30 C	2 2	5.30	4.94 2.0E-43	2.94	294	1.57	0.74 1.0E-43	8.45 1.0E-43	8.46 1.0E-43	1.38 1.0E-43 R19751.	1.13	4.03	25.49	0.08	8.11	4.78 1.0E-43	3.04 1.0E-43 AL13790	1.89 1.0E-43 AI67541
Most Similar (Top) Hit RAST E N	31518 0.72	32013 2.24 3.0E-43	32014 2.24 3.0E-43	32404 4.29	8.38 3.0E-43 AA45882	34554 1.87 3.0E-43	35822 0.58 3.0E-43	7.67 2.0E-43 AI190784	32454 1 13 2 0E-43 BE22277	7000 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	32833 1.32	5.50	4.94 2.0E-43	27080 2.94	27081 2.94	27142 1.57	30788 0.74 1.0E.43	32280 8.45 1.0E-43	32281 8.46 1.0E-43	30542 1.36 1.0E-43 R19751.	33655 1.13	4.03	34574 25.49	36052 0.66	36812 8.11	37332 4.78 1.0E-43	3.04 1.0E-43 AL13790	31079 1.89 1.0E-43 A167541
Expression (Top) Hit Top Hit. Signal Value	0.72	19038 32013 2.24 3.0E-43	19038 32014 2.24 3.0E-43	19390 32404 4.29	20757 8.38 3.0E-43 AA45862	21411 34564 1.87 3.0E-43	22415 35622 0.56 3.0E-43	12991 7.67 2.0E-43 A1190784	19152 32154 1.13 2.0E-43 BE22277	TCCCAR SEA OF SE	19862 32933 1.32	20901	23823 4.94 2.0E-43	14391 27080 2.94	14391 27081 2.94	1.57	30788 0.74 1.0E.43	19279 32280 8.45 1.0E-43	19279, 32281 8.46 1.0E-43	17847 30542 1.36 1.0E-43 R19751.	20528 33655 1.13	20660 4.03	21428 34574 25.49	22837 36052 0.66	23564 36812 8.11	24028 37332 4.78 1.0E-43	24520 3.04 1.0E-43 AL13790	1.89 1.0E-43 AI67541

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	Top Hit Database Source		HUMAN	I HUMAN	NT.			NT					T_HUMAN		NT IN	TN	TN TN	TN	EN LA		EST_HUMAN /	EST_HUMAN	EST HUMAN	TN	TN TN			THUMAN	I	EST HUMAN	TN.	T_HUMAN		EST HUMAN
	Top Hit Acesslon No.	11418322 NT	5.1	5.1	.1	11423497 NT	11423497 NT	.2	.1	11627389 NT	11418086 NT	11418099 NT		5031886 NT	29.1	29.1	34.2		19.1	4505846 NT	39.1	220948.1	4W954050.1	30.1	5.0E-44 AJ280880.1		5.0E-44 AI568523.1		3.2	3E883178.1	1	18.1		3.0E-44 AA169851.1
	Most Similar (Top) Hit BLAST E Value	8.0E-44	8.0E-44	8.0E-44 A122298	8.0E-44 X94354	8.0E-44	8.0E-44	8.0E-44 Y10498	8.0E-44 L29139	8.0E-44	8.0E-44	8.0E-44	7.0E-44 R06035.	7.0E-44	7.0E-44 AF0487	7.0E-44 AF0487	7.0E-44 AL1632	7.0E-44	7.0E-44 AF2319	7.0E-44	7.0E-44 AU1598	8.0E-44 Z20948.	6.0E-44 AW954	5.0E-44 A.128980	5.0E-44		5.0E-44	5.0E-44	4.0E-44	4.0E-44 BE8831	4.0E-44 L21948	4.0E-44 BE1788	4.0E-44	3.0E-44
	Expression Signal	3.41	6.23	6.23	2.67	0.47	0.47	3.78	1.36	4.09	1.38	2.55	0.69	1.05	2.58	2.58	254	1.12	1.12	1.9	228	96.0	1.76	3.3	2.72		4.96	2.34	3.75	99:0	0.78	0.61	5.38	5.77
	ORF SEQ ID NO:	31032	26300	26310	34206	36097	36098	37064	37808	31073	30976	30808		27696	28381	28382	29231	29581	29582	30476	33908	31756	37702				33607		28816	33131	33005		37153	28500
	Een SEQ ID NO:	24835	13839	13639	21129	22884	22884	23787	24283	24673	25009	25186	13423	14958	15732	15732	16594	16958	16958	17860	207702	18793	24372	13102	13124		20483	22038	16167	20050	20863	21469	23866	15859
	Probe SEQ ID NO:	12460	870	870	8437	10238	10236	11117	11688	12207	12248	12580	\$	2228	8887	2962	3843	4217	4217	5142	8085	8012	11781	288	323		7788	9284	3408	23.70	8169	87777	11202	3094

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Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEÇ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession Na.	Top Hit Detabase Source	Top Hit Descriptor
3870	10020	29280	1.37	3.0E-44	3.0E-44 AA337234.1	EST_HUMAN	EST42299 Endometrial tumor Homo sapiens cDNA 5' end similiar to similiar to siphe-1-entiproteinase F
9419	22097	35260	0.55			N	Sus scrofa domestica submardilary aportrucin mRNA, complete cds
1027	13787	28446	2.84	2.0E-44	482885 NT	NT	Homo sapiens DEAD/H (AspGlu-Ala-Asp/Pils) box polypeptide 1 (DDX1) mRNA
1027	13787	26447	2.64	2.0E-44		L	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/Hs) box polypeptide 1 (DDX1) mRNA
1185	13937	26602	3.36	2.0E-44	TN 0025083	LN.	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1185	13937	20003	3.36	2.0E-44	TN 0025083	FZ.	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1289	14038	26711	4.06		2.0E-44 AF133588.1	IN	Homo sapiens RAB36 (RAB36) mRNA, complete cds
1347	14095	28770	67	2.0E-44	2.0E-44 BE485325.1	EST HUMAN	hw14g06.x1 NCI_CGAP_Lu24 Homo septiens cDNA clone IMAGE:3182938 3' stimiter to SW:OXYB_HUMAN P22059 OXYSTEROL-BINDING PROTEIN.;
2147	14877	27012	222	2.0E-44	15.	NT	Homo sapiens tissue-type bone marrow zinc finger protein 4 mRNA, complete cds
2816	15327		1.31	2.0E-44	5901933	N	Home sapiens adaptor-related protein complex 4, sigma 1 subunit (CLAPS4), mRNA
3463	16219	28873	1.13	2.0E-44	D87675	¥	Homo sapiens DNA for amyloid precursor protein, complete cds
4531	17266	29899	<u>z</u> .	2.0E-44	179.1	EST HUMAN	PM4-SN0016-120500-003-g04 SN0016 Homo sepiens cDNA
6004	18785	31747	1.87	2.0E-44	11449901	1	Homo saplens chemokine (C-C motif) receptor 9 (CCR9), mRNA
6738	17927	30502	3.31	2.0E-44	2.0E-44 AF038968.1	N	Homo sepiens general transcription factor 2-I (GTF2I) mRNA, atternatively apticed product, complete cds
7313	19996	33074	4.57	2.0E-44	11419226 NT	N.	Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA
7313	19896	33075	4.67	2.0E-44	11419226 NT	Z	Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA
8327	21020	34155	29.0	20E-44	TN 0729077	N	Homo sapiens vesicle transport-related protein (KİAA0917), mRNA
8327	21020	34156	0.67	2.0E-44	TN 0759077	IN	Homo saplens vesicle transport-related protein (KIAA0917), mRNA
8517	21209	34352	1.58	2.0E-44	BE389058.1	EST_HUMAN	601286914F1 NIH_MGC_44 Homo sepiens cDNA clane IMAGE:3813586 51
				,			TCBAP1E2795 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens
11883	24456		1.62	2.0E-44	2.0E-44 BE244902.1	EST HUMAN	CUNA Cime 1 CBAP2785
3/8	2007		4.	Z.UE-44		Z	TOTO Supports Cat eye syntrome critomoscrop legion, caroname 1 (CECX.1), micro
2	12880	25507	2.43	1.0E-44		Ł	Homo septens Misshapen/NiK-related kinase (MiNK), mRNA
51	12880	25508	2.43	1.0E-44		TN	Homo sapiens Misshapen/NIK-related kinase (MINK), mRNA
999	13347	25975	2.44	1.0E-44 AW853	132.1	EST_HUMAN	RC1-CT0249-030300-028-h12 CT0249 Homo sapiens cDNA
1175	13928		1.9	1.0E-44	1.0E-44 AW994803.1	EST_HUMAN	RC1-BN0039-110300-012-501 BN0039 Homo sapiens cDNA
1567	14314		5.78	1.0E-44	1.0E-44 AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
722	14949	27687	3.74	1.0E-44	1.0E-44 AA434554.1	EST HUMAN	zw33d02.r1 Sceres_total_fetus_Nb2HF8_9w Homo sepiens cDNA clone MAGE:773763 5' similar to contains THR.t3 THR repetitive element;
,,,,,	7,070	27899	2.77	4 OF 44		ECT LI BAAN	ZW53d02.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone.IMAGE:773763 5' similar to
777	Bt et	7/000	1,00	10.1	1	ESI TOMPIN	California III II I I I I I I I I I I I I I I I

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																						_				_					
	Top Hit Descriptor	z188g11.r1 Sceres_testis_NHT Hamo sepiens cDNA clone IMAGE:729476 51	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, 154 protein, 154 protein, 154 protein, 154 protein, 154 protein, 154 protein, 155 p	complete cds; and L-type calcium charmel a>	ea01c09.s1 Sceres_NH-IMPu_S1 Homo sapiens cDNA clone IMAGE:811984 3'	Homo explens alpha satelite DNA, M1 monomer type	Homo sapiens elpha satelite DNA, M1 monomer type	EST379147 MAGE resequences, MAGJ Homo sepiens cDNA	EST379147 MAGE resequences, MAGJ Hamo sapiens curva	Homo sepiens chromosome 21 segment HSZ10009	px88g07xf NCI_CGAP_GC8 Homo sapiens cUNA cione IMAGE:ZU09026 3	AV714608 DCB Hamp sepiens CONA dans DCBBYECS 5	Homo sepiens Sushi domain (SCR repeat) containing (BR65A6.2), mrthA	RCI-CT0198-150900-011-C08 C10198 Homo septiens CUNA	RC1-C70198-150999-011-C08 C70198 Hama espleme aDNA	Homo sepiens hypothetical protein FLJ10379 (FLJ10379), m:NNA	Home sapiens hypothetical protein FLJ10378 (FLJ10378), mrthA	Hamo septens mRNA for KIAA0896 protein, pertial cds	Homo explans TRK-fused gene (NOTE: non-etendend symbol and name) (1FG) midNA	Hamo sepiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA	CMC-NN0005-130300-283-b09 NN0005 Homo seplene cDNA	EST90893 Synovial sercoma Homo septens cDNA 5 end	wbggc06.x1 NCI_CGAP_Pr28 Hamo sepiens cDNA clone IMAGE:2313802 3' similar to contains L1.t1 L1 reportitive element:	au83h07.x1 Schneider fetai brain 00004 Homo sepiens cDNA clone IMAGE:2782809 3' similar to	SW-R13A, HUMAN P40429 60S RIBOSOMAL PROTEIN L13A;	Homo eapiens ADP-ribosylation factor GTPses activating protein 1 (ARFGAP1), mRNA	Homo septens chromosome 21 segment HS210003	CAM-CN0044-180200-515-f01 CN0044 Homo sapiens cDNA	togoto XI NCL CGAP_CLL1 Hamo septens cDNA done IMAGE:2116453 3' similiar to SW:PAX1_MOUSE PO6084 PAIRED BOX PROTEIN PAX-1.;	z/22003.s1 Sceres_bedts_NHT Homo sapiens cDNA clone IMAGE:727877.3' similar to contains element TAR1 repetitive element;	Homo sapiens MCP-1 gene and enhancer region
ממו וומען	Top Hit Database Source	EST HUMAN		¥	EST HUMAN	LΝ	NT	EST HUMAN	EST HUMAN	L	EST_HUMAN	EST HUMAN	Ę	EST HUMAN	EST HUMAN	M	Ä	ΙN	M	NT	EST HUMAN	EST_HUMAN	FST HUMAN		EST HUMAN	NT	LN⊤	EST_HUMAN	EST HUMAN	EST HUMAN	TN
5	Top Hit Acession No.	1.0E-44 AA398099.1		1 0F.44 AF196779.1		1.0E-44 AJ130755.1				1.0E-44 AL163209.2	1.0E-44 Al337183.1	1.0E-44 AV714808.1	10092884 NT	1.0E-44 AW846967.1	4W846967.1	8922391 NT	N 1822391 NT	AB023212.1	5174718 NT	5174718 NT	4W802763.1	AA377995.1	R OF AS AIRTRAPS 1		6.0E-45 AW157570.1	11418213 NT	5.0E-45 AL163203.2	BF333627.1	A1623788.1	AA397781.1	Y18933.1
	Most Similar (Top) Hit BLAST E Velue	1.0E-44		1 05.44	1.0E-44	1.0E-44 /	1.0E-44/	1.0E-44 AW9670	1.0E-44	1.0E-44	1.0E-44	1.0E-44	1.0E-44	1.0E-44	1.0E-44 AW8469	9.0€-45	9.0E-45	9.0E-45 AB02321	8.0E-45	8.0E-45	8.0E-45 AW8927	8.0E-45 AA37796	R OF AR		6.0E-45	6.0E-45	5.0E-45	5.0E-45 BF33362	6.0E-45 AI52378	5.0E-45 AA39778	5.0E-45 Y18933
	Expression Signal	0.96		1 44	3.73	\$	1.04	86.0	96'0	98.0	0.69	4.04	3.92	3.17	3.17	1.38	1.38	1.31	3.12	6.41	0.68	16.0	70,7		4.09	1.65	1.03	3.65	62.1	8.76	1.31
 	ORF SEQ ID NO:	27746		78244		30385	30386	33988	33989	34380			37427	37496	37497	28906		L										27453			
	Exan SEQ ID NO:	15590		45.480	16485	1		20857	20857	Ĺ_	!	L	1	<u>. </u>	L	L	1	Ł	L	L	1	1	<u> </u>	1	16709	L	L		<u>L</u>	1	1
	Probe SEQ ID NO:	2280		2362	3742	5048	5048	8163	8163	8544	8924	10836	11518	11683	11583	4539	4639	6552	2527	5023	4140	8008	7876	3	3960	12556	872	1995	3204	6426	6269

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Γ	-							Π				_	7								_							<u> </u>		٦				٦
	Top Hit Descriptor	Homo sapiens MCP-1 gene and enhancer region	Homo sapiens mRNA for inducible mitric code synthase, complete cds	Horino sapiens mRNA for inducible nitric odde synthase, complete cds	Homo sapiens zinc finger protein 277 (ZNF277), mRNA	Homo sapiens zinc finger protein 277 (ZNF277), mRNA	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA	Homo sapiens programmed cell death 5 (PDCD5), mRNA	Homo saplens golgin-like protein (GLP), mRNA	H.eaplens ART4 gene	801194440F1 NIH MGC 7 Hama septems cDNA done MAAGE:3538425 5	nc28e07.s1 NCI_CGAP_Pr1 Homo sepiens cDNA clone IMAGE:1009284 similar to contains element L1	repellitve element;	yd35f07,r1 Soares fetal liver splean 1NFLS Homo sapiens cDNA clone IMAGE:110245 5	Mus musculus dynein, axon, heavy chain 11 (Dnahct1), mRNA	Mus musculus dynein, axon, heavy chain 11 (Dnahc11), mRNA	AV723976 HTB Homo septens cDNA clone HTBAAG01 5'	Homo sapiens golgi autoantigen, golgin subfamily a, 2 (GOLGA2) mRNA	Homo sapiens chromosome 21 segment HS21C027	Homo sapiens chromosome 21 segment HS21C027	H.sapiens DNA for endogenous retroviral like element	Homo sepiens chromosome 21 segment HS21C018	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5	Human acsinophil Charcot-Layden crystal (CLC) protein (lysophospholipase) gene, promoter and exon 1	601467793F1 NIH MGC_67 Homo septens cDNA clone IMAGE:3870638 5	RCD-LT0001-150200-032-d11 LT0001 Homo sepiens cDNA	ts56a01.x1 NCL_CGAP_Kid8 Homo explens cDNA clone IMAGE:2232552.31	MR0-HT0923-190800-201-s02 HT0823 Homo saplens cDNA	ea87712.r.1 Strategene fetal retina 937202 Homo eaplens cDNA clone IMAGE:838319 5' similar to	TR:G1144569 G1144569 R-SLY1.;	xp72a03.x1 NCI_CGAP_Ov40 Homo sapiens cDNA clone IMAGE:2745868 3'	xp72a03.x1 NCI_CGAP_Ov40 Homo eapiens cDNA clone IMAGE:2745888 3'	Homo sepiens celcium chennel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA	601284350F1 NIH_MGC_44 Hamo sepiens aDNA done IMAGE:3505183 5
	Top Hit Databasa Source	NT	LN	TN	F	노	FN	. LN	N	TN	EST_HUMAN			EST HUMAN	F	NT.	EST_HUMAN	NT	NT	M	Ę	Ę	NT	E	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN		EST_HUMAN	EST_HUMAN	EST HUMAN	NT	EST_HUMAN
Sign of	Top Hit Acesston No.	5.0E-45 Y18933.1	5.0E-45 AB022318.1	5.0E-45 AB022318.1	11496268 NT	11496268 NT	11418704 NT	4759223 NT	TN 8923698	4.0E-45 X95828.1	4.0E-45 BE265622.1		4.0E-45 AA228220.1	T71480.1	6753651 NT	6753651 NT	3.0E-45 AV723976.1	4758451 NT	3.0E-46 AL163227.2	3.0E-45 AL163227.2		2.0E-45 AL163218.2	2.0E-45 A.1243213.1	2.0E-45 L01665.1	2.0E-45 BE782184.1	¥.	2.0E-45 Al636786.1	1.1		2.0E-45 AA458770.1	2.0E-45 AW270280.1	2.0E-45 AW 270280.1	11418157 NT	1.0E-45 BE389855.1
	Most Similar (Top) Hit BLAST E Value	5.0E-45	5.0E-45	5.0E-45	5.0E-45	5.0E-45	5.0E-45	5.0E-45	5.0E-45	4.0E-45	4.0E-45		4.0E-45		3.0E-45	3.0E-45	3.0E-45	3.0E-45	3.0Ё-46	3.0E-45	3.0E-45	2.0E-45	2.0E-45	2.0€.45	2.0E-45	2.0E-45	2.0E-45	2.0E-45		2.0E-45	2.0E-45	2.0E-45	2.0E-45	1.0E-45
	Expression Signal	1.31	0.79	67.0	1.02	20.1	67.0	8.	2.50	95.6	2.42		0.82	1.35	1.36	1.36	1.1	3.74	13.43	13.43	2.35	2.24	1.22	5.15	122	0.78	0.48	18.28		4.16	1.76	1.75	3.93	1.6
	ORF SEQ ID NO:	31670	31717	31718	31842	31843	34000	34773	37617	26536	27750				31890	31891		34526	30008	36069			28441	32194	33274	34145	35318	38633		37073	37400	37401		
	SEQ ID NO:	18713	18756	18756	18874	18874	20868	21630	24292	13877	15014		21546	16085	18920	18920	21043	21382	22854	22854	25314	15223	15795	19197	20181	21007	22138	25130		23707	24089	24089	24987	13185
	Probe SEQ ID NO:	5920	5974	5974	9609	9609	8174	8030	11697	1121	2280		8855	4066	6142	6142	8350	088	10206	10206	12670	2508	3029	6429	7510	8314	9485	10705		11120	11488	11488	12711	120

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wm3178 x1 NCI_COAP_UI4 Homo espiens dDNA done INAGE:2437575 3' similar to contains MER19.t2 MER19 reportative element: MER19 reportative element: MER19 reportative definent: MER19 reportative definent: MER19 reportative definent: MER19 reportative definent: MER19 reportative definent: MER19 reportative definent: MER19 reportative defined: MER1	TOP HIT Detabases Source Source T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN T HUMAN	t Similar AST E AST AST AST AST AST AST AST AST AST AST	Most Similar (Top) Hit BLAST E Value 8.0E-46 6.0E-46 6.0E-46 6.0E-46 6.0E-46 6.0E-46 4.0E-46 4.0E-46 4.0E-46 7.0E-46 al Signal Signal 3.90 3.90 10.94 10.94 10.94 1.07 1.07 1.07 1.08 6.86 6.86 6.86 6.86 2.43 2.43 2.43 2.43 2.43 2.43 2.43 2.43	ORF SEQ. ID NO: 28208 32868 32863 32413 32413 32413 32570 27140 27140 27140 27140 300834 300834 310144 277884	Exan SEQ ID NO: 15464 19804 13012 13012 16275 1687 19687 17442 1744 1744	Probe SEQ ID NO: NO: NO: NO: NO: NO: NO: NO: NO: NO:	
Homo sapiens mitogen-activated protein kinase kinase kinase kinase 3 (MAP4K3), mRNA H. sapiens ig tembda light chain variable region gene (7c.11.2) germline; ig-Light-Lambda; VLambda	NT	3.0E-46 4506376 NT 3.0E-46 Z73690.1 NT	3.0E-46				4362
ion to septiens y Awressociation 33 NOs protein minuty, compress cos tomo sabiens miltoen-activeted brotein kinasa kinasa kinasa kinasa (MAP4K3), mRNA	Z	AF160212.1 4506378	3.0E-46				4362
The section of the se		, 6,666.7	2 0				
John Capitale D'O' IN INTERESTATION OF CONTINUE AND PROPERTY AND PROPERTY (CE COSE) AND A CONTINUE CONTINUE CONTINUE AND PROPERTY (CE COSE) AND A CONTINUE CONTINUE CONTINUE AND A CONTINUE		ADVIENCE: 1	1.V.F			₋Ⅱ	3466
iono saniana DNA for Human P2XM, completa cda	FN	ARM02050 4	4 0F 48				12513
luman ig germline gamma-3 heavy-chain gene V region, partial cds	NT	M36852.1	4.0E-48				5350
tuman ig germilne gamma-3 heavy-chain gene V region, partial cds	NT	M36852.1	4.0E-46	2.43			5350
lomo sapiens mRNA for KIAA0622 protein, partial ods	NT	AB014522.1	4.0E-48				4384
formo septems mRNA for KLAAU622 protein, perties cos	L	AB014522.1	4.0E-46				<u>\$</u>
Innan eroogerous retoway K I VL-1/2	ž	M18048.1	4.0E-46			\perp	2/43
uman endocencus natrovinus RTVI12	NT	MIROAR 1	4 OF 48	280	l		77.43
186c03.xt NCL_CGAP_Lu24 Homo sepiens cDNA clone IMAGE:3008836 3' similær to gb:X14008_me1 YSOZYME C PRECURSOR (HUMAN);contains element MER37 repetitive element ;	EST_HUMAN	AW770544.1	4.0E-46	6.86			1699
186c03.x1 NCI_CGAP_Lu24 Homo explens cDNA clone IMAGE:3008836 3' similar to gb:X14008_ma1 :YSOZYME C PRECURSOR (HUMAN);contains element MER37 repetitive element ;	EST_HUMAN	AW770544.1	4.0E-46				1089
o54e00.¢1 NCI_CGAP_SS1 Homo espiens cDNA clone IMAGE:1104520 3' similar to gb:X53741_ms1 IBULIN-1, ISOFORM A PRECURSOR (HUMAN);		AA801143.1	4.0E-46	1.4			929
162c08.s1 Sogres_testis_NHT Homo saplens cDNA clone IMAGE:726926 3'		AA398381.1	5.0E-46	0.47		١.	9615
V4-ST0212-120100-075-f09 ST0212 Homo saplens cDNA		AW582253.1	5.0E-46			l _	9895
02021164F1 NCI_CGAP_Bm67 Hamo sepiens cDNA clone IMAGE:4156670 5		BF347228.1	5.0E-46				6842
esi38f07.x1 NCI_CGAP_Kid11 Homo espiens cDNA clone IMAGE:3258757 3' similar to TR:075202 375202 HOMOLOG OF RAT KIDNEY-SPECIFIC;		BF590442.1	5.0E-46				9838
d81g01.x1 Lupski_dorsal_root_ganglion Homo sapiens cDNA done IMAGE:3279408 3'	EST_HUMAN	BE677194.1	5.0E-48			l	3519
d81g01.x1 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'	EST_HUMAN	BE677194.1	5.0E-46				3519
omo sapiens chromosome 21 segment HS21C010		AL163210.2	5.0E-48	8.9			199
01478409F1 NIH MGC 68 Hamo sepiens oDNA clane IMAGE:3880995 5		BE784971.1	6.0E-46	2.04			11364
o42e04.x1 NCI_CGAP_Ut1 Homo sepiens cDNA clone IMAGE:2706654 3' similar to gb:L08069 DNAJ ROTEIN HOMOLOG 2 (HUMAN);		AW513244.1	6.0E.46	0.72			7116
A GENE.;	EST_HUMAN	AI635448.1	6.0E-46	10.94			9038
59810 x l NCI CGAP Kide Home sepiens cDNA clone IMAGE-2232835 3' similar to TR: 0e0363 0e0363							
IER 19 repetitive element;	EST_HUMAN		6.0E-46				2750
m31f08x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:24375753' similar to contains MER19.t2							
Top Hit Descriptor	Top Hit Detaberse Source	Top Hit Acession No.	Most Similar (Top) Hit BLAST E Value	Expression Signal			Probe SEQ ID NO:
	316 mya						

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	H. sepiens ig iembde light chain variable region gene (7c.11.2) germilne; ig-Light-Lambda; VLambda	wj49c04.x1 NCI_CGAP_Lu19 Homo sepiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR repetitive element;	Human mRNA for KIAA0061 gene, partial cds	ne08a09.s1 NCI_CGAP_Co3 Homo sepiens oDNA done MACE:880408 3' similar to contains THR.b2 THR necessitive element:	227a11.s1 Soares_fatal_liver_spleen_1NFLS_S1 Homo sepiens cDNA clone IMAGE:431996 3'	Homo sapiens Bruton's tyrosine kinese (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete ods	259e02.rl Scenes_beets_NHT Hamo septens cDNA clone IMAGE:720650 5' similar to SW:RSP1_MOUSE	Mus musculus anem tall associated protein (Stap), mRNA	601445137F1 NIH MGC 65 Homo septems cDNA clone IMAGE:3849297 51	y32d01.r1 Soares fetal liver spleen 1NFLS Homo saplens cDNA done IMAGE:200977 5	xq78h03.x1 NCI_CGAP_Lu34 Homo sepiens cDNA clone IMAGE:2756789 3'	Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA	Homo sapiens KiAA0565 gene product (KIAA0555), mRNA	EST390625 MAGE resequences, MAGP Homo saplens cDNA	EST48b095 WATMI Hamo seplens cDNA clone 48b095	Inp78b02.s1 NCI_CGAP_Pr2 Homo sepiens oDNA clone MAGE:1132395 similar to gb:X78717 H.sepiens MT-11 mRNA_(HUMAN);	Homo sapiens mRNA for KIAA0980 protein, partial cds	7092b01x1 NCI_CGAP_Ov18 Hamo saplens cDNA clone IMAGE:36437053'	Homo saplens centaurin-eighe 2 protein (HSA272195), mRNA	Homo saplens centauth-eigha 2 protein (HSA272195), mRNA	7062601x1 NCI_CGAP_Ov18 Hamo sapiens cDNA clone IMAGE:3843705 3'	df50e03.y1 Marton Fetal Cochies Hamo septems aDNA alone IMAGE:2488861 51	df50e03.y1 Morton Fetal Cochles Homo sapiens cDNA done IMAGE:249861 5	602072284F1 NCI_CGAP_Bm67 Hamo sepiens cDNA clone IMAGE:4215398 5	602072284F1 NCI_CGAP_Bm67 Hamo sepiens cDNA clane IMAGE:4215398 5	AV716377 DCB Hamo espiens aDNA clane DCBAIE03 5'	Homo sepiens Xq pseudoautosomel region; segment 1/2
jie Exon Pro	Top Hit Database Source	N.	EST_HUMAN	N	HST HIMAN	EST_HUMAN	¥		ESI HOMAN	EST HIMAN	EST HUMAN	EST_HUMAN	LN TN	TN	NT	EST_HUMAN	EST_HUMAN	EST HUMAN	Ę	EST_HUMAN	¥	M	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	눌
Sing	Top Hit Acession No.	3.0E-46 Z73680.1	3.0E-46 AI831462.1	3.0E-46 D31765.1	2 DF-46 AA488648 1	2.0E-46 AA678248.1		Ţ,	2.0E-46 AA388286.1 ES	2 0F-46 RFR9151 1	2.0E-46 H48391.1	2.0E-46 AW 277214.1	4502694 NT	7682177 NT	7682177 NT	1.0E-46 AW978516.1	1.0E-46 H97330.1	1.0E-46 AA631912.1		1.0E-46 BF194707.1	8923762 NT	8923762 NT	1.0E-46 BF194707.1	1.0E-46 AW023178.1	1.0E-46 AW023178.1	1.0E-46 BF631102.1	1	1.0E-46 AV715377.1	9.0E-47 AJ271735.1
	Most Similar (Top) Hit BLAST E Value	3.0E-46	3.0E-48	3.0E-46	2 OF 46	2.0E-48	2.0E-46		2.0E-40	2 OF 46	2.0E-48	2.0E-46	1.0E-46	1.05-46	1.0E-48	1.0E-48	1.0E-46	1.0E-48	1.0E-48	1.0E-46	1.0E-46	1.05-48	1.0E-48	1.0E-46	1.0E-48	1.0⋶-48	1.0E-46	1.0E-48	9.0E-47
	Expression Signal	1.2	7.59	2.19	7.64	1.66	3.43		12	1.68	1.5	3.38	79.7	1.23	1.23	3.44	3.08	4.65	3.17	6.88	8.14	8.14	5.27	1.53	1.53	2.28	2.28	2.37	6.18
	ORF SEQ ID NO:	30082	34483	37474	28086		27070		30238	7		30902	28628	5688	27000	27745	27857	28654		31322	31617	31618	31322	37865	37868	31115	31116		
1	Exan SEQ ID NO:	17456	21330	24163	13588	14301	14383		1/045	20063	25179	25170	13961	14313	14313	15005	15120	16005	17549	18409	25080	25080	18409	24338	24338	24564	24564	25032	13522
	Probe SEQ ID NO:	4724	8647	11584	2,7	1554	1637		1987	890	12257	12575	1211	1566	1566	2279	2399	3243	4818	5613	5888	5888	10770	11747	11747	12044	12044	12778	750

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					5	יייו ווייחם סופ	Oligio Excitationed Expression in Digital
Probe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Detabase Source	Top Hit Descriptor
4879	17606	30229	3.02		9.0E-47 AW 770928.1	EST_HUMAN	M83604.X1 NCI_CGAP_Lu24 Homa sapiens cDNA clone INACE:3009534.3' similar to TR:075703 075703 HYPOTHETICAL 12.4 KD PROTEIN.;
6284	19057	32037	0.0	9.0E-47	11425439 NT	NT	Homo sapiens zino finger protein ZNF286 (ZNF286), mRNA
12631	25270	30725	2		11417988 NT	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
1801	14541	27252	6.88		8.0E-47 Y18536.1	NT	Homo saplens HLA-C gene, exon 5, Individual 18323
1801	14541	27253	6.88		8.0E-47 Y18536.1	NT	Homo sapiens HLA-C gene, excn 5, individual 19323
2722	15429	28167	1.04	8.0E-47	6463965 NT	Ę	Homo sepiens protein phosphatase 2, reguletory subunit B (B56), epsiton isoform (PPP2R6E) mRNA
3024	15790	L	1.89		8.0E-47 AJ229043.1	Z	Homo sapiens 959 lds contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
3613	16366		99'0		8.0E-47 AB041926.1	Z	Homo sapiens mRNA for GCK family kinase MINK-2, complete cds
3613	16366	28010	0.68		8.0E-47 AB041926.1	M	Homo sapiens mRNA for GCK family kinase MINK-2, complete cds
12004	25169		1.38		7.0E-47 AV683284.1	EST_HUMAN	AV683284 GKC Homo seplens oDNA clane GKCASH11 5'
2650	15285	28000	1.68		6.0E-47 AL163246.2	IN	Homo septens chromosome 21 segment HS210048
8682	21284	34423	0.40	6.0E-47	U77054.1	EST_HUMAN	HSU77054 Human Homo saplens cDNA clone N7
9176	21846	35012	6.78		6.0E-47 AI695189.1	EST HUMAN	ESBINOZYI NGL CGAP_K0411 Hamo septems cDNA done IMAGE:2296659 3'
9812	22285	35450	99.0		6.0E-47 AB042824.1	NT	Homo sapiens RECQL5 bets mRNA for DNA helicase recQ5 bets, complete ods
9612	22285	35451	99.0		6.0E-47 AB042824.1	NT	Hamo septens RECQL5 beta mRNA for DNA helicase recQ5 beta, complete cds
6482	19249	32240	6.67	5.0E-47	11423972 NT	IN	Homo sapiens CDC37 (cell division cycle 37, S. cerevisiae, homolog) (CDC37), mRNA
10696	23387		123		5.0E-47 M78590.1	EST_HUMAN	EST00738 Fetal brain, Stratagene (oat#836208) Homo sapiens cDNA olone HFBCF07
1378	14128	26801	320	4.0E-47	TN 9527554	TN	Homo saplens E1A binding protein p300 (EP300) mRNA
6733	19567	32599	6.1		4.0E-47 BE93898.1	EST HUMAN	MR4-TN0108-280800-201-404 TN0108 Homo sepiens cDNA
8379	21072	34210	2.42		4.0E-47 BE616483.1	EST HUMAN	801280488F1 NIH_MGC_39 Homo septems oDNA done IMAGE:3622437 5
8378	21072	34211	2.42		4.0E-47 BE616483.1	EST HUMAN	601280486F1 NIH_MGC_39 Hamo saplens cDNA done IMAGE:3622497 5
8516	21208	13676	19.0		4.0E-47 AW993777.1	EST_HUMAN	RC3-BN0034-220300-015-f06 BN0034 Homo sapiens cDNA
						1	xx88b07.x1 NCI_CGAP_Lym12 Homo septiens cDNA done IMAGE:2848597 3' similar to SW::NT6_MOUSE
11635	24232		2.83		4.0E-47 AW 51 5509.1	EST HUMAN	GOAZSZ VITAL IN TEGRALION STIE FROTEIN IN 1-6, [1];
531	13316	25950	2.05		3.0E-47 BE907634.1	EST_HUMAN	601497639F1 NIH_MGC_70 Harno septens cDNA done IMAGE:3899721 5
531	13315		2.05		3.0E-47 BE907634.1	EST HUMAN	601497639F1 NIH_MGC_70 Homo sepiens cDNA done IMAGE:3899721 5
799	13571	76232			3.0E-47 N57483.1	EST HUMAN	ly54b04.s1 Scares_multiple_sclerosis_2NbHMSP Hamo sepiens cDNA done IMAGE:277327 3'
924	13691	26355	10.25		3.0E-47 AL163284.2	NT	Homo sapiens chromosome 21 segment HS210084
3296	16058	70782	62'0	3.0E-47	4504116 NT	M	Homo seplens glutamete receptor, londropic, lainete 1 (GRIK1) mRNA
3948	16698		27.5		3.0E-47 U83181.1	NT	Homo sapiens nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds
4329	1	29698	1.32		3.0E-47 M12959.1	ᅜ	Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds
2652	18707	31659	5.41		3.0E-47 AW 408800.1	EST HUMAN	UHHF-BM0-edic-07-0-UI,r1 NIH_MGC_38 Homo sepiens cDNA clone IMAGE;3063205 5

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2259	18707	31660	5.41	3.0E-47	3.0E-47 AW408800.1	EST_HUMAN	UI-HF-BM0-edxc4-07-0-UI.r1 NIH_MGC_38 Hamo sepiens cDINA clane IMAGE:3063205 5'
6469	19236		1.78	3.0E-47	3.0E-47 At222413.1	EST_HUMAN	ch04e07.x1 Sceres_NFL_T_GBC_S1 Hamo septems aDNA clane IMAGE:18437153'
8732	21424	34569	0.71	3.0E-47		EST HUMAN	EST375889 MAGE meequences, MAGH Hamo sepiens cDNA
8732			17.0	3.0E-47	3.0E-47 AW963796.1	EST_HUMAN	EST375869 MAGE resequences, MAGH Homo sepiens oDNA
143	12958	25600	1.61	2.0E-47	4505318 NT	NT	Homo sapiens myosh phosphatase, target subunit 2 (MYPT2), mRNA
947	13713		2.69	2.0E-47		NT	Homo saplene chromosome 21 segment HS21 0009
247	13713	26378	2.69	2.0E-47	2.0E-47 AL163209.2	NT _	Homo sepiens chromosome 21 segment HS210009
1560	14307		96.0	2.0E-47		EST_HUMAN	wq96b02.x1 NCI_CGAP_GC8 Homo septens cDNA clone IMAGE:2478851 3'
1588	14334	27022	1.75	2.0E-47	TN 6012897	Ę	Homo sapiens KIAA0428 gene product (KIAA0428), mRNA
1673	14418	27111	3.41	2.0E-47	2.0E-47 AA524514.1	EST HUMAN	ng43h12.s1 NCI_CGAP_Cc3 Homo sepiens cDNA done IMAGE:837607 3'
4313	17052	729677	2	2.0E-47	4504888	TN	Homo saplens ring finger protein (C3HC4 type) 8 (RNF8), mRNA
4351	17090	29722	1.5	2.0E-47	2.0E-47 AA569592.1	EST HUMAN	mf23g07.s1 NCI_CGAP_Pr1 Hamo sapiens cDNA clone IMAGE:914652
4351	17090	28723	1.5	2.0E-47	2.0E-47 AA568592.1	EST_HUMAN	mf23g07.s1 NCI_CGAP_Pr1 Hamo sepiens aDNA done IMAGE:914652
4471	17206	29832	1.98	2.0E-47	5174648	N _T	Homo sapiens RewRex activation domain binding protein-related (RAB-R) mRNA
4761	17403	30121	1.3	2.0E-47	2.0E-47 AW985168.1	EST_HUMAN	EST377239 MAGE resequences, MAGI Homo sepiens cONA
2898	18490	31411	1.12	2.0E-47	2.0E-47 AF073921.1	NT.	Homo sepiens regulator of G-protein signaling 6 variant form (RGS6) mRNA, complete cds
5887	18673	31615	1.23	2.0E-47	2.0E-47 BE778475.1	EST_HUMAN	601463832F1 NIH_MGC_67 Homo sapiens cONA clane IMAGE:3867487 5'
2883	18873	31616	1.23	2.0E-47	2.0E-47 BE778475.1	EST_HUMAN	601463932F1 NIH_MGC_67 Homo sapiens cONA clane IMAGE:3867487 5'
7598	25116		1.43	2.0E-47	1	NT	Homo sapiens 5-hydroxyfryptamine 1D receptor pseudogens with an Alu repeat insertion
7864	69902	33886	1.92	2.0E-47	1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
7864	50569	98988	1.92	2.0E-47	2.0E-47 D87675.1	TN	Homo sapiens DNA for emyloid precursor protein, complete cds
8618	21310		1.67	2.0E-47	2.0E-47 AF071771.1	NT	Homo sepiens SPH-binding factor mRNA, partial cds
6826	15022	35222	0.77	2.0E-47	TN 828138 NT	M	Homo sapiens BTG family, member 3 (BTG3), mRNA
11451	23218	36451	1.27	2.0E-47	2.0E-47 M78125.1	NT	Human tyrosine khase receptor (ad) mRNA, complete cds
							y92e08.s1 Soares infant brain 1NIB Homo sepiens cDNA done IMAGE:29966 3' similiar to contains OFR
12077			1.75	2.0E-47	ı	EST HUMAN	repetitive element;
1384	14131	28804	7.35	1.0E-47	1.1	EST_HUMAN	qp89h03.x1 Soares_fetal_lung_NbHL19W Homo saplens cDNA clone IMAGE:1831189 3'
5017	17738		1.96	1.05-47	1.0E-47 AW813906.1	EST_HUMAN	RC3-ST0197-130400-017-h02 ST0197 Homo septems cDNA
9044	19426	32441	6.70	1.0E-47	1.0E-47 AI880896.1	EST HUMAN	et19e00.xt Berstead earte HPLRB6 Homo septens cDNA clone IMAGE:2355586 3' similar to gb:M22995 RAS-RELATED PROTEIN RAP-1A (HUMAN):
8707	<u> </u>	<u> </u>	0.56	1.0E-47	£8.1	EST HUMAN	h84a11.x1 Source_NR_T_GBC_S1 Homo sepiens dDNA clone IMAGE:2978972.3' similar to gb:M283.28 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
10254	1_	36112	228	1.0E-47	Γ	Į.	Peplo hamadryas alcohol dehydrogenase class I (ADH) gene, 5' region

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Probe SEQ ID NO: 1607 11080 1128 1128 1128 11483		§ 0	Signal Si		AF223391.1 BE888196.1 BE888196.1 BE888196.1 BE888196.1 BE888196.1 ANT23240.1 BE33198.1 ANT23240.1 ANT24240.1 ANT24240.1 ANT24240.1 ANT24240.1 ANT24240.1 ANT24240.1 ANT24240.1 ANT24240.1 A	Top Hit Detablese Source Source Source Source Source EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN NT NT NT NT NT NT NT NT NT NT NT NT NT	Top Hit Detablese Source Homo sapiens calchun channel alphatE subunit (CACNATE) gene, excris 7-49, and partial cde, alternatively solute acidem channel alphatE subunit (CACNATE) gene, excris 7-49, and partial cde, alternatively solute acidem calchanges acidem channel alphatE subunit (CACNATE) gene, excris 7-49, and partial cde, alternatively solute acidem calchanges aci
9022	21712	34866	1.74	6.0E-48 AF02681	AF026816.1 11427428	NT	Homo sapiens putative oncogene protein mRNA, partial ods Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA
9588 3304 8474 11603 10878	22241 17876 21186 24202 23558		3.00 3.00 3.00 3.00 3.00 3.00 3.00 3.00	6.0E.48 5.0E.48 5.0E.48 5.0E.48 4.0E.48	AA189080.1 4826891 BE064410.1 AW 890299.1 Ale20420.1	EST_HUMAN NT EST_HUMAN EST_HUMAN EST_HUMAN	zq45b06.s1 Stratagene hNT neuron (#937233) Homo saplens cDNA clone IMAGE:632627 3' similar to contains Alu repetitive element. Homo saplens phosphodiesterase 1A, calmodulin-dependent (PDE1A) mRNA RC4-BT0311-141199-011-h06 BT0311 Homo saplens cDNA MR0-NT0039-010500-002-708 NT0039 Homo saplens cDNA tu47a02.x1 NCI_CGAP_Pr28 Homo saplens cDNA clone !MAGE:2254154 3'
1364	14112	26786	1.27	3.0E-48		EST_HUMAN	AV690064 GKC Homo sepiens cDNA dane GKCDRE12 57

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	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA	Homo seplene chromosome X open reading frame 6 (CXORF6) mRNA	htt4b12.x1 NCI_CGAP_GU1 Hamo septens aDNA done IMAGE:2972255 3' similer to SW:DCRB_HUMAN AN PS6555 DOWN SYNDROME CRITICAL REGION PROTEIN B.;	Т	Г	Inv03f05.s1 NCI_CGAP_Pr22 Homo septens cDNA clone MAGE:1219137 3' similer to contains PTR5.b1	Т	Т		TCBAP1D3842 Pediatric pre-B cell acute lymphoblastic leukernia Baykor-HGSC project=TCBA Homo	Т	Т	Т	Homo septens mRNA for KIAA1501 protein, pertial cds	Homo sapiens v-rei avian reticuloendotheliosis viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (p55)) (RELA), mRNA	П	П	AN 601305064F1 NIH_MGC_39 Homo septens cDNA clone IMAGE:3639782 5		Home saplens displatin resistance-associated overexpressed protein (LOC51747), mRNA	Homo septens amyold beta (A4) precursor protein (protesse neatn-II, Alzheimer disesse) (APP), mRNA	Homo septens RNA binding modif protein 6 (RBM6) mRNA	Homo saplens chromosome 21 segment HS21C102	Homo saplens chromosome 21 segment HS21C046	Human endogenous retrovinal DNA (4-1), complete retrovinal segment	kd17c01x1 NCI_CGAP_Co18 Homo septens cDNA clone IMAGE;2075904 3' similar to TR:O14598 O14598 AN SIMILARITY TO U73941;
Top Hit Derbabese Source	LΝ	F	EST HUMAN	EST HUMAN	¥	NAMI IL TAB	EST HIMAN	EST HUMAN	EST HUMAN	MAN ILI TOD	EST HUMAN	EST HUMAN	N	F	¥	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	뉟	N.	۲	N.	NT	EST_HUMAN
Top Hit Acession No.	4885170 NT	4885170 NT	3.0E-48 AW 664531.1	3.0E-48 BE084571.1	3.0E-48 AF087913.1	3 OF 48 4 4 REDOCK 4	2.0E-48 RER14170 1	2.0E-48 AA631940.1	2.0E-48 H24278.1	2 OE 48 DE344045 4	2.0E-48 AA613171.1	2.0E-48 AA613171.1	2.0E-48 AB040934.1	2.0E-48 AB040834.1	11498238 NT	AV7434	2.0E-48 AA465007.1	2.0E-48 BE737154.1	2.0E-48 H24278.1	7706534 NT	4502166 NT	5032032 NT	1.0E-48 AL163302.2		1.0E-48 M10976.1	1.0E-48 AI889077.1
Most Similer (Top) Hit BLAST E Value	3.0E-48	3.0E-48	3.0E-48	3.0E-48	3.0E-48	3 05 48	3 OF 48	2.0E-48	2.0E-48	2 05 40	2.0E-48	2.0E-48	2.0E-48	2.0E-48	2.0E-48	2.0E-48	20E-48	2.0E-48	2.0E-48	1.0E-48	1.0E-48	1.0E-48	1.0E-48	1.0E-48	1.0E-48	1.0E-48
Expression Signal	15.26	15.28	0.75	247	9.0	3.44	0.50	17.	5.15	5	0.61	0.61	4.77	4.77	3.35	1.33	4.27	1.86	1.34	2.3	17.13	3.77	30.36	96.0	1.8	1.17
ORF SEQ ID NO:	27422	27423	29017				36708	25495		7000	31438			33183	33197	34084	30486	30820		25511	26283	28691	27350	28894	30388	31948
SEQ ID	14705	14705	16375	18394	l	20064	22467	12873	13949	47724	18516	18516	20098	20096	20100	20947	17888	25232	13949	12883	13623	14023	14648	16238	17780	18971
Probe SEQ ID NO:	1969	1969	3622	280	6949	929	10784	4	1197	7077	5724	5724	7419	7419	7432	8253	12041	12367	12716	54	858	1273	1911	3481	5061	6195

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.		Top Hit Detablese Source
9198	18971	31947	1.17		1.0E-48 AI889077.1	EST_HUMAN	td17c01.x1 NCI_CGAP_Co16 Hamo sepiens cDNA clone IMAGE:2075904.3' similar to TR:014598 014598 SIMILARITY TO U73941;
6407	19176		0.94	1.0E-48	1.0E-48 Y18000.1	NT	Homo saplens NF2 gene
9200	19265	32268	0.71	1.0E-48	1.0E-48 AB028994.1	NT	Homo saplens mRNA for KIAA1071 protein, partial cds
88	19266	32267			1.0E-48 AB028994.1	NT	Homo sapiens mRNA for KIAA1071 protein, partial cds
7157	19844	32913			4755137 NT	NT	Homo sepiens huntingtin (Huntington disease) (HD) mRNA
8730	21422	34568	0.76	1.0E-48	4758695 NT	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 13 (MAP3K13), mRNA
8730	21422	34567			4758695 NT	TN	Homo sapiens mitogen-activated protein kinase kinase kinase 13 (MAP3K13), mRNA
1 3	21801	34966	0.84		4502838 NT	NT	Homo sapiens Chedials-Higashi syndrome 1 (CHS1) mRNA
94 88	21838	35004			1.0E-48 AB033071.1	NT	Homo saplens mRNA for KIAA1245 protein, pertial cds
<u>8</u>	22134	35314			BF30488	EST_HUMAN	601888096F1 NIH_MGC_17 Homo sepiens cDNA clone IMAGE:4122119 5'
10289	22917	36127	4.08		11429808 NT	NT	Homo saplens B cell linker protein (SLP65), mRNA
10289	22917	36128	4.08		1.0E-48 11429808 NT	NT	Homo saplens B cell linker protein (SLP65), mRNA
2002	14737	27461	1.13		AB026497.1	NT	Mus musculus MysPDZ mRNA for myosin containing PDZ domain, complete cds
2962	18744	31704	3.43		10048417 NT	NT	Mus muscultus T-box 20 (Tbx20), mRNA
2962	18744	31705	3.43	8.0E-49	10048417 NT	NT	Mus musculus T-box 20 (Tbx20), mRNA
8194	20888	34028	3.17	8.0E-40		NT	Human Inostita 1,4,5 trisphosphate receptor type 1 mRNA, partial cds
88	22539	35733	1.15		8.0E-49 AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
135	13171	25814	1	7.0E-49	5729990 NT	IN	Homo saplens protessome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
135	13171	25815	1	7.0E-49	5729990 NT	NT	Homo saplens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
훬	13171	25814	1.73	7.0E-49	6729990 NT	NT	Homo sapiens protessome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
훷	13171	25815		7.0E-49	5728990 NT	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
8	13171	25814		7.0E-49	5729990 NT	INT	Homo saplens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
ଞ୍ଚ	13171	26815	2.94	7.0E-49	6729990 NT	IN	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
1 38	13951	20615	3.4	7.0E-49	7.0E-49 AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
20.0	200	2000	****	L		100	wf25h04.x1 Soares_NRT_GBC_S1 Homo septems cDNA clone IMAGE:2356063 3' similar to TR:054923
2 6	101/3	2000	7.17	701	7.0E-49 AIBO/191.1	TOT HUMAN	OSASZS ROECTB.;
<u> 1</u>	3	2000	2	1.0C-48	ALI 20857. I	NOMOL 183	WINTERFORCES ST. 102 (a) Indiany III. Intrinst. J. Indian Butter Brown Control
5716	18173	30862	0.67	7.0E-49	7.0E-49 AI807191.1	EST_HUMAN	054023 RSEC15.
8	13005	25646	19 12	S OF 40	6 OF 40 AW731740 1	FST HIMAN	be55g05.xf NIH_MGC_10 Homo septens cDNA clone MAGE:2800504.3' strillar to gb:X17206.40S RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20632 Mouse LLRep3 protein mRNA from a repetitive element, complete (MOUSE):
Ş	16837	29484	127	8 OF 49	8 0F-49 At 162091 1	Т	DKF207814138 at 781 (syncovm: hamv2) Homo sanlens cDNA close DKF25781A138 3
1						٦	

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Table 4
Single Exon Probes Expressed in Brain

Top Hit Descriptor	AU140742 PLACE4 Homo expiens cDNA clone PLACE4000148 5	hd44602x1 Sogres NFL_T_GBC_S1 Hamo supiens aDNA done IMAGE:2912378 3' similar to TR:095636 O95636 CAMP-REGULATED GUANINE NUCLEOTIDE EXCHANGE FACTOR II.;	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA	UHH-BI3-80-4-05-0-UI.s1 NCI_CGAP_Sub5 Homo septens cDNA clone IMAGE:3068048 3'	EST77625 Pencreas tumor III Homo sapiens cDNA 5' end	EST77525 Pancreas tumor III Homo saplens cONA 5' and	zj29c08.s1 Scares_fetai_liver_spieen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451694.3'	Homo sapiens chromosome 21 segment HS21C010	Homo sapiens chromosame 21 segment HS21C010	2p29c07.r1 Strategene neuroopithelium (#837231) Homo sepiens cDNA clone IMAGE:610990 5' eimiliar to TR:0233229 0233226 RTVL-H PROTEIN, ;contains LTR7.t3 LTR7 LTR7 repetitive element;	Homo sepiens putative fumor suppressor ST13 (ST13) mRNA, complete cds	Homo saplens similar to ribosomal protein S27 (metallopanstimulin 1) (H. saplens) (LOC83382), mRNA	xi08b01.x1 NC_CGAP_Lt4 Homo septens cDNA done IMAGE:2675593 3' similar to WP:B0350.2B CE06703;	Homo sepiens UDP-N-acetyt-alpha-D-galactosamine:polypeptide N-acetytgalactosaminytransfenase 8 (GaINAo-T8) (GALNT8), mRNA	Homo saplens UDP-N-acetyt-alpha-D-galactosamine:polypeptide N-acetygalactosaminytransferase 8 (GaINAc-T8) (GALNT8), mRNA	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA	Homo sepiens copine III (CPNE3), mRNA	Homo septens copine III (CPNE3), mRNA	z/80/05.r1 NCI_CGAP_GCB1 Homo septems cONA done IMAGE:882977 5	Homo septems glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) connes, complete cds	H. sepiens mRNA for acetyl-CoA carboylese.	2831005-1 Soares retina N2b4HR Homo sepiens cDNA done IMAGE:300584 5 stimilar to contains L1.t3 L1 repetitive element;	Human type IV collagen (COL4A8) gene, excn 40	EST25e12 WATM1 Homo saplens cDNA clone 25e12
Top Hit Database Source	EST HUMAN /	EST_HUMAN C			EST_HUMAN	EST_HUMAN E	EST_HUMAN E	EST_HUMAN 2	NT IN	NT TN	EST_HUMAN	1		EST_HUMAN C						THUMAN	<u> </u>			Į.	EST_HUMAN E
Top Hit Acession No.	6.0E-49 AU140742.1	_	9910293	D010283 NT	4W452218.1	6.0E-49 AA386556.1	6.0E-49 AA388556.1	4A707567.1	5.0E-49 AL163210.2	1.2	5.0E-49 AA172121.1		11436355 NT	4.0E-49 AW189533.1	11525737 NT	11526737 NT	7662209 NT	11425374 NT	11425374 NT	4.0E-49 AA210798.1	3.1		_		
Most Similar (Top) Hit BLAST E Value	6.0E-49	6.0E-49 AW5112	6.0E-49	6.0E-49	6.0E-49 AW 4522	6.0E-49	8.0E-49	8.0E-49 AA70756	5.0E-49	5.0E-49 AL 163210	5.0E-49	5.0E-49 U17714.1	5.0E-49	4.0E-49	4.0E-49	4.0E-49	4.0E-49	4.0E-49	4.0E-49	4.0E-49	4.0E-49 AF24078	3.0E-49 X08968.1	3.0E-49 AA016131	3.0E-49 U46999.1	3.0E-49 H39479.1
Expression Signal	46.0	0.69	0.45	0.45	2.6	2.6	2.6	2.03	7	7	3.49	4.25	2.64	47.84	0.95	0.95	80	0.47	0.47	421	4.1	1.73	1.9	233	11.87
ORF SEQ ID NO:	32109	33078	35478	35479	37202	87878	37580		20117	26118	27235	28201	28678	1Z85Z	32930	32931	33488	34604	34605			25961		30264	33081
Exan SEQ ID NO:	19119	19997	22285	22285	23910	24257	24257	25151	13470	13470	14527	15459	16029	13296	19858	19858	20374	21465	21455	25368	24730	13330	15364	17651	20002
Probe SEQ ID NO:	88 84	7314	9633	5833	11248	11661	11661	12362	695	9892	1786	2754	3267	512	7172	7172	7710	8763	8763	12221	12306	32	2654	4923	7319

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	Top Hit Acession Database No. Source	3.0E-49 AA337581.1 EST_HUMAN EST42572 Endometrial tumor Homo septems cDNA 5' end	2.0E-49 BE165680.1 EST_HUMAN MR3-HT0487-150200-113-001 HT0487 Homo sapiens cDNA	49 N26446.1 EST_HUMAN yx23406.r1 Source melenocyte 2NbHM Homo septiens cDNA clone IMAGE:282571 5'	oz8802_x1 Sorres, serrescent, fibroblasts, NbHSF Homo sepiens oDNA done IMAGE:1082403 3' similar to gb:W31470 RAS-LIKE PROTEIN TC10 (HUMAN);contains Alu repetitive element,contains element MER22	:1 EST HUMAN	49 BF511846.1 EST_HUMAN UHH-BIA-aps-d-02-0-UI.st NCI_CGAP_Sub8 Homo septens cDNA done IMAGE:3088638 3'	8.1	EST HUMAN	2.0E. 49 AF163864.1 INT Homo septens SNCA isoform (SNCA) gene, complete ods, attennatively spilood	EST_HUMAN	TN 7887554	49 BE255216.1 EST_HUMAN 601115769F1 NIH_MGC_16 Homo septems cDNA clone IMAGE:3356273 5	7.1 EST_HUMAN	AND HARDA A SOURCE HI MAN ORAST CLIANINE NICH FORDER CONSIGNATION OF SUBLINIT	0.1 EST HUMAN	3.1 EST HUMAN	EST_HUMAN	EST_HUMAN	49 BE398110.1 EST_HUMAN 601290330F1 NIH_MGC_8 Homo septens cDNA clone IMAGE:3620863 5	EST HUMAN		N25884.1 EST_HUMAN	11321580 NT	49 11321580 [NT Homo saplens succinate CoA ligrase, GDP-forming, alpha subunit (SUGLG1), mRNA	49 9694184 NT Homo seplens RNA binding modif probein 7 (LOC51120), mRNA	BE408340.1 EST_HUMAN	9.2 EST_HUMAN	AV751477.1 EST_HUMAN	11427369 NT	11418322	60 AF101475.1 NT Homo sepiens glycine N-methyltrænsferese (GNMT) gene, complete cds
S 2001 : 1125 2:15:112	Top Hit Database Source	EST_HUMAN	EST_HUMAN	Г	0288d0 gb:M31	EST HUMAN	EST_HUMAN	EST_HUMAN		NT	EST_HUMAN		HUMAN	EST_HUMAN		EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	Г		Γ	THUMAN				EST_HUMAN	EST_HUMAN	EST_HUMAN			LNI
	Top Hit A	49 AA337581.1	49 BE165980.1	2.0E-49 N26446.1		2.0E-49 AI167357.1	20E-49 BF611846.1	40 AV717838.1	2.0E-49 M86033.1	49 AF163864.1	1.0E-49 BF035327.1		1.0E-49 BE255216.1	1.0E-49 BF131007.1	1 OF 40 H18201 1	1.0E-49 AW984640.	49 AV703000.1	49 AV703000.1	49 BE398110.1	1.0E-49 BE398110.1	1.0E-49 N25884.1	 	N25884.1	1	-		BE40834	1.0E-49 AL043129.2	AV75147	_	1	9.0E-60 AF101475.1
	Most Similar (Top) Hit BLAST E Value										5 1.0E-	11 1.0E-49												39 1.0E-49	39 1.0E-49				1.05-49	32 1.0E-49	1.0E-49	1.4 9.0E-
	Expression Signal	1.98	294	1.92		0.68	0.74		1.74	2.07		1.11	4.82	6.82	8			0.62			227				0.69	0.68	1.29		1.43	3.32	2.46	-
	ORF SEQ ID NO:	37226		28630		30110		32414				26978			24724		ĺ.	32870	32878	32879	32960	L			33796		34721		36907			
	SEQ ID	23933	13425	15979		17478	17490	L	20693	25250	13648	14292	14534	18080	18787	L	1_	19805		19811	19886	Ŀ			20872	L	1			23942	24677	17865
	Probe SEQ ID NO:	11272	846	3218		4748	4758	6637	7998	12316	879	1548	<u>1</u>	5275	Agor.	5992	7117	7117	7123	7123	7200		7200	7977	7707	8575	1688	10026	10979	11281	12215	4637

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						30	
Probe SEQ ID NO:	Exan SEQ (D NO:	ORF SEQ ID NO:	Expression Signal	Most Similer (Top) Hit BLAST E Vetue	Top Hit Acession No.	Top Hit Databese Source	Top Hit Descriptor
6310	25421		0.95	9.0E-50 BE2957	BE295738.1	EST_HUMAN	601176250F1 NIH_MGC_17 Homo septens cDNA clane IMAGE:3531588 5'
168	12980	25619	4.05		8.0E-50 AL163202.2	LN L	Homo sapiens chromosome 21 segment HS21C002
702	13477		2.54	8.0E-50	8.0E-50 X95097.2	IN	Homo sapiens mRNA for VIP receptor 2
702	13477			8.05-50	8.0E-60 X95097.2	۲N	Homo sapiens mRNA for VIP receptor 2
1758	14500		2.82	8.0E-50	4501890 NT	Z.	Homo sapiens actinin, alpha 1 (ACTN1) mRNA
2703	15410	28147	1.48	8.0E-50	4828658 NT	Z	Homo saplens capping protein (actin filternent) muscle Z-line, beta (CAPZB), mRNA
2833	14691		15.7	8.0E-50 D90334	1	TN.	Homo sapiens hepatocyte growth factor(HGF) gene, exon 18
11385	23002	37293	1.28	8.0E-50	8.0E-50 AA633467.1	EST HUMAN	np62d06.s1 NCI_CGAP_Br2 Homo septens dDNA clone IMAGE:1130891 3' similar to gb:J05459 GLUTATHIONE S-TRANSFERASE TESTIS/BRAIN (HUMAN);
88	13383	20015		7.05-50	7.0E-50 BE089591.1	EST HUMAN	QV0-BT0703-280400-211-608 BT0703 Homo sepiens cDNA
2889	19604				BF091922.1	EST HUMAN	RC6-TN0073-150900-011-A12 TN0073 Homo septens cDNA
6687	19604				7.0E-60 BF091922.1	EST_HUMAN	RC8-TN0073-150900-011-A12 TN0073 Homo sapiens cDNA
7205	19890	32968	0.0		7.0E-50 AA627822.1	EST HUMAN	IngSe12.s1 NCI_CGAP_Co9 Homo sepiens cDNA done IMAGE:1148208 3' similar to gb:X88391 60S RIBOSOMAL PROTEIN L6 (HUMAN);
10656	23347		_		7.0E-50 AI872137.1	EST HUMAN	wm55g11.x1 NCL_CGAP_Ut2 Hamo sapiens cDNA clane IMAGE:2439908 3'
4309	17048				6.0E-50 BE794381.1	EST_HUMAN	601580565F1 NIH_MGC_7 Homo septens CDNA clane IMAGE:3943577 5
8112	20808		29.9	6.0E-50 BE04407	BE044076.1	EST HUMAN	ho36h04.x1 NCI_CGAP_Utt Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3 MER29 repetitive element;
10717	23406	36646	12.6	6.0E-50 AA31207	AA312079.1	EST_HUMAN	EST182775 Jurkst T-cells VI Homo septens cDNA 5' end
10717	23406	36647	12.6	6.0E-50 AA31207	AA312079.1	EST_HUMAN	EST182775 Jurket T-cells VI Homo sepiens oDNA 5' end
1785	14526	27233	1.1	5.0E-50	8.1	EST_HUMAN	CM0-BT0792-300500-398-b05 BT0792 Homo sapiens cDNA
1785	14528	27234	1.1	5.05-50		EST_HUMAN	CM0-BT0702-300500-398-b05 BT0792 Homo sapiens cDNA
9000	21680		92.3	5.05-50	5.0E-50 AA557883.1	EST HUMAN	n/45h10.s1 NCL_CGAP_Pr4 Homo septens cDNA clone IMAGE:1043683 similar to contains PTR5.t3 PTR5 repetitive element :
							no54e09.s1 NCI_CGAP_SS1 Homo sepiens cDNA clone IMAGE:1104520 3' similar to gb:X53741_ma1
897	3005		1.71	4.0E-50	_	EST HUMAN	FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
344	16197	28847		4.0E-50	.2	NT	Homo sapiens chromosome 21 segment HS210048
6238	19041	32018	86.0	4.0E-50 11	11440683 NT	.	Homo sapiens cysteinyl-tRNA synthetase (CARS), mRNA
7135	19822	32888	1.95	4.0E-50 BE08753	6.1	EST_HUMAN	QV1-BT0681-280300-127-f12 BT0681 Homo sapiens cDNA
1931	14667		4.13	3.0E-50 M18048.	1	NT	Human endogenous retrovirus RTVL-H2
3283	16054	28703	1.24	3.0E-50	3.0E-50 AA746142.1	EST HUMAN	ob03f08.s1 NCI_CGAP_Ktd3 Homo seplens cDNA clone IMAGE:1322827 3'
3734	16487	28124	1.14		3.0E-50 AW755254.1	EST HUMAN	CMYA5 Human cardiac musole expression library Homo sapiens oDNA clone 4151936 similar to CMYA5 Cardiomyopathy associated gene 5

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	Human ankyrin (ANK1) cerre, exon 2	Homo sapiens interfeutin 17 receptor (IL17R) mRNA	Homo septions protein phosphatase 2, requirement services (RRR) such section (DDD) and a services (RRR)	Homo sections probably three-2 mentiletons enthants B (DER) all to the control of	Homo sablens chromosome 21 segment HS24/2ng	Homo sablens T-cell hamphome investment and metashada 1 (TIAMA) mRNA	Novel human gene mapping to champeome X	Homo septens 26S proteesome essociated part homoton (POH1) mPN/A	Homo saplens mRNA for nucleoportn 155	Human Ku (p70/p80) subunit mRNA complete orts	Human Ku (070/080) subunit mRNA complete cris	Homo saplens RNA binding most protein 3 (RBN3), mRNA	191-09-XI NOI_CGAP_Part Homo esplens CONA done IMAGE:2224720 3' similer to gb:M26328 KERATIN, TYPF I CYTOSKFI FTAI 18 (14 INAM)	Note I turner dene menoling to chomosome 22	ye47c08.r1 Soares infant brain 1NIB Homo saplens cDNA clone IMAGE 53233 57 similar to arbitatat 22 and a	RETROVIRUS-RELATED POL POLYPROTEIN (HUMAN) contains (TR5 modifies alessed)	ruman hinRNP C2 protein mRNA	a04d06.y1 Human Pancreatic Islets Homo sapiens cDNA 5	Homo septens ubquitta protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA	#20a05.1 Stratagere NT2 neuronal precursor 937230 Homo sepiens cDNA clone IMAGE:964890 5' similar to TR-0233278 G233278 BTM H DDOTTEN	003 X NCI CCAP Kidta Home seniore contact literations of	UI-HBITAGE-02-0-UI-STACL COAP Subst Homo services CDNA close NAA CESTAGE SUBSTACE OF	di34f09.35 NGL CGAP_KId5 Homo septens cDN4 clone IMAGE:1325609 similar to SW:NME1_MOUSE P35436 GLUTAMATE INMIDAT RECEPTOR SUBINITEDS:II ON 1 DEBCY IDCOLD.	0634709.05 NCI_CGAP_KI45 Homo septens cDNA clone INAGE:1325009.3 struiter to SW:NME1_MOUSE	601470446FINIH MAG RY Home series ANA About MACE Series E	Homo saplens diacylghyard kinase lota (DGKI) gene, even 23
le Exon Probe	Top Hit Database Source	I IN												T HUMAN	Ž			Ĭ,	EST HUMAN IN		EST HIMAN TO	Τ	Τ	Г	Γ	Т	오
Sing	Top Hit Acession No.	U50083.1	11526280	5453949 NT	5453949 NT	AL163203.2	8	5.0E-51 AL 133204.1	5031980 NT	5.0E-51 AJ007558.1	1		5803136	_				3.0E-51 M29063.1		4507798 NT	2.0E-51 AA233352 1	Γ	2.0E-51 AW137826.1 E				11
	Most Similar (Top) Hit BLAST E Value	6.0E-51		6.0E-51	6.0E-51		5.0E-51	6.0E-51	5.0E-51	5.0E-51	5.0E-51 M30938.	5.0E-51	5.0E-51	3.0E-51	3.0E-51	- -	3.0E-51 R15914.	3.0E-51 N	3.0E-51 A	2.0E-51	2.0E-51 A	2.0E-51 A	2.0E-51 A	2.0E-51 AI732851	2.0E-61 AI732854	2.0E-51 B	2.0E-51 AF219927.1
	Expression	0.67	1.51	1.52	1.62	11.81	1.98	96.0	0.99	8.67	1.52	1.52	4.18	3.65	1.97		3	4.86	0.47	201	5.16	1.67	0.78	0.7	0.7	3.06	0.61
	ORF SEQ ID NO:	35511	37169	37425	37428	26207	20219	28400	27038	28052	22316	28317	37203	28571	29659		33246			25798	27124	29107	29820	30837	30838	31663	H
	Exan SEQ ID NO:	22314	23884	24115	24115	13546	13557	15557	14349	15315	16875	16875	23911	13908	17031		20152	21430	25430	13155	14427	16469	17194	18155	18155	18709	19894
	Probe SEQ ID NQ:	3995	11221	11515	11515	774	785	970	1 8 83	ğ	3925	3926	11249	1163	4292		7473	8738	88	357		3716	4458	5352	5352	5925	7209

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Oligie Extri Probes Extri essect in Drain	Most Similar Top Hit Acession (Top) Hit Top Hit Descriptor Signal Signal Velue Source	33116 1.06 2.0E-51 7662349 NT Homo sepiens cell recognition molecule Caspr2 (KIAA0868), mRNA	34432 1.72 2.0E-51 BE901994.1 EST_HUMAN 601676787F1 NIH_MGC_21 Homo sapiens cDNA clone !MAGE:3959613 5'	3E901994.1 EST_HUMAN	0.96 2.0E-51 11037064 NT	1.45 20E-51 AB17078.1 EST HUMAN Q16298 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR;	5.68 2.0E-61 BE165980.1	0.8 2.0E-51 AB007928.1	1.77	2.67 2.0E-61 AA378659.1 EST_HUMAN	20E-61/Al732851.1 (EST HUMAN	8.52 2.0E-61 A1732861.1 EST HUMAN	23 200	4503528 NT	20.32 1.0E-61 AV742248.1 EST HUMAN	1.0E-61 BE779039.1 EST_HUMAN	1.0E-51 T18862.1 EST_HUMAN	49.0	33819 0.81 1.0E-51 BF434359.1 EST HUMAN PROTEASE;	2 1.0E-51 AV780590.1	36520 1.39 9.0E-62 R91638.1 EST HUMAN SP:YGAF_ECOLI P37339 HYPOTHETICAL PROTEIN IN GABP 3/REGION;	36521 1.39 9.0E-52 R91638.1 EST HUMAN SP:YGAF_ECOLI P37339 HYPOTHETICAL PROTEIN IN GABP 3/REGION;	9.0E-52 AA777621.1 EST HUMAN	8.0E-52 AA720574.1	26915 1.65 8.0E-52 X84900.1 NT H.sepiens mRNA for laminin-5, alpha3b chain
		118	4432	4433	34768	35281	35336	35366	36139	36232	30837	30838	150	31017	+	30294	30789	33322	33619		36520	36621	-	25805	28915
	ORF SEQ ID NO:	8	9	 	Ĭ	"	ı			ı	l					1	ı	1	ŀ			1	1	l	l.
	Probe Exan ORF SE(SEQ ID SEQ ID ID NO: NO:	7357 20038 33	21291	21291		9412 22090	ì	<u> </u>	ı	10370 23018	L	Ì	L	L	_l	L.	L	7549 20219	7803 20498	1	10587 23282	<u> </u>	<u> </u>		1482 14229

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1650	14396	27085	3.13	8.0E-52	11968028 NT	ŢŃ	Homo septions hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
1650	14396	27086	3.13	8.0E-62	11968028 NT	FN	Homo sepiens hypothetical protein FLJ13556 shallar to N-myo downstream regulated 3 (FLJ13556), mRNA
3976	14396	27085	6.6	8.0E-52	119880Z8	NT	Homo sepiens hypothetical protein FL113556 striller to N-myc downstream regulated 3 (FLJ13559), mRNA
3976	14396	27086	99	8.0E-52	11968028	Į,	Homo sapiens hypothetical protein FL/13556 shrifar to N-myc downstream regulated 3 (FL/13556), mRNA
7417	20094	33178	19:0	L	TN 58691411	Į.	Homo saplens transforming growth factor, beta-induced, 68kD (TGFBI), mRNA
7177	20094	33170	0.67	8.0E-52	11416585 NT	NT	Homo sapiens transforming growth factor, beta-Induced, 68kD (TGFBI), mRNA
8911	21602	34745	2.04		7.0E-52 W 56471.1	EST HUMAN	2259a08.11 Soeres_peretryndd_tumor_NbHPA Homo septens cDNA clone IMAGE:328578 5' similar to contains Alu repetitive element:
1164	13918		0.78		6.0E-52 BE072409.1	EST_HUMAN	QV3-BT0537-271229-049-407 BT0537 Homo sepiens cDNA
1689	14433	27129	4.27	6.0E-52	6.0E-62 AF108907.1	Ę	Homo septens S164 gene, partial ods; PS1 and hypothetical protein genes, complete ods; and S171 gene, partial ods
5641	18436	31340	0.86		-	EST HUMAN	0944f04.x1 Soares_testis_NHT Homo sepiens cDNA clone IMAGE:1838047.3'
11170	23837	37119	1.84		6.0E-52 BF048172.1	EST HUMAN	12/41/04.y/ NCI_CGAP_BM52 Homo septens dDNA done (MAGE:228/671.5' similar to SW:PGBM_MOUSE Q05783 BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR:
8282	21959	35132	9.0	L	11437385 NT	Į.	Homo sepiens FSHD region gene 1 (FRG1), mRNA
1723	14486	27165	132	4.0E-52	4501922 NT	M	Homo sapiens adenylate cyclase activating potypeptide 1 (pttuitiary) receptor type I (ADCYAP1R1) mRNA
1780	14521	27225	1.02	4.0E-52	4758843 NT	N.	Homo sepiens nucleoparin 155\D (NUP155) mRNA
3906	16856	29297	080	4.0E-52	4507500 NT	N.	Homo sapiens T-cell lymphome invasion and metastasis 1 (TIAM1) mRNA
5204	18012	30633	1.33	4.0E-52	4506132 NT	IN	Homo sapiens phosphoribosyl pyrophosphate synthetase associated protein 2 (PRPSAP2) mRNA
5204	18012	30634	1.33	4.0E-52	4508132 NT	L	Homo sapiens phosphorbosyl pyrophosphate synthetase essociated protein 2 (PRPSAP2) mRNA
7938	20633	33760	1.74		BE622032.1	EST HUMAN	601440687F1 NIH_MGC_72 Hamo septens cONA clane IMAGE:3916836 67
8432	21125	34263	5.48	4.0E-52	Į.	NT	Homo sapiens hydroxysteroid (17-beta) dehydrogenase 4 (HSD17B4), mRNA
12143	24631		5.11	4.0E-52	11418177	L	Homo saplens Ran GTP ass activating protein 1 (RANGAP1), mRNA
12627	24930		5.23	4.0E-52	4.0E-52 AB002059.1	NT	Homo septems DNA for Human P2XM, complete cds
4071	16815		10.57		1437042	N	Homo sapiens hypothetical protein FLJ10675 (FLJ10675), mRNA
540	13332	25962	2.88			NT	Human endogenous retrovinst DNA (4-1), complete retrovinsi segment
240	13332	25963	288	ŀ	2.0E-52 M10976.1	NT	Human endogencus retroviral DNA (4-1), complete retroviral segment
							_

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potential element [human, endogenous retroviral element RTVL-Hp1,
18056 30884 4.35 1.0E-62/M29426.1 NT
1.05-02 Mi29420.1

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Top Hit Acession Databetee Top Hit Descriptor No. Source	1,0E-52 X07292.1 NT Human eldolase C gene for fructbee-1,8-bisphosphate adolase	1.0E-52/AL163227.2 NT (Hamo saplens diromosome 21 segment HS21C027	INT IN	D.1 EST_HUMAN	2 NT	NT	1426321 NT	4505064 NT Homo sepiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B) mRNA	9.0E-53 AF001446.1 (NT Homo septens care binding factor alpha1 subunit (CBFA1) gene, exon 3	7.0E-53 BF238465.1 EST_HUMAN 601904771F1 NIH_MGC_64 Homo septens CDNA done IMAGE:4132793 5	1	HOMAN	758543	S.1 COL HOMAN	N N	705414 NT	.1 EST_HUMAN	EST_HUMAN	.1 EST HUMAN	4.0E-63 BF128701.1 [EST_HUMAN 60181008867 NIH_MGC_48 Homo estima cDNA clone IMAGE:4053977 5	Homo sepiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, ARCOARGA (NT	EST HUMAN	LN NT	11526297 NT [Homo sepiens Mil.1 protein (Mil.1), mRNA	BE160025.1 EST_HUMAN	3.0E-53 Y10389.3 NT H.sapiers graf gene	3.0E-53 Y10388.3 NT H.sapiers graf gene	3.0E-53 S72043.1 [NT GIF-growth Inhibitory factor (human, brain, Genomic, 2015 nt]	2835090 NT	5901953 NT	3 8923599 NT Homo septens hypothetical protein FLI20644 (FLI20644), mRNA
Most Similer (Top) Hit BLAST E Vatue	1.0E.	1.0E-	1.0E-	1.0E	1.0E-5	1.0E-5	1.0E-52	9.0E-53	9.0€-53	7.0E-53	7.05-53	6.0=-53	5.05-53	3.0E-33 AWO1330	4.0E-53 AL 163285	4.0E-53	4.0E-53	4.0E-53	4.0E-53	4.0E-53	2 OF A3	3.06-53	3.0E-63	3.0E-53	3.0E-5	3.0E-6	3.0E-	3.0E-	3.0E-53	3.0E-53	3.0E-53
Most Similar Signal (Top) Hit Signal BLAST E	5.31 1.0E-	1.2 1.0E-	0.75 1.0E-	1.03 1.0E~	1.39 1.0E-5		2.09 1.0E-52	1.05 9.0E-53	1.96 9.0E-53	3.18 7.0E-53					2.76 4.0E-53.A		0.66 4.0E-53	'		2.78 4.0E-53	1 77 1	L		0.82 3.0E-5	0.85 3.0E-5	1.04 3.0E-5	1.04 3.0E-5	12.52 3.0E-4			2.79 3.0E-6
<u> </u>	33090 5.31					36596 1.61		1.05			4.92	30422 1.02	29448 228	0.10	2.76	30125 1.03		79.0	37126 2.78			29014 0.74	30803 0.7	31243 0.82	31846 0.85				34597 0.65	8.41	

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Table 4
Single Exon Probes Expressed in Brain

					;	151 - 150 P	
Probe SEQ ID NO:	SEQ ID	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
445	13231		582	2.05-63	2 0F-53 AA386558 1	EST HIMAN	EST77525 Pancrase timor III Homo saviene cDNA 57 and
	<u> </u>						Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44 like nibosomal protein
2327	15052	27788	2.79	2.0E-53	2.0E-63 U78027.1	NT	(L44L) and FTP3 (FTP3) genes, complete cds
2538	15253		8.73	2.0E-53	4502318 NT	ŢN	Homo sapiens ATPase, H+ transporting, lysosomal (vacuoler proton pump) 31fQ; Vacuoler proton-ATPase, subunit E; V-ATPase, subunit E (ATPase, mRNA)
27.20	15436	28172	1.48	2.0E-53	TN 2167915	Į.	Homo septens core-binding factor, runt domain, alpha subunit 2; transfocated to, 1; cyclin D-related (CBFA2T1) mRNA
2728	15436	28173	1.46	2.0E-53	TN218151N1	 	Homo sepiens core-binding factor, runt domain, alpha subunit 2; transiocated to, 1; cyclin D-related (CBFAZT1) mRNA
3239		28651	3.72	2.0E-53	2.0E-53 AF083822.1	TN	Homo sapiens dhydropyridine receptor alphe 2 subunit (CACNA2D1) gene, excn 6
4038		29411	2.63	2.0E-63		N	Human Krueppel-related DNA-binding protein (TF34) gene, pertial cds
5340		30804	2.67	2.0E-53		Т	PM1-CT0396-170800-001-g03 CT0396 Homo saplens cDNA
5340		30805	2.67	2.0E-53		EST_HUMAN	PM1-CT0396-170800-001-g03 CT0396 Homo saplens cDNA
2770		33500	1	2.0E-53	2.0E-63 AW975598.1	EST_HUMAN	EST387707 MAGE resequences, MAGN Homo sepiens cDNA
8308	21975		3.82	2.0E-53	2.0E-53 AW 245676.1	EST_HUMAN	2822885.5prime NIH_MGC_7 Homo sepiens aDNA clane IMAGE:2822865 5
1428	14175	26860	1.51	1.0E-53	11	TN	Homo sapiens Xq pseudoautosomal region; segment 2/2
200	16162	28813	1.08	1.0E-63	1.0E-63 AB028898.1	L	Homo sapiens DNA, DLECt to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
6593	18356	32370	1.52	1.0E-63	-	HUMAN	CM4-NN1029-150800-543-e02 NN1029 Homo septens cONA
7147	19834	32903	0.68	1.0E-53	=	T	RC5-BN1058-270400-031-D01 BN1058 Homo septems cDNA
7836		33658	9.54	1.0E-63			19571.seq.F Human fetal heart, Lambda ZAP Express Homo septiens cDNA 5
8987	21677	34826	5.91	1.0E-53	1.0E-53 X79536.1	NT.	H.saplens mRNA for hnRNPcore protein A1
11833	24417	37757	1.41	1.0E-53		Į.	H saplens mRNA for myosin-IE
11833		37758	1.41	. 1.0E-53		۲	H.saplene mRNA for myosin-IE
11955		37255	2.29	1.0E-53	AW 245422.1	T_HUMAN	2822943.3prime NIH_MGC_7 Hamo expiens cDNA clane IMAGE:2822943.3°
5210		30651	6.18	9.0E-54	4508786 NT		Homo sepiens IQ modf containing GTPease activeding protein 1 (IQGAP1) mRNA
202	13015	25655	2.4	8.0E-54	BE386785.1	T_HUMAN	801272863F1 NIH MGC 20 Homo expiens cONA clone IMAGE:3614031 5
1827	14506	27278	1.77	8.0E-54	4504610 NT		Homo sepiens insulin-like growth factor 2 receptor (IGF2R) mRNA
5845	18633	31568	26.87	8.0E-54	TN 00057000 NT	TN	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCAB), mRNA
Į	-		,			Г	al79c12.s1 Soares teetis NHT Homo sapiens cDNA clone 1377046.3' similar to contains MER30.t3 MER30
e)	13200	25845	127	7.0E-54	 ج	EST HUMAN	repolitive element;
223	\$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$	27273	. 8.	7.0E-54	7.0E-54 Y16645.1		Homo sapiens mRNA for monocyte chemotactic protein-2
2202	14830	27067	6.38	7.0E-54	7.0E-64 N27177.1	EST HUMAN	yw68d12.s1 Soares_placenta_8b09weeks_2NbHP8b09W Homo septens cDNA clone IMAGE:257399 3' similar to contains LTR7.b3 LTR7 repetitive element;
	l					7	

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Table 4

					JIS	igle Exon Pro	Single Exon Probes Expressed in Brain
Probe SEO ID	Exon SEO ID	ORF SEQ	Expression	Most Similar (Top) Hit	Top Hit Acession		
NO:	Ö	ID NO:	Signal	BLAST E Value	<u>\$</u>	Source	Top Hit Descriptor
10028	22676	35892	2.08	7.0E-54	TN 00071411	Į	A selection of the sele
11047			1.74	L		5	Home services additional to nuclear ractor related to kappa B binding protein (H. sapiens) (LOC83182), mRNA
11047	23717	36987	1.74	7.0E-54		L	Homo seriens populative modeln (GLP), mrNA
11261	23923		4.35	7.0E-54	A/160186	EST HUMAN	db67g03x1 Source_folal_heart_NbHH19W Homo septens cDNA clone IMAGE:1705204.3' similar to contains OFR:t1 OFR repetitive element:
11811	24400	37736	1.48	7.0E-54	7.0E-64 AF111167.2	NT	Homo septems fun dimerization protein cens partial cets: offer offer cens can a
11811	24400	87737	04.	7.0E-54	7.0E-54 AF111187.2	<u> </u>	University of the control of the con
Z	12850	25465	1.41	6.0E-64	6.0E-64 AB003618.1	Ę	Home services DNA 6-141/CO
376	13201	25846	6.83	6.0E-54		5	Home environment in the first of the parties cos
376	13201	25847	6.83	6.0E-64		 	Home enviore in the factor of the control of the co
3277	16038	28688	0.77	6.0E-54		Ę	Homo geniene historieucal protein DNF 2003 (UKF 20434M036), mRNA
3986	16734	29368	196	6.0E-54		Į.	Home sorious debutte the series of Chest C
4429	17165	29794	98.0	8.0E 64	6.0E-64 AV754746.1	EST HIMAN	AV754740 TP Home emission CLUND MYNA
4792	17523	30145	1.78	6.0E-54	4505806 NT	LN	Homo seniore phosphare account of the senior phosphare account
4819	17550		1.15	6.0E-54	6.0E-54 Y09845.1	LN	Headens shir post decrease need 1-4-masse, catasyde, alpha polypoptide (PIK4CA) mRNA
11432	23199	38430	1.51	8.0E-64	97.1	EST HIMAN	RCS-ST0492-454000 044-90 ST0402-U
2146	14876	27811	3.78	5.0E-54 P51523	Γ	SWISSPROT	ZINC FINGER PROTEIN BA (ZINC FINGER PROTEIN INC.)
2	12980		13.34	4.0E-54	.g	LN	Tubes belancer beta outh mRNA resta At-
888	13703	26368	67.5	4.0E-54 AA30678	13	FST HIMAN	EST177696 Jurkat T-cells VI Home septems CDNA 5 and similar to give raidehyde-3-phosphete
1798	14538	27248	3.22	4.0E-54 D38521.1		NT NT	Himon mBNA for VIA ACCET
<u>138</u>	14538	27249	3.22	4.0E-541		Z	Human mRNA for Kladnot7 come postul colo
3100	15962		-	4.05-54	4 0F-54 A 103-50-8-4 1	Γ	wd2dd11xf Sogres NFL T 9BC S1 Homo sepiens cDNA done IMAGE:2329269 3' semilar to TR:002711
85	12918	25555	4.47	3.0E-54		EST HIMAN	EST18832 CAL
1585	14312		0.94	3.0E-54		Т	Edition of Control Cardinating (FICC) certified Homo sapiens cond. Significant
2574	15288	28025	96:0	3.0E-64	T	Т	DKEZAGERTA A 224 (224)
283 783	15342		1.34	3.0E-64 AI908757.		T	11-81180-191300-007 BT180 Home Sapiens CDNA clone DKFZp434E0731 5
2814	18803	31531	1.74	3.0E-64	502434		Homo services BAX con-contract to the contract
7288	19071	33048	2.1	3.0E-54 AA844061	-	T HUMAN	BIOCOOR ST SOME PARTHER AND A LICENTAL AND A LICENTAL MICHAEL CONTRACT OF THE
7288	19971	33049	21	3.0E-54 AA844081	-	Т	a02c08.sf Sogres paraffyrnid frimm NH-IDA Home and All All All All All All All All All Al
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Table 4
Single Exon Probee Expressed in Brain

					IIIO	gie Exon Pro	Single Exon Probes Expressed in Brain
Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similer (Top) Hit BLAST E Value	Top Hit Acesslon No.	Top Hit Detablese Source	Top Hit Descriptor
10949			1.83	3.0E-54	11434806 NT	LN LN	Homo sapiens goldi autoentiden, coldin subfamily e. 5 (GOI GAS) mRNA
11024	23696	39959	4.93	3.0E-54	3.0E-54 BF345600.1	EST_HUMAN	802019408F1 NCL_CGAP_Brief Homo sepiens cDNA clone IMAGE:4155121 5
11341	24031	37335	3.26	3.0E-54	3.0E-64 AA393362.1	EST HUMAN	270/12.r1 Soares_bests_NHT Home septens cDNA clane IMAGE:727727 5' similar to TR:G191315 G191315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN
12056		31119	2.98	3.0E-54	3.0E-54 AW954559.1	EST HUMAN	EST366829 MAGE measurement MAGE Homo sentime ANNA
12097			2.51	3.0E-54	3.0E-54 AW748965.1	EST HUMAN	RC1-BT0313-131189-011-b00 BT0313 Home services CDNA
627	13406		8.86	2.0E-54	5031900 NT	Į.	Homo saciens killer cell lectralitie recentra subfamily G. member 1 (K) RG41 mDNA
1344	14092	28767	0.96	2.0E-54		NT	Homo sepiens nuclear antigen Sp100 (SP100) mRNA
1530	14286	28972	1.37	2.0E-54	2.0E-54 AA655008.1	EST HUMAN	nt78e08.s1 NCI_CGAP_Pr3 Homo sepiens cDNA done IMAGE:1204600 similar to contains element L1 repositive element
2541	15255	27895	1.22	2.0E-54	2.0E-54 AW183175.1	EST HUMAN	au62g03.y1 Schneider fetal brain 00004 Homo sepiens cDNA clone IMAGE:2783784 5' stritter to SW:XUL1 HUMAN 013816 CVII IN HOMAN OG 1
2608	15320	28062	1.66	2.0E-54	02	NT	Homo septens chromosome 21 segment HS24C010
2896	15063	28311	1.52	2.0E-64	1.45	EST HUMAN	wy60b12x1 Soares_NSF_F8_9W_OT_PA_P_31 Home explens oDNA clone IMAGE:2552927 3' similar to TR:062084 062084 PHOSPHOI IPASE ONE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFI
3311	16071	28721	1.18	2.0E-54	Γ	Z E	Homo sepiens mRNA for phospholipase C-beta-1b (Pt.CB1 gene)
3536			3.2	20E-64	2.0E-54 AA532925.1	T_HUMAN	n45509.s1 NCI_CGAP_Pr9 Hamo septems cDNA clone IMAGE:995488 semiler to gb:X53777 60S RIBOSOMAL PROTEIN L29 (HUMAN):
4181	16921		2.08	2.0E-54	4502842 NT		Home septens chaperonin containing T-complex survivit 6 (CCTA) mRNA
4826	17558	30178	1.02	20E-54	7706446 NT	Ę	Homo septens peoble/septinine detrainese troe III (LOCS1702) mRNA
5368	18188	30880	1.64	2.0E-54	4759069 NT	Z	Homo explens amail inducible cytolane subfamily A (C/a-C/a), member 14 (SCYA14) mbNA
5516	18314	31216	12	20E-64	2.0E-64 BE047864.1	T HUMAN	Ex3c11.y1 NCI_CGAP_Bm52 Hamo septens cDNA done IMAGE:2291348 5
5875	18480	31386	5.04	2.0E-64	1426657		Homo saplens KIAA0100 gene product (KIAA0100), mRNA
2//1	18582	31489	13.89	20E-64	1.1		Homo septens mRNA for KIAA1501 protein, pertial cds
5	18562	31490	13.80	2.0E-54		NT	Homo eaplens mRNA for KIAA1591 protein, pertial cds
8220	19324	32331	0.68	20E-54			Homo sepiens EVI5 homolog mRNA, complete cds
67.13	19628	32672	0.08	2.0E-54	2.1	TN	Homo sepiens mRNA for KIAA0005 protein, perfal cds
67.13	19628	32673	0.055	2.0E-54		Į.	Homo eaplens mRNA for KIAA0995 protein, pertial cds
7023	19715	32772	8.8	2.0E-54	11426544 NT		Homo sapiens neurofficomin 1 (neurofficomatosis, von Recklinghausen disease, Watson disease) (NF1), mRNA
9529	22182	35366	4.11	2.0E-54	2.0E-54 AB001025.1		Homo sapiens mRNA for brain nenodine receptor, complete cats
88	22558	35753	0.70	2.0E-64	212		Homo sapiens Janus kinase 2 (a profesh tyrosine kinase) (JAK2) mRNA
10021	22689	35885	101	2.0E-54	11416762 NT		Homo sepiens sendopically defined colon cancer entitien 10 (SDCCAG10), mRNA
10021	22669	35886	1,9	2.0E-54	11416762NT		Hamo saplens serdiogically defined colon cencer antigen 10 (SDCCAG10), mRNA

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Probe SEQ ID 58 SEQ ID 58 SEQ ID 58 SEQ ID 58 SEQ ID 58 SEQ ID 58 SEQ ID 59 SEQ ID 59 SEQ ID 59 SEQ ID 50	Single Exon Probes Expressed in Brain	Exon ORF SEQ Expression (Top) Hit Top Hit Acession (Top) Hit Top Hit Acession No. Signal BLAST E No. Source Source	19324 32331 1.57 2.0E-54 AF008915.1 NT Homo septens EVI5 homotog mRNA, complete cds	24321 2.86 2.0E-54 7857454 NT Homo explens bescedillo (zebrafiah) homolog 1 contraining BRCT domain (DES4) mona	T HUMAN	9.1 EST HUMAN	1.0E-64 AA412409.1 EST HUMAN	T	9.0E-55 BE081469.1 EST HIMAN	8.0E-55 Y07829.2 NT	Z	8.0E-55 AW409714.1 EST HUMAN	21395 0.8 7.0E-55 AW103839 1 For Hilliam Denses Records 1 CBC_S1 Homo septens oDNA clone IMAGE:2803522 3' similar to TR:080385	34932 1.28 7.0E-55 AA899581 1 FST HILLIAN	34968 2.16 7.0E-55 AU139809.1 FST HIMAN	7.0E-55 A1561056.1 EST HUMAN	1 EST HUMAN	EST HUMAN	37412 2.45 6.0E-55 AB040834.1 NT	27205 1.19 5.0E-56 AA704971.1 EST_HUMAN	27206 1.19 5.0E-55 AA704971.1 EST HUMAN	30096 1.81 5.0E-55 AW 206021.1 EST_HUMAN	32271 1.85 5.0E-55 4502240 NT	32212 1.86 5.0E-55 4502240 NT	32340 1.34 5.0E-55 4505952 NT	32341 1.34 5.0E-55 4505052 NT	32718 0.83 6.0E-66 7382477 NT	32955 0.7 5.0E-55 11434422 NT	33718 0.72 5.0E-55 11528491 NT	34777 3.63 6.0E-55 4506302 NT	1.75 5.0E-55 BE064386.1 EST_HUMAN	35786 1.77 5.0E-55 AB014511.1 NT
	-			121	88					41	44	18	100					33						1								
	-	<u> </u>		_			Ш		L				 		L			_						┸								

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	Top Hit Descriptor				The familia A (Opena)	mental tribulation At (row 11A1) micket	mRNA	to septers cDNA done IMAGE:3390043 3' similar to	12 (12 (12 (12 (12 (12 (12 (12 (12 (12 (and manual type, Z (FSMAZ) micha	AKC HONA	COO HOW	4 / IBES/4 mon	1 (COLEY 1) HEAVE	71	Amo emisso o'ON #	MIN SEPTEMBER	In Information of the Informatio			water comment	ANT PROPERTY OF THE PROPERTY O	CONA	THE CONTRACTOR STATE FOR	THE INTERNATION OF THE PROPERTY OF	See IMA OF 342489 91	s CDNA clone IMAGE:1884185 3' similar to contains		AAOORED E	Spendera) (MSDR) mDNA	1 man () man	CLA I SINTER (NELTERINZ) INTENA, COMPIETE COS
Single Exon Probes Expressed in Brain	Top Hit	Homo sections mRNA for KIAA0811 postering and	Homo sepiens nei (chicken Like 2 (NET 1.2) mDNA	Homo sariens mecanillo (sekrafie), handon 4 metalla DOCT 3	Hamo saplens RNA binding moff problem V chromosome familia.	Homo sepiens predicted osteoblast protein (GS3784) mBNA	Homo septens predicted osteoblast protein (GS3786) mRNA	7j52b10x1 Soeree_NSF_F8_GW_OT_PA_P_S1 Homo sepiens cDNA done IMAGE:3380043 3' similar to contains [-1 t3 1 manething algorithm algorithms.]	Homo series protestore (program maxweds) subustituting the total of (100) 1111	Home sapiens tribescome (presons movement) subtent, spins 1998, 2 (POMAZ) mRNA	Homo saplens discriptivend kinese germs (900) (DGKG) mBNA	Homo seriens discreptional kinese germas (ONO) (OOO)	Homo seciens ubiquiting private and Format 1 (11862/11 PMA)	Homo sepiens Xo pseudosupermel region: segment 1/2	Homo sepiens chromosome 21 segment HS210310	43c5 Human ratina cDNA randomiv primed sublibrary Homo seniors CNA	801886575F2 NIH MGC 17 Homo servine chala class ILA CE: 41272226 ET	PM1-HT0803-090300-001-009 HT0903 H-000-0-0010	Homo stolens chromosome 21 sermon IIS310084	Human endocemore naturalise pHE 4 (EDVo)	Human endodenous retroying DNA (4-1) complete retroying enumers	Homo sapiens syntach-binding protein 1 (STXRD1) mRNA and femalest	CM1-HT0876-150800-357-003 HT0876 Homo septems cDNA	UITHE-BNO-846-5-08-0-ULT NIT MIGC 50 Home seniors CIDNA Avea IMA CE: 3078275 F	hr76h08.xt NCI CGAP Kid11 Homo seriens cDNA cime IMACE 212463 2	hr76h08.x1 NCI CGAP Kid11 Homo senione obiNA close INA CE-3434489 31	eme8h06.a1 Strategene achtzo brain 311 Homo sapiens cDNA cione IMAGE:1684185 3' similar to contains	OVO-RN0147-280400-213-006 EN0147 U	AU10344 HEMBA1 Homo services of NA close HELMA Accesses at	Homo sapiens mannas & photographic (callon photographic straight and Anna Anna Anna Anna Anna Anna Anna	Orcholacus cunicatus New Zealand with a lander to	Homo sapiens mRNA for KIAA0803 protein pertial cuts
gle Exon Pro	Top Hit Database Source	L	Į	Ę	LN	NT	IN	EST HUMAN	N-	Z	Z	LZ.	Z	Z	12	EST HUMAN	EST HUMAN	EST HUMAN	Ę	Į	F	F	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	FST HIMAN	EST HUMAN	7	IN	
Sin	Top Hit Acession No.	5.0E-55 AB014511.1	5453785 NT	11417972 NT	4826973 NT	7861713 NT	7861713 NT	4.0E-55 BF061411.1	6180	4506180 NT	4503314 INT	4603314 NT		5.1	92				57			4507286 NT	Ī							4505080	-	
	Most Similar (Top) Hit BLAST E Value	5.0E-55	5.0E-55	6.0E-66	4.0E-55	4.0E-55	4.0E-55	4.0E-55	4.0E-55	4.0E-55	4.0E-55	4.0E-55	4.0E-55	4.0E-55/	4.0E-55/	4.0E-65	4.0E-55 E	3.0E-55 E	3.0E-55	2.0E-55 X57147.1	2.0E-55 M10978	2.0E-65	2.0E-55 BE71990	2.0E-55 A	2.0E-66 B	2.0E-55 B	2.0E-55 A	2.0E-55 B	2.0E-55 AU11934	1.0E-55	1.0E-55 U09823.	1.0E-55 AB02071
	Expression Signal	1.77	2.48	273	4:50	1.78	1.78	1.7	70.0	0.97	6.47	6.47	2.29	1.21	8.37	2.3	3.05	1.5	1.85	1.98	1.13	13.79	2.91	0.76	0.52	0.52	6.23	0.72	1,95	3.01	8.22	3.53
	ORF SEQ ID NO:	35787	35964		26075	26853	26854		27482	27483	27542	27543	27771							25807		26049	30090	33162	34804	34805		-	36798	25558	25636	26543
	Econ SEQ ID NO:	22585	22770	24626	13434	14169	14169	14250	14754	14754	14811	14811	15033	15310	20936	23859	24574	24536	24993	13164	13321	13413	17455	25113	21654	21664	21747	21828	23550	12921	12997	13883
	Probe SEQ ID NO:	20037	10122	12137	667	1424	1421	1504	2019	2019	2079	2079	308	2696	8242	11194	12057	11998	12721	368	88 88	\$	4733	2 2 3	8963	88 88	8008	9140	10870	88	184	1127

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RF SEQ Expression (Top) Hit Acession Database ID NO: Signal BLAST E No. Source	25470 8.58 4.0E-56 AF141349.1 NT Homo sapiens bets-tubulin mRNA complete cds	3.1 EST HUMAN	7.28 4.0E-56 4507728 NT	28158 7.28 4.0E-36 4507728 NT Homo septens tutrulin, beta polypeptide (TUBB) mRNA	25929 3.49 4.0E-68 AF003528.1 NT regions Papers X-linked anhibitrofitic ectodormal dysplasia protein gene (EDA), exon 2 and flanking repeat	T HUMAN		4.0E-56 AF217508.1 NT	N N	2.02 4.0E-58 AF043349.1 NT	1 EST HUMAN	1 EST HUMAN	4.17 3.0E-66 8924029 NT	1.54 3.0E-56 AA325826.1 EST HUMAN	L1 EST_HUMAN	1.61 3.0E-56 AF055096.1 NT	767042 NT	4.27 3.0E-56 AL163288.2 NT	902085 NT	31302 2.12 3.0E-56 4759163 NT Homo sapiens sparc/osteonectin, owov and leazal-like domains proteoglycan (testican) (SPOCK) mRNA	31303 2.12 3.0E-56 4759163 NT Homo septens spendosteomecth, cwrcv and leared-like domains and activities (American American	1.15 3.0E-58 4504970 NT	32982 1.15 3.0E-66 4504970 NT Homo septens LIM binding domain 2 (LDB2) mRNA		D63479.2 NT	1.38 3.0E-56 11434956 NT	1.71 3.0E-56 AB042558.1 NT	2013 NT	
	25470		28157	28158	25929	28074	28075	31912	319/13	36288	36784	36765	26742	28527	28528		29728	29759	29902	31302	31303	32547	32981	32982	34550	35562	36240	36571	37239
Exan SEQ ID NO:	3 12854	14902		15419	13297	16331	15331	18941	18941			Ш			_	16567	17093		17260	18383	18303			19908		_	23025	23333	23945
Probe SEQ ID NO:	82	2173	2712	2712	2815	2836	2836	6164	6164	10403	10841	10841	1319	3122	3122	3815	4366	4390	4534	5598	5598	6775	7223	7223	8715	9713	103.70	10642	11284

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	Top Hit Descriptor	Homo expiens mRNA for KJAA0880 protein, partial cds	Homo eaplens mRNA for KIAA0960 protein, partial cds	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA	Homo eapiens mRNA for KIAA0837 protein, pertial ods	Homo sapiens mRNA for KIAA0837 protein, partial cds	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA	Homo eapiens SH3-domain binding protein 1 (SH3BP1), mRNA	Homo septens SH3-domain binding protein 1 (SH3BP1), mRNA	Homo sepiens mRNA for KIAA1342 protein, pertiel cds	Homo suplens ang GDS-ASSOCIATED PROTEIN (SMAP), mRNA	Homo sepiens amg GDS-ASSOCIATED PROTEIN (SWAP), mRNA	Homo saplens NME7 (NME7), mRNA	Homo saplens NME7 (NME7), mRNA	Homo sapiens Kruppel-Ike factor 8 (KLFB), mRNA	Homo saplens phosphatidylinositid 4-kinase 230 (pi4K230) mRNA, complete cds	Homo sepiens phosphetidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5	Homo saplens large conductance calcium- and voltage-dependent potassium channel alpha subunit (Madit) mRNA, complete cds	Homo saplens Xq peeudoeutoecmal region; segment 1/2	Hamo saplens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)	Homo sepiens ublquitin protein ligase E3A (human papillome virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA	no13f07.s1 NCI_CGAP_Pr1 Homo explens cDNA done IMAGE:1008037 similar to SW:RS10_HUMAN P46783 40S RIBOSOMAL PROTEIN S10.	EST54770 Hippocampus II Homo saplens cDNA 5' end	7733b10.x1 NCI_CGAP_CL11 Homo sapiens cDNA done IMAGE:3296443 3' similar to WP:Y47H9C_2	733510.X1 NCI_CGAP_CL1 Homo seplens cDNA clone IMAGE:3296443 3' semilar to WP:Y47H9C.2	CE20283;	Homo sapiens cell-line tsA201a chioride ion current inducer protein I(Cin) gene, complete cds	RC3-CT0254-110300-027-d10 CT0254 Homo septens cDNA
3011103	Top Hit Database Source	NT	LN	L	LN	LN	-	 	F	N	ト	F	5	누	누	N	L	NT	LN	\ L	NT	Ť	ST HUMAN	EST HUMAN	POT LIMAN	ATURNOUS TO	EST_HUMAN		EST_HUMAN
	Top Hit Acession No.	8.0E-57 AB023177.1	8.0E-57 AB023177.1	7862263 NT	1.4	14.1	8923349 NT	11545732 NT	11545732 NT	3.1	7667592 NT	7857592 NT	7242158 NT	7242158 NT	TN 6265009	21	7.0E-67 AF012872.1	7.0E-57 AF020503.1		4-		4507798 NT	1 2	5.1	;	T		П	
	Most Similar (Top) Hit BLAST E Value	8.0E-57	8.0E-57	8.0E-67	8.0E-67 AB02064	8.0E-57 AB02064	8.0E-67	8.0E-57	8.0E-57	8.0E-57 AB03776	7.0E-57	7.0E-57	7.0E-67	7.0E-67	7.0E-57	7.0E-57 AF01287	7.0E-67 A	7.0E-57	7.0E-57 U11058.2	5.0E-67 A	4.0E-57 A	3.0E-57	3.0E-57 AA23027	3.0E-67 AA34833	2 OF 57 B		3.0E-57 B	3.0E-57	3.0E-57
	Expression Signal	12.87	12.87	0.64	1.7	1.7	3.29	2.74	1.99	2.07	1.71	1.71	6.0	0.0	1.08	1.39	1.39	0.95	96.0	263	1.67	0.78	16.24	2.99	8		0.95	1.74	62.34
	ORF SEQ ID NO:		32138		83 4 23			31028	31028		28083	28094	28625	28656	28677	29246	29247		30088		28125	02292		27848	28454		28152	28955	
	Exan SEQ ID NO:	19141	19141	20030	20312	20312	17889	24828	24828	25060	16350	15350	16006	19006	16027	16608	16608	17135	17462	25310	16480	13558	14056	15111	15414		15414	16305	16438
	Prabe SEQ ID NO:	6372	6372	7349	7648	7848	11460	12459	12473	12820	2639	2639	3244	3244	3285	3858	3828	4398	4730	12785	3738	786	1308	2390	2,002		2707	3550	3685

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Probe SEQ ID NO:	Een SEQ ID NO:	ORF SEQ ID-NO:	Expression Signal	Most Similar (Top) Hit BLAST E Vatue	Top Hit Acessian No.	Top Hit Datebase Source	Top Hit Descriptor
5639	18721	31680	124	3.0E-67	11225608 NT	TN	Homo sapiens anglotensin I converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA
9033	18813	31773	3.23	3.0€-57	3.0E-57 BE796537.1	EST HUMAN	601589898F1 NIH_MGC_7 Homo septens cDNA clone (MAGE:3944302 5'
8044	20738	33871	3.77	3.0E-57	3.0E-57 W28130.1	EST_HUMAN	42/8 Human retina cDNA randomly primed sublibrary Homo saplens cDNA
8070	20764	33892	2.16	3.0E-57	11545798 NT	N	Homo saciens hypothetical protein FLJ11656 (FLJ11856), mRNA
9070	20764	33893	2.16	3.0E-57	11545798 NT	NT	Homo sepiens hypothetical protein FLJ11666 (FLJ11656), mRNA
8179	20873	34008	0.7	3.0E-57	11427757 NT	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
8328	21021	34157	0.73	3.0E-57		IN	Human fames y pyrophosphate synthetese mRNA, complete ods
8757	21449	34596	4.17	3.0E-57	3.0E-57 AU117859.1	EST_HUMAN	AU117659 HEMBA1 Hamo sepiens cDNA clane HEMBA1001910 5'
9149	21880	35047	1.03	3.0E-57	11545798 NT	Į,	Homo septems hypothetical protein FL111656 (FL111656), mRNA
8149	21880	35048	1.03	3.0E-67	11545798 NT	NT	Homo sepiens hypothetical protein FLJ11656 (FLJ11656), mRNA
10825	23508	36747	.2.85	3.0E-57	3.0E-57 AW248374.1	EST_HUMAN	2820473.5prime NIH_MGC_7 Homo septens cONA clone IMAGE:2820473 5
12101	25381	30616	8.38	3.0E-57	3.0E-57 W 23871.1	EST_HUMAN	zb45d11,r1 Sceres fetal Jung_NbHL19W Homo septens cDNA clone IMAGE:306549 5
12480	25281		232	3.0E-57	3.0E-57 AW178575.1	EST_HUMAN	RC0-HT0112-080999-001-C06 HT0112 Homo sepiens cDNA
12823	24928	31010	1.48	3.0E-57	3.0E-57 AJ003849.1	EST HUMAN	AJ003849 Selected chromosome 21 cDNA library Homo sepiens cDNA clone MPIpi10-1L1
1487	14234	26919	1.39	2.0E-67	2.0E-67 AF246219.1	NT	Homo sepiens SNARE protein kinase SNAK mRNA, complete cds
1487	14234	26920	1.39	2.0E-57		. LN	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3432	16188		1.24	2.0E-57		NT	Homo sapiene chromosome 21 segment HS21C004
3910	16560	28301	67.0	2.0E-57		EST_HUMAN	WR0-BT0551-080300-103-b03 BT0551 Homo sepiers cDNA
4474	17209	20834	6.73	2.0E-57	2.0E-57 AL163283.2	LN	Homo sapiens chromosome 21 segment HS21C083
CRAS	18370		1 84	2.05.57	2 0E-57 44018131 1	PST HIMAN	2831c05.11 Scenes retina N254HR Homo sepiens cDNA clone IMAGE:380584 5' similar to contains L1.t3 L1 promittus alement
							7/80/04.x1 NCI CGAP Ov18 Homo seniens cDNA clone IMAGE:3570068.3' similar to containe TAR1 H
5043	18725		33.81	2.0E-67	2.0E-67 BF115266.1	EST_HUMAN	MER22 repetitive element;
2909	18846	31810	0.06	2.0E-57	11431281 NT	Z	Homo sepiens small inducible cytokine subfamily A (Cys-Cys.), member 22 (SCYA22), mRNA
8529	21221	34363	1.08	2.0E-57	2.0E-67 AF045452.1	IN.	Homo sepiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
9748	22397	35602	1.86	2.0E-57	2.0E-67 AF067722.1	N.	Homo sepiens 17-bete-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exone 3 and 4
10526	23171	36338	0.49	2.0E-57	11434330 NT	Ę	Homo sepiens KIAA1085 protein (KIAA1085), mRNA
10525	23171	36399	0.49	2.0E-57	11434330 NT	Ę	Homo sepiens KIAA1065 protein (KIAA1065), mRNA
11238	23901	37189	2.42	20E-57	11424084 NT	Z	Homo sepiens hypothetical protein FLJ20041 (FLJ20041), mRNA
11238	23901	37190	2.42	2.0E-57	11424084 NT	Ę	Homo expleme hypothetical protein FLJ20041 (FLJ20041), mRNA
8593	21285		3.62	1.0E-57	1.0E-57 BE043031.1	EST_HUMAN	ho32s08.x1 NCLCGAP_Lu24 Homo septens cDNA clone IMAGE:3039062.3' similer to TR:000246 000246 HYPOTHETICAL 9.3 KD PROTEIN;
12249	24696		5.08	1.05-67		EST HUMAN	ha33d06.x1 NCI_CGAP_Kid12 Homo sepiens aDNA clone IMAGE:2875499 3' similar to contains THR.b3 THR receifthe element:

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Table 4
Single Exon Probes Expressed in Brain

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Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Detabase Source	Top Hit Descriptor
1267	14016		10		2.0E-58 BE208632.1	EST_HUMAN	be08b07.y1 NIH_MGC_7 Homo septens cDNA clone IMAGE:2823733 5' similar to gb:X80391 60S RIBOSOMAL PROTEIN L6 (HUMAN); gb:X81987 M.musculius mRNA for TAX responsive element binding protein (MOUSE);
5273		30708	3.4		2.0E-58 BE907186.1	EST HUMAN	801499961F1 NIH_MGC_70 Homo septens cDNA clone IMAGE:3901911 5'
5273		30734			2.0E-58 BE907186.1	EST_HUMAN	601499961F1 NIH_MGC_70 Hamo septens cDNA clone IMAGE:3901911 5'
2966	18748	31709	1.12		2.0E-58 BF513488.1	EST_HUMAN	UI-H-BW 1-ems-g-11-0-UI.s1 NCI_CGAP_Sub7 Homo septens cDNA clone IMAGE:3071060 3'
							em57e02.x1 Johnston frontal cortex Homo sepiens cDNA clone IMAGE:1539674 3' similar to WP-ZK328.1 CE05065 UBIQUITIN CONJUGATING ENZYMEY, RECOVERIN SUBFAMILY OF EF-HAND CALCIUM
9031	18811	31771	1.88		2.0E-58 AI124874.1	EST_HUMAN	BINDING PROTEIN;
6062	1884	31803	0.8	2.0E-58	2.0E-58 R92567.1	EST_HUMAN	yq08h06.r1 Soeres fetal liver spleen 1NFLS Homo saplens cDNA done IMAGE:196379 5
6828		32511	1.12		2.0E-58 AI291407.1	EST_HUMAN	qm84c01.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:18954243'
7056	i	32809	2.83	2.0E-58	2.0E-58 AF134838.1	LN	Homo sepiens endocytic receptor Endo180 (ENDO180) mRNA, complete ods
7056		32810	2.83	2.0E-58	2.0E-58 AF134838.1	Į.	Hamo sepiens endacytic receptor Endo180 (ENDO180) mRNA, complete cds
10641		38570	21.77	2.0E-58	2.0E-58 BF307745.1	EST_HUMAN	801890812F1 NIH MGC_17 Hano saplens cONA done IMAGE:4131891 5'
10885	23585	35813	2.43	2.05-58	2.0E-58 AW872641.1	EST_HUMAN	hm25f08.x1 NCI_CGAP_Thy Home septens cDNA clone IMAGE:30136713'
705	13480	28128	0.86	1.0E-58	1.0E-58 M65134.1	Ę	Human complement component C5 mRNA, 3'end
1046	13805	28464	241	1.06-58	TV 0724540 NT	5	Homo saidens NADH dehufmoornasse (rithinstones) 1 hats subcommulae 0 (2000 B20) (ND) (EDO)DAIA
1304		28728	1.61	1.0E-58	1.0E-58 AW957182.1	EST HUMAN	EST389252 MAGE resequences. MAGD Homo serviens cDNA
1304	14053	28727	1.61	1.05-58	1.0E-68 AW967182.1	EST HUMAN	EST369252 MAGE resequences, MAGD Hamo sepiens cDNA
1376	14124	26798	1.13	1.0E-58	1.0E-58 AJZ38093.1	N.	Homo sapiens partial AF-4 gene, excres 2 to 7 and Alu repeat elements
2805		28251	2.37	1.0E-58	4750160 NT	F	Homo sepiens stand regulatory element binding transcription factor 2 (SREBF2) mRNA
2834		27462	1.6	1.0E-58	5174444 NT	LN	Homo seplens G protein-coupled receptor 69A (GPR69A) mRNA
3526		28938	0.88	1.0E-58	4758081 NT	NT	Homo seplens chandratin suifate proteoglycan 2 (versican) (CSPG2) mRNA
3228		28939	0.88	1.0E-58	4758081 NT	NT	Homo sapiens chondroltin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
49 3	Ì	30256	4.75	1.0E-58	1.0E-58 AI141063.1	EST_HUMAN	oz/3h01.x1 Soares_NhHMPu_S1 Homo sepiens cDNA clone IMAGE:1678129 3'
5751	18543	31465	1.31	1.0€-58	1.0E-58 BE061890.1	EST_HUMAN	RC1-BT0254-290100-015-e01 BT0254 Homo sepiens cDNA
9764	19508	32533	9.0	1.0E-58	11422031 NT	NT	Homo sepiens hypothetical protein (LOC51280), mRNA
8013	20708		0.5	1.0E-58	1.0E-58 AW973537.1	EST_HUMAN	EST385637 MAGE recequences, MAGM Homo septens cDNA
8768	21460	34609	0.88	1.0E-58	4505314 NT	Ę	Homo sepiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA
8880	21571	34714	16.0	1.0E-58	1.0E-58 AV751001.1	EST_HUMAN	AV751001 NPC Hamo septens cDNA clane NPCACH09 51
8070	21669	34818	0.98	1.0E-58		EST HUMAN	z/99f06.r1 Sceres_testis_NHT Homo septens cDNA clone IMAGE:730497 5'
8979	21669	34819	0.08	1.0E-58	1.0E-58 AA412397.1	T_HUMAN	2199/05.r1 Sceres_bests_NHT Homo septens cDNA clone INAGE:730497 5'
10086	22734	32949	1.21	1.0E-58	11432994 NT		Homo sepiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2), mRNA

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Single Excit Flores Expressed in Diani	Con ORF SEQ Expression (Top) Hit Accession ORF SEQ Expression (Top) Hit Descriptor Top Hit Descriptor Signel BLASTE No. Source	4371 2.11 1.0E-68 X63392.1 NT H.sepiens immunoglobulin keppa light chein verleble region L14	37739 1.57 1.0E-58 D81405.1 NT	27691 29.49 8.0E-59 4507378 NT	33904 2.49 8.0E-59 AI781963.1 EST HUMAN	1.74 6.0E-59 BF035327.1 EST_HUMAN	33970 0.61 6.0E-59 AI750970.1	4490 27189 1.32 5.0E-59 AW157281.1 EST HUMAN TR:O75789 O75789 GANGLIOSIDE-INDUCED DIFFERENTIATION ASSOCIATED PROTEIN 1.	27190 1.32 6.0E-59 AW157281.1 EST HUMAN	28530 6.98 5.0E-59 Al807484.1	23978 6.55 5.0E-59 X83497.1 NT	30526 7.5	34544 1.04 5.0E-59 11421778 NT	35443 1.62 5.0E-59 AV76288	36745 3.78 5.0E-59 11434908 NT	28210	31138 1.03 4.0E-59 11034810 NT	1.91 4.0E-59 AF057720.1 NT Homo sepiens 17-bets-hydroxysteroid dehydrogenese IV (HSD17B4) gene, promoter region and exon 1	6.13	25666 4.58 3.0E-59 7862247 NT	27147 8.2 3.0E-59 4505860 NT	27148 8.2 3.0E-59 4505860 NT	27585 5.59 3.0E-59 AB029035.1 NT	27586 5.59 3.0E-59 AB029035.1 NT	29634 3.77 3.0E-69 450.2014 NT Homo sepiens A kinese (PRKA) enchor protein 1 (AKAP1), mRNA	28535 3.77 3.0E-59 4502014 NT	29189 1.45 3.0E-59 4508044 (NT	30007 0.98 3.0E-59[AL163284.2 NT	
																												l	
	Be Econ ID SEQ ID NO:	11780 24371	11816 24404	225 14953	8080 20774	173 15536	8144 20838	1748 14490	1748 14490	3124 15889	4810 17345	6892 17958	1	1	10823 23508	776 13548	5450 18249	12203 25238	9 12836	219 13030		1705 14448	2125 14856		15891				4738 17470
	Probe SEQ ID NO:	÷	ξ	121	Ø.	Ĺ		=	-	မြ	4		80	ă	ĕ	_	, A	74			1,		Ä	2	3,	<u>ب</u>	8	¥	47

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Top Hit Descriptor	Homo sepiens protein tyroeine phosphatase, receptor type, T (PTPRT), mRNA	Human prohormone converting enzyme (NEC2) gene, exon 2	Homo saplens hypothetical protein PRO1741 (PRO1741), mRNA	Homo seplens nuclear receptor co-repressor 1 (NCOR1), mRNA	Human mRNA for dbl proto-oncogene	Human mRNA for dbi proto-oncogene	H. sapiens CKII alpha gene.	H. sapiens CKI siphe gene	Homo sapiens gemme-gluternytransferasse-like activity 1 (GGTLA1), mRNA	MR0-FT0144-250700-002-e10 FT0144 Homo sepiens cDNA	EST180633 Jurket T-cells V Homo sepiens cDNA 5' end	RC0-NT0036-100700-032-e07 NT0036 Homo sepiens cDNA	fn07h04x1 NIH_MGC_17 Hamo septens cDNA clone IMAGE:2961654 5	fh07h04.x1 NIH_MGC_17 Homo sapiens cDNA done IMAGE-2961654 51	y49h09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:208673 5 similar to	SP:POL_FENV1 P31702 POL:POLYPROTEIN;	we36c12.x1 NO_CGAP_Kid11 Homo sepiens cDNA clone IMAGE:2300182 3' similar to TR:Q86542 Q86542 RTVL-H PROTEIN ;contains LTR7.b1 LTR7 repetitive element;	Homo saplens alpha-tubulin mRNA, complete cds	601176757F1 NIH_MGC_17 Hamo sepiens oDNA clane IMAGE:3631927 61	ye25c09.r1 Stratagorre lung (#837210) Homo sepiens cDNA clone IMAGE:118768 5' similar to SP:S21348 S21348 HYPOTHETICAL PROTEIN 4 - :	Homo sapiens Xdha mRNA for xanthine dehydrogenase, complete cds	Homo sapiens Xdha mRNA for xanthine dehydrogenase, complete cds	0e56h11.81 NCL_CGAP_GCB1 Homo septens dDNA clone IMAGE:1309029 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE.	Homo sepiens mRNA for transcription factor	601111851F1 NIH_MGC_16 Hamo septens cDNA clone IMAGE:3352692 57	801111951F1 NIH_MGC_16 Homo sepiens cDNA clone IMAGE:3352692 5'	Homo saplens zinc finger protein 275 (ZNF275), mRNA	Homo saplens 3-hydraxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA	Homo sepiens 3-hydraxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA	Homo sepiens mRNA for transcription factor	EST389849 MAGE resequences, MAGO Homo septens cDNA
Top Hit Detribese Source		1 LN			TN	Į,	Z	F		EST_HUMAN N	EST_HUMAN E	EST_HUMAN F	EST HUMAN 1	EST HUMAN	Г	EST HUMAN S	EST_HUMAN C	П	Г	EST HUMAN S	Г	F	EST HUMAN	Т	T_HUMAN						EST HUMAN E
Top Hit Acession No.	7427522 NT	.1	8924074 NT	6464137 NT	1	1	4	1	11417866 NT	20.1	14.1	3F365554.1	20E-59 AW410898.1	2.0E-59 AW410898.1		161604.1	9.1	L	1.1	4-	_	2	1.0E-59 AA748468.1		1.4	14.1	11419630 NT	11428849 NT	8840		8.0E-60 AW977845.1
Most Similar (Top) Hit BLAST E Value	3.0E-59	3.0E-59 M95981	3.0E-59	3.0E-50	3.0E-59 X12556	3.0E-59 X12556.	3.0E-59 X70251.	3.0E-59 X70251	3.0E-59	2.0E-59 BF37333	2.0E-59 AA3097	2.0E-59 BF36555	20E-59	2.0E-59		2.0E-59 H61604.	2.0E-59 AIC3180	2.0E-59 L11645.	1.0E-59 BE2964	1.0E-59 T92522	1.0E-59 D11456.	1.0E-59 D11456.	1.0E-59/	1.0E-59/	1.0E-59 BE2568	1.0E-59 BE2568	1.0E-59	1.0E-59	1.0E-50	.1.0E-59	8.0E-50/
Expression Signal	1.57	26.0	2.12	1.94	1.18	1.16	78.0	0.87	6.04	0.71	6.32	1.19	2.6	2.8		1.31	2.93	4.65	3.03	0.83	1.19	1.19	2.47	1.08	76.0	76.0	0.86	0.54	0.54	12.88	0.85
ORF SEQ ID NO:	30143		31872	33020	33653	33654	35794	35795					36663	36864		37274	31126	30719		. 28934	27870	27871		33227	33392	33393	35210	35337	35338	33227	28178
SEQ ID NO:	17520	17713	18904	19943	20527	20227	22592	22592	24746	20357	22190		23421	23421		23970	24595	25263	12974	14276		15133	15335	20135	20283	20283	22039	22157	22457	20135	13520
Probe SEQ ID NO:	4789	4990	6126	7259	7832	7832	9944	8944	12327	7603	9537	10425	10734	10734		11311	12091	12805	169	1529	2412	2412	2823	7462	7197	7817	9282	9504	9504	10760	747

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Top Hit Descriptor Source	1597 NT Homo sapiens wref-1 murine leukemia viral oncogene homotog 1 (RAF1), mRNA	EST HUMAN 601336446F1 NIH MGC 44 Homo septens cDNA clone IMAGE:3690395 5	Г			EST HUMAN QV4-NN1146-250900-423-f01 NN1146 Homo sapients oDNA	EST HUMAN RC3-L10023-200100-012-401 L10023 Homo septens cDNA	d60h11.x6 NCI_CGAP_Kid3 Homo sepiens cDNA clone IMAGE:1534053 5' similar to SW;UDP_MOUSE. EST_HUMAN P52824 URIDINE PHOSPHORYLASE:	ı		Ox58409.X1 Sources, NIH1MPu_S1 Homo sepiens cDNA done IMAGE:1880337.3' similar to EST HUMAN SW:FORM MOUSE Q05880 FORMIN;	644 NT Homo septens profine dehydrogenese (profine addass) (PRODH) mRNA	T HUMAN			ab07h04.r1 Strategene king (#837210) Homo saplens cDNA clone IMAGE:840151 5' similar to contains EST_HUMAN LTR10 trapetitive element;			NT Human ber protein mRNA, 5' end	NT Homo seplens solute cerrier (SLC25A18) mRNA, complete cds; nuclear cene for mitochondrial product	Т	1757967 NT Homo septens v-raf murithe sarcoma West oncogene homolog B1 (BRAF) mRNA	T	Inn01f12.y5 NCI_CGAP_Co9 Homo septens cDNA clone IMAGE:1076495 5' strailer to contains THR.t1 THR	Т			
Top Hit Acession No.	11433597 NT	3.0E-60 BE562611.1 E	1.1	W31190 NT	3.0E-60 AJZ71735.1 N	3.0E-80 BF365143.1 E		3.0E-60 AI792814.1	5174844	5174644 NT	3.0E-80 Al040235.1 ES	5174644	3.0E-60 BF102612.1 E	427120	11427120 NT	3.0E-60 AA485286.1 E	-		2.0E-60 M24603.1 N	2.0E-60 AY008285.1	AW978005.1 ES	2.0E-80 4757867 N	20E-60 AF231919.1 NT			5	4603044 N	TNIAACANA
Most Similar (Top) Hit BLAST E Value	4.0E-80	3.0E-80	3.0E-80	3.0E-80	3.0E-90	3.0E-80	3.05-60	3.0E-90	3.0E-80	3.0E-80	3.0E-90),	3.05-60	3.05-80	3.0E-80	3.0E-80	3.0E-80	2.0E-80	2.0E-80	2.0E-80	205-80	2.0E-80,	2.0E-80	20E-00	10 C	20E-00 AF004877	2.0E-80 /	2.0E-80	O OF AN
Expression Signal	123	4,44	4.44	1.92	1.94	0.57	2.12	1	4.97	4.97	0.51	4.32	0.47	1.28	1.26	2.06	3.8	7.35	1.29	1.50	1.96	0.00	0.73	88.0	1.87	0.50	2.43	274
ORF SEQ ID NO:	37220	27305	27306				31260	30508	34132	34133	34310	34477	35398	37107	37108		25474	28831	27155	27106	28160	28069	29285	31962	32168	32303	30683	30594
Exan SEQ ID NO:	23929	14590	14590	14600		18090	18351		20805	20995	21174	21333	22212	23820	23829	25297	12857	14151	14468	14467	15421	16321	16645	18083	19169	19378	17919	47040
Probe SEQ ID NO:	11267	1852	1852	1862	4424	5294	5554	6856	8301	8301	8482	9841	8228	11162	11162	12686	82	1404	1715	1724	2714	3596	3865	8208	80	6615	6750	R7EO

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Top Hit Descriptor	Homo sapiens PXR2b protein (PXR2b), mRNA	Homo saplens PXR2b protein (PXR2b), mRNA	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'	601300938F1 NIH_MGC_21 Hamo septens cDNA clone IMAGE:3635480 5'	Homo saplens PR02014 mRNA, complete cds	601109238F1 NIH_MGC_16 Hamo sepiens cDNA clone IMAGE:3350145 5'	nn68h09.s1 NCI_CGAP_Ler1 Homo sapiens cDNA clone IMAGE:1088897 3'	Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochandrial product	AU130689 NT2RP3 Hamo sepiene cDNA clone NT2RP3001263 5	lg-beta/B29≕CD79b (atternatively spliced) [human, B cells, mRNA Partial, 375 nt]	Human autosomal dominant polycystic kichey disease protein 1 (PKD1) gene	Homo sapiens general transcription factor 2-I (GTF2I) mRNA, complete cds	Homo sapiens napsin A mRNA, complete cds	Homo saplens napsin A mRNA, complete cds	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5	Homo sapiens T-cell lymphome investon and metastasis 1 (TIAMI) mRNA	Homo saplens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA	Homo sapiens chromosome 21 segment HS21C079	Homo sapiens amykidd beta (A4) precursor protein (protesse nedn-II, Alzhetmer disease) (APP), mRNA	Homo saplens 959 lds config between AML1 and CBR1 on chromosome 21q22; segment 1/3	Homo saplens T-cell lymphoma invasion and motastasis 1 (TIAM1) mRNA	Homo sapiens ATPase, Ca++ transporting, plasma membrane 1 (ATP2B1) mRNA	Homo sepiens DKFZP568B023 protein (DKFZP568B023), mRNA	AV731140 HTF Homo sapiens cDNA clone HTFARB01 6	AF150190 Human mRNA from cd34+ stem cells Homo sapiens cDNA clone CBDAGB04	EST14323 Testis tumor Homo sepiens cDNA 5' end	EST14323 Testis tumor Homo sepiens cDNA 5' end	Homo saplens hypothetical protein PLJ11026 (FLJ11026), mRNA	QV3-HT0513-060400-147-d01 HT0513 Homo saplens cDNA	QV3-HT0513-080400-147-d01 HT0513 Hamo sapiens cDNA	yv53d11.s1 Soares fetal liver spieen 1NFLS Homo sapiens cDNA clone IMAGE:246453 3' shnilar to gb:L25444 6cS RIBOSOMAL PROTEIN L35A (HUMAN);
Top Hit Databese Source	TN	TN	EST_HUMAN	EST_HUMAN	LN	EST_HUMAN	EST HUMAN	TN	EST_HUMAN	IN.	IN	N _T	L	ĮN	EST_HUMAN	NT.	NT.	NT	IN IN	LN TN	TN	LN	TN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	N	EST_HUMAN	EST HUMAN	EST_HUMAN
Top Hit Accession No.	T708670	TN06670 NT	BE409310.1			6.0E-61 BE257400.1	П	6.0E-61 AY008285.1	6.0E-61 AU130689.1			7.1	6.0E-61 AF090386.1	6.1	0.1	4507500 NT	4506008 NT	9.2	4502166 NT		4507500 NT	4502286 NT	7881637 NT	4.0E-61 AV731140.1	3.0E-61 AF150190.1	3.0E-61 AA301233.1	3.0E-61 AA301233.1	8922829 NT	2.0E-61 BE168410.1	2.0E-61 BE168410.1	
Most Similar (Top) Hit BLAST E Value	7.0E-61	7.0E-61	6.0E-61	6.0E-61 BE40931	6.0E-61	6.0E-61	6.0E-61	6.0E-61	6.0E-81	6.0E-61 S79249.1	6.0E-61 U24498.	6.0E-61 AF03573	0.0E-01	6.0E-61	6.0E-61 BE40931	5.0E-61	5.0E-81	. 5.0E-61 AL16327	5.0E-61	5.0E-81 AJ22904	5.0E-81	5.0E-61	4.0E-81	4.0E-61	3.0€-61	3.05-61	3.0E-61	2.0E- 0 1	2.05-61	2.0E-61	2.0E-61 N53039.
Expression Signal	1.04	1.04	2.95	1.62	15	26.0	2.63	1.58	75.6	3.37	1.82	1.67	1.35	1.35	1.62	1.73	2.22	2.58	3.27	1.78	1.07	3.38	0.87	3.51	0.09	0.64	0.64	1.52	0.82	0.82	-
ORF SEQ ID NO:	25583	25584	25705		26719	27061	27078	27.583	28711	31682	33003	33282	37384	37385	26226	25789	27112	28444	28608		25789	30416	31438		34151		34428	25906			27097
Exen SEQ ID NO:	12941	12941	13067	13565	14047	14372	14389	14854	16063	18723	19927	20189	24075	24075	13565	13149	14419	15798	15956	16712	13149	17799	18517	24582	21013	21288	21288	13271	13942	13942	14406
Probe SEQ ID NO:	5034	268	250	28	1288	1628	1643	2123	3301	5941	7242	7518	11474	11474	12265	330	1674	3032	3183	3963	4941	2080	£229	12068	8320	8598	8596	\$	1190	1190	1680

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Probe	Exam	į,	Most Similar		Teb ∰	
	SEQ ID ON: NO:	Signal	(Top) HR BLAST E Value	I op Hit Acession No.	Detabase Source	Top Hit Descriptor
2847 1	15357	1.04	2.0E-81	2.0E-61 N39397.1	EST_HUMAN	yy03f11.r1 Scares melanocyle 2NbHM Homo sepiens cDNA clone IMAGE:270189 5'
	19102 32090	0.98	2.0E-61	11428188 NT	\ L	Homo sapiens ATPase, H+ transporting, lysosomal (vacuotar proton pump) non-catalytic accessory protein 14 (110/116kD) (ATPetv1A), mRNA
8913 2				AV694317.1	EST_HUMAN	AV604317 GKC Homo sepiens cDNA clone GKCELG06 5
	22012	0.99	20€-61	AB011108.1	NT	Homo sapiens mRNA for KIAA0538 protein, pertial cds
		1.67	2.0E-61	2.0E-61 AW 500258.1	EST_HUMAN	UI-HF-BNO-ekd-f-12-0-UI.r1 NIH_MGC_50 Hamo sepiens cDNA clane IMAGE:30787745
10150 2	22798 38014	2.3	2.0E-61	11421778 NT	NT.	Homo sapiens polymerase (RNA) III (DNA directed) (39kD) (RPC39), mRNA
10799 23	23482	1.81	2.0E-61	11419729 NT	LN	Homo sepiens ribosomei protein L44 (RPL44), mRNA
756 13	13528 26188	1.11	1.0E-61	5453829 NT	N.	Homo sapiens origin recognition complex, subunit 2 (yeast homolog)-like (ORC2L) mRNA
1851 14	14589 27304	3.71	1.0E-81	9005983 NT	FN	Homo sapiens zona pellucida giyoqrotein 3A (sperm receptor) (ZP3A), mRNA
2193	14922 27856	1.42	1.05-61	1.0E-61 AW827281.1	EST HUMAN	xn11b09.y1 NCI_CGAP_LI5 Homo sepiens cDNA done IMAGE:2893389 5' similar to contains element MSR1 recettive element:
L			1.0E-61	Γ	EST HUMAN	801273513F1 NIH MGC 20 Homo sapiens cDNA clone IMAGE:3614887 5'
			1.0E-61	2319	N N	Hamo sepiens KIAA0806 gene product (KIAA0806), mRNA
3715 16	16468 29106	1.2	1.05-61	1.0E-61 BE174455.1	T HUMAN	QV2-HT0577-140300-077-g06 HT0577 Homo sepiens cDNA
4407 17	17144 29773	0.81	1.0E-61	4759249 NT	Į	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
4407 17	17144 29774	0.81	1.0E-61	4759249 NT	LN.	Homo sapiens TRAF family member-essociated NFKB activator (TANK) mRNA
		8.11	1.0E-61			UI-H-BW0-4ft-b-08-0-UI.s1 NCI_CGAP_Sub8 Hamo septens cDNA dane IMAGE:2732871 3'
		8.11	1.0E-61	31.1	T_HUMAN	UI-H-BW0-ajt-b-08-0-UI.s1 NCI_CGAP_Sub6 Homo sepiens cDNA clone IMAGE:2732871 3'
4905 17	17632 30247	0.75	1.0E-61	1.0E-61 AL163210.2	LNT.	Homo sapiens chromosome 21 segment HS21C010
		1.62	1.0E-61 M76423.	1	INT	H. saplens carbonic anhydrase VII (CA VII) gene, exons 4,5,6, and 7, and complete cds
5603 18	18308 31310	0.79	1.0E-61	7862303 NT		Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
	18584 31511	1.29	1.0E-81	11416891 NT		Homo sapiens survival of motor neuron 1, telomeric (SMN1), mRNA
	19461 32482	7.11		M30135.1	NT.	Human P40 T-cell and mast cell growth factor (hP40) gene, complete cds
	19684 32732	0.67	1.0E-61	4759171 NT	LN	Homo sapiens SC35-Interacting protein 1 (SRRP129), mRNA
	19780 32845	1.42	1.0E-61	8923130 NT	LN	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
	19780 32846	1.42	1.0E-81	8923130 NT	TN	Homo sepiens hypothetical protein FLJ20128 (FLJ20128), mRNA
8033 20	20728 33861	3	1.0E-61	11034840 NT	LN.	Hano sapiens growth harmone releasing hormone (GHRH), mRNA
200	24044		40.4	4 00 00 4 00 00 4	Ļ	Homo sapiens mannosidase, beta A, Iyeosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
Ш			100	,	100000	NEO BRIOGRAM AND AND BRIDGED LESS CONTRACTOR OF THE STATE
	21002	7.73	1.05.01	AW888/20.1	NOW N	Mrvd-Druck Code 400-0 10-10 I Druck of The Sapiets CLANS Home carians cacher 48 (CDH48) mRNA
L			100.0	TIN CORROLL	F	Homo september XIAA0074 mmtain (XIAA0074) mRNA
1			2 10 10	11420032 IN	F-2	Home carbons artists alone 4 (ACTINA) mana
j	╽		1.00.01	0/007411		

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	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accesion No.	Top Hit Database Source	Тор Hit Descriptor
10855	23535	36780	1.40	1.0E-61	1.0E-61 AB044550.1	IN	Hono sapiens P/OKcl.19 mRNA for ubiquitin-conjyugating enzyme E2, complete ods
11006	23678	36935	1.53	1.0E-61	1.0E-61 AB007830.1	IN	Homo saplens mRNA for CSR2, complete cds
12007	25273	30726	3.02	1.0E-61	11430460 NT	LN L	Homo saplens fow density thoprotein-related protein 2 (LRP2), mRNA
12007	25273	30727	3.02	1.0E-61	11430460 NT	Z.	Homo saplens low density lipoprobain-related protein 2 (LRP2), mRNA
12659	24959	30888	11.58	1.0E-61	11418127 NT	IN	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
10255	22903	36113	1.45	9.0E-62 BE0643	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
4614	17249	20885	1.1	8.0E-62 AAB304	8.1	EST HUMAN	0085h11.s1 NCI_CGAP_GCB1 Homo septens cDNA clone IMAGE:1354725 3' similer to SW:POI_MLVRK P31705 POLYPROTEIN;
1085	13843	28501	1.62	7.0E-62	7.	EST HUMAN	AV714334 DCB Homo septens cDNA done DCBAMA08 5
3407	16253	28907	0.74	7.0E-62 P17480	P17480	SWISSPROT	NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1) (AUTOANTIGEN NOR-60)
5826	18615	31547	0.64	7.0E-62	11427985 NT	TN.	Homo saplens hypothetical protein (FL/20281), mRNA
11323	24014	37317	7.1	7.0E-62	AI20868	EST_HUMAN	qg58a04.x1 Soeres lestis. NHT Homo sepiens dDNA clone IMAGE:1830150 3' similar to TR:015103 015103 HYPOTHETICAL 27.3 KD PROTEIN.;
2888	15764	-	1.42	6.0E-62		LN LN	Human zho finger protein ZNF131 mRNA, pertial cds
3379	16138		4.1	6.0E-62 1	11418255 NT	NT	Homo sapiens CGI-66 protein (CGI-66), mRNA
	20196	33280	3.03	6.0E-62 AI76280		EST HUMAN	wi04d02x1 NCI_CGAP_CLL1 Home expiens cDNA clone IMAGE2389251 3'
7525	20198	33290	3.03	6.0E-62 A176280	Al762801.1	EST_HUMAN	wi04d02.x1 NCI_CGAP_CL1 Homo septens cDNA clane IMAGE:2389251 3'
	20679	\vdash	0.72	6.0E-62 AW 50112	4.1	T_HUMAN	UI-HF-BP0p-att-d-08-0-UI_r1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072833 5'
8155	20849	33981	1.45	6.0E-62	11431130 NT	NT	Homo sepiens CGI-18 protein (LOC51008), mRNA
9254	21933	35106	3.27	6.0E-62	6.0E-62 AW814393.1	EST_HUMAN	MR3-ST0203-130100-025-e09 ST0203 Homo sepiens cDNA
407	13192	25840	2.8	5.0E-62		EST HUMAN	wo51e07.x1 NCI_CGAP_LL28 Homo septens cDNA done IMAGE:2547204 3' stimiter to SW:GG95_HUMAN Q08379 GOLGIN-95, ;contains element MER22 repetitive element;
2406	15127	27863	4.25	6.0E-62	6.0E-62 AJ271735.1	Z	Homo sapiens Xq pseudosutosomal region; segment 1/2
2406	15127	27864	4.25	5.0E-62 AJ27173	5.1	Z	Homo saplens Xq pseudosubscamal region; segment 1/2
	15312	28048	1.35	5.0E-62 U39487.	1	IN	Human xantitine dehydrogenasse/oxidase mRNA, complete cds
	16312	28040	1.35	5.0E-62 U39487	-	LZ.	Human xanthine dehydrogenese/coddese mRNA, complete cds
3413	16171	28820	2.92	5.0E-62	4506758 NT	FN.	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
4203	17032	20880	2.6	5.0E-62	5.0E-62 AA431093.1	EST HUMAN	2w78e09.s1 Soares_testis_NHT Homo sepiens cDNA clone IMAGE:782344 3' similar to SW:NRDC_RAT P47245 NARDILYSIN:
L	2130	34278	9.55	5.0E-62	67.28		Homo saplens ryanodine receptor 3 (RYR3) mRNA
	22095	35267	6.45	5.0E-02	AW410687.1	T_HUMAN	fn07g09.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2961616 5'
	23804	37180	2.85	5.0E-62	11426574		Homo saplens muscle specific gene (MG), mRNA
11231	23894	37181	2.85	5.0E-62	11425574 NT		Homo sapiens muscle specific gene (M8), mRNA

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Single Exon Probes Expressed in Brain

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Probe SEQ ID NO:	Esan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8438	21130	34287	5.82	3.0E-62	3.0E-62 Al632733.1	EST HUMAN	ws33f04.x1 NCI_CGAP_Kid11 Homo sepiens cDNA clone IMAGE:2299903 3' similar to conteins THR.t2 THR repositive element;
1209	13960	28627	236	2.0E-62		TN	Homo sapisns chromosome 21 segment HS21C084
8673	21365		4.89	2.0E-62	2.0E-62 BF329911.1	EST_HUMAN	RC0-BN0284300500-031-e05 BN0284 Homo sapiens oDNA
8673	21365	34512	4.89	2.0E-62	2.0E-62 BF329911.1	EST_HUMAN	RC0-BN0284-300500-031-e05 BN0284 Homo sapiens cDNA
10072	22720		3.8	2.0E-62	2.0E-62 AF224669.1	LN	Homo saplens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
11689	24284		4.81	2.0E-62		EST HUMAN	QV4-BT0257-081199-017-e03 BT0257 Homo septens cDNA
1021	13781	26443	1.87	1.0E-62			Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
1536	14283	28970	11.01	1.0E-62 L78810.1		LN L	Homo sapiens ADP/ATP carrier problem (ANT-2) gene, complete cds
1704	14531	06626	70 7	4 OF A2	1 0F-62 A 4625207 1	NALE: H TAR	eff0e11.rt Soeres_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1047404 5' similar to WP:K01H12.1 CFR3488
2915		28328	80	1.0E-82 AL03904		EST HUMAN	DKFZp568F104 r1 568 (synonym: hftd2) Homo septens cDNA clone DKFZp568F104 5
4317	<u> </u>		0.71	1.0E-82	3.1	EST HUMAN	QV0-HT0483-280200-135-h12 HT0493 Homo septens cDNA
4490	17228	29855	1.57	1.0E-62	TN 1923201	LN	Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA
5071	17790		6.0	1.0E-62 L23503.	4	N.	Human glucagon-like peptide-1 receptor (GLP-1) mRNA, complete cds
							Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal
92	18972	31948	98.0	1.0E-82	1.0E-82 U52111.2	Ž	protein L18a (RPL18a), Ca2+/Catmodulin-dependent protein kinase i (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleutodystrochy protein >
78	L	L	10.0	1.0E-82	5	EST HUMAN	ab05c02.s1 Stratagene fetal retine 937202 Homo sapiens cDNA clone IMAGE:839906 3'
7045	19736	32796	2.94	1.0E-62	1.0E-62 AA722878.1	EST_HUMAN	2989110.s1 Soeres fetal_heart_NbHH19W Homo septens aDNA dane IMAGE:409771 3'
7045	19736		294	1.0E-62	1.0E-62 AA722878.1	EST_HUMAN	2089710.s1 Soares_fetal_heart_NbHH19W Homo septens cDNA clone IMAGE:409771 3*
8655	21347	34401	0.5	1.05-82	1.0E-62 AA280050.1	EST_HUMAN	2883e07.r1 NCI_CGAP_GCB1 Hamo sepiens cDNA clone IMAGE:705080 5
8968		34797	2.13	1.0E-62	7662289 NT	LΝ	Homo saplens KIAA0763 gene product (KIAA0763), mRNA
8858		34798	2.13	1.0E-62	7662289 NT	IN	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
8000			2.02	1.0E-62 X15533.	1	LN	H. saplens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9
6008			2.02	1.0E-62		FN	H. sapiens tycocomel acid phosphatase gene (EC 3.1.3.2) Exon 9
9457	20022	35177	3.54	1.0E-62 AA465170	-	EST_HUMAN	as33d08.s1 NCI_CGAP_GCB1 Homo sepiens cDNA clone IMAGE:815055 3'
11339	24029	37333	2.01	1.0E-62 Z78698.		ĮN.	H.saplens flow-scried chromosome 6 Hindill fragment, SC8pA14D8
11866	24450	37782	1.52	1.0E-62	11424055 NT	LN.	Homo sapiens exosome component Rrp48 (LOC56915), mRNA
12474	24838		2.25	1.0E-62	11418322 NT	L	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
12873	24966	30390	2.99	1.0E-62	11430460 NT	L	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
88	13130	25765	2.59	9.0E-€3	06.1	EST_HUMAN	QV4-ST0234-181199-037-105 ST0234 Homo saplens dDNA
8	15068		1.53	9.0E-63 C18159.		EST_HUMAN	C18159 Human placenta cDNA (TFujiwara) Homo sapiens cDNA clone GEN-558C10 5

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4020	16706	28395	7.42	L	9.0E-63 AB002348.2	M	Homo saplens mRNA for KIAA0350 protein, pertial cds
4020	16786	20398	7.42		9.0E-63 AB002348.2	LN TN	Homo saplens mRNA for KIAA0350 protein, partial cds
5164	17895	37798	3,05	9.0E-63	11418185 NT	ΙN	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
5379	18179	30869	1.63		9.0E-63 Y15056.1	NT	Homo sapiens mRNA for PkB kinase
7082	19772	32837	38.6	9.0E-63	11426985 NT	NT	Homo saplens nucleopartn 88kD (NUP88), mRNA
7724	20387	33501	0.81	9.0E-63	4885544 NT	NT TA	Homo saplens pyruvate defrydrogenase kinase, isoenzyme 3 (PDK3) mRNA
8224	20918	34055	1.38		11421160 NT	Ā	Homo sapiens Ras association (RaiGDS/AF-6) domain family 2 (RASSF2), mRNA
10816	23499	36736	2.03	9.0E-83	7882289 NT	NT	Homo saplens KIAA0763 gene product (KIAA0763), mRNA
10816	23499	36737	2.03	9.0E-63	7662289[NT	NT	Homo sapiens KIAA0783 gene product (KIAA0763), mRNA
2343	15066	27803	1.32	8.0E-63	4557734 NT	Ę	Homo sapiens monoamine oxidase A (MAOA), nuclear gene encoding mitochondrial protein, mRNA
2373	15095	27834	2.06	8.0E-63	F031810 NT	Ā	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
3454	16210	28861	3.02		8.0E-63 AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3454	16210	28862	3.02		8.0E-63 AF198349.1	NT	Galfus gallus Dach2 protein (Dach2) mRNA, complete cds
4234	16975	29600	3.31		8.0E-63 AL163268.2	NT	Homo saplens chromosome 21 segment HS21 C068
808	13675		2.09		7.0E-63 AI872137.1	EST_HUMAN	wm55g11.xt, NCI_CGAP_Ut2 Hamo saplens aDNA clone IMAGE:2439908 3'
							noc3f02.rt NCI_CGAP_Pr1 Homo sepiens cDNA clone IMAGE:745947 similar to gb:Y00361 60S
822				İ	AA420803	ESI HUMAN	RIBOSOWAL PROTEIN (TOWAN),
8773		34612			=	¥	Homo sepiens G protein-coupled receptor 51 (GPR51), mRNA
3315	16075	28726	0.84		4.0E-63 AL163278.2	NT	Home saplens chromosome 21 segment HS21C078
3788	16540	29174	1.16		4.0E-63 AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, pertial cds
3788	16540	29175	1.18		4.0E-63 AB014607.1	NT	Homo saplens mRNA for KIAA0707 protein, pertial cds
සුසු		32115			4.0E-63 AW750372.1	EST_HUMAN	CM3-BT0595-190100-072-a09 BT0595 Homo sapiens cDNA
සෙස	19123	32116	3.64		4.0E-63 AW7503721 ·	EST_HUMAN	CM3-BT0595-190100-072-a09 BT0595 Homo sapiens cDNA
11077	23747	37021	2.3		4.0E-63 AW134709.1	EST_HUMAN	UI-H-BI1-abq-a-02-0-UI.s1 NCL_CGAP_Sub3 Homo sapiens cDNA done IMAGE:27124823'
11077	23747	37022	2.3		4.0E-63 AW 134709.1	EST_HUMAN	UI-H-BI1-abq-a-02-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA done IMAGE:2712482 3'
11846	24430	37771	4.32		4.0E-63 AA362834.1	EST_HUMAN	EST72607 Ovary II Homo sapiens cDNA 5" end similar to similar to zinc finger protein family
1928	14664	27377	2.82		3.0E-63 AB018260.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
2782	15487	28225	2.28		3.0E-63 J00310.1	N	Human Met-tRNA-i gene 1
2824		26836	11.81	3.0E-63	9	ħ	Homo saptens zinc finger protein 144 (Md-18) (ZNF144), mRNA
2869	19151	32150	32.78		11545810 NT	LN.	Homo saptens hepatocelluler cercinoma entigen gene 520 (LOC63928), mRNA
5005	22258	35444	1.15		3.0E-63 BE876158.1	EST_HUMAN	601485666F1 NIH_MGC_69 Hamo sapiens cDNA clane IMAGE:3888263 5'
9805		35445	1.15		3.0E-63 BE876158.1	EST_HUMAN	801485856F1 NIH_MGC_69 Home saplens cDNA clone IMAGE:3888253 5'
186	12989	25639	1.09		2.0E-63 U07804.1	NT	Human DNA topoisomerase i mRNA, partial cds

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Probe SEO ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression. Signal	Most Simitar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Databese Source	Top Hit Descriptor
<u>\$</u>	13006	25847	1.68	2.0E-63	4885226 NT	F	Homo sapiens eyes absent (Drosophile) homolog 2 (EYA2), mRNA
\$	<u> </u>	<u> </u>		2.05-63		-	Homo sapiens glutamate-cysteine !gese (gamma-glutamylcysteine synthetase), catalytic (72.8kD) (GLCLC) mRNA
807	1_	26244		20E-83		F	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
1550	14306			20E-83	AB030388.1		Homo sepiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds
1559	14306		1.43	2.0E-63	1.1	Ę	Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds
1760	14502	27203	1.1	2.0E-63	2.0E-63 BE410739.1	EST_HUMAN	801301627F1 NIH_MGC_21 Hamo septens cDNA clane IMAGE:3636103 5
9.5	15917	28563	3.44	2.0E-83	45021 68 NT	<u> </u>	Homo sapiens amyold beta (A4) precursor protein (protesse neofn-II, Alzheimer dissesse) (APP), mRNA
3279	1				2.0E-63 AF109718.1	NT	Homo sapiens chromosome 3 subtelomento region
3885	l		3.74	2.0E-63		NT	Homo sapiens polycystic kldney disease-associated protein (PKD1) gene, complete cds
4813	17544	30169	1	2.0E-83	2.0E-63 AF111167.2	INT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
888	1_		98'0	2.0E-63		Į.	Homo sapiens glutaminyl-peptide cyclotransferase (glutaminyl cyclase) (QPCT), mRNA
518	l			2.0E-83	11419429 NT	¥	Homo sepiens similar to ectonucleotide pyrophosphetase/phosphodiesterase 3 (H. sepiens) (LOC63214), mRNA
578	<u> </u>			2.0E-63	BF373541.1	EST HUMAN	QV1-FT0170-040700-285-005 FT0170 Homo septens cDNA
578	18585			2.0E-63	1.1	EST_HUMAN	QV1-FT0170-040700-265-c05 FT0170 Hamo septens cDNA
9083	18871	31837	0.84	2.0E-63	11421940 NT	12	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA
8083	L			2.0E-63	11421940 NT	z	Homo sepiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKARZB), mRNA
						r 	Human garmiine T.cell receptor beta chain Doparnine-beta-hydroxylasse-like, TRY1, TRY2, TRY3, TCRBV2751P, TCRBV2751P, TCRBV2251A2N1T, TCRBV1353, TCRBV2751P, TCRBV251A1T, TCRBV1353,
		_	<u>.</u>				TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2PT, TCRBV7S2A1N4T,
6002	L		1.5/	2.0E-63	2.0E-63 U00039.1	FIX	Lynn seriene MiCT mDNA merial rde
2	_			Z.UE-02	I	121	TOTAL SEPTEMBER OF THE TOTAL SEPTEMBER OF THE
9849					2.0E-63 AB032369.1	LN	Homo suppers Milk I mrkry, perter cas
6975	19456	32477	1.45		1	LN.	Homo sepiens Carbonic anhydrase-related protein 10 (LOC56624), mRNA
6975	19456	32478	1.45		9910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56834), mRNA
7678	20342	33454	0.87	2.0E-63	2.0E-63 AB046844.1	INT	Homo sapiens mRNA for KIAA1624 protein, pertial cds
77.43	20277	00762	83	2.0E.83	TN 31816311		Homo septens similar to seme domain, immunoglobulin domain (ig), short basic domain, secreted, semenhorin) 34 (H. sapiens) (LOC69222), mRNA
200	1			20.0	A 4 8 8 2 4 4		Home seulone chromosoma 21 samment HS2(C)(1)
8	1			2.0E-00	4442040	E P	Homo centene litreeth femily member 3R (KIP3R) mRNA
7080					- `	2	TOTAL COMPANIES AND TOTAL COMPANIES OF THE STATE OF THE S
8952	21643	34792	1.35	2.0E-63	11420949 NI	Z	HOMO SEPONTS KINOSIA ISATILY INSTITUTOS OD (NITOD), INIVAN

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	Homo sapiens chromosome 21 segment HS21C018	25/18b05.81 Sceres_fetal_Lung_NbHL19W Homo sepiens cDNA clone IMAGE:302385 3' similar to gb:X17206 40S RIBOSOMAL PROTEIN S4 (HUMAN);	Homo sapiens neuredn III-apha gene, partial ods	Homo sapiens neureich III-alpha gene, pertial ods	Homo sapiens econitases 2, mitochondrial (ACO2), mRNA	HSCZVD111 normalized infant brain cDNA Homo saplens cDNA clone c-zvd11	HSCZVD111 nomwalized infent brein cDNA Homo septens cDNA clone c-zvd11	HSCZVD111 normalized infant brain cDNA Homo sepiens cDNA done c-zvd11	HSCZVD111 normalized infant brain cDNA Homo subjens cDNA clone c-zvd11	Homo saplens Xq pseudosutosomal region; segment 2/2	QV0-ST0215-060100-083-b09 ST0215 Homo saplens cDNA	ULH-Bi3-atth-02-0-Ui.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068763 3'	UHH-BI3-eth-02-0-UI.s1 NCI_CGAP_Sub5 Hamo septens aDNA done IMAGE:3068763 3'	Hama seplens chromosome 21 segment HS21C047	Homo sapiens chromosome 21 segment HS21C007	fm50b07.x1 NCI_CGAP_Ktd11 Homo sepiens oDNA clone IMAGE:2161625 31	601155232F1 NIH_MGC_21 Homo sepiens aDNA clans IMAGE:3139038 5	601508968F1 NIH_MGC_71 Homo septeme aDNA done IMAGE:3910336 51	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA	y098b02.r1 Stratagene lung (#637210) Homo sapiens aDNA clane IMAGE:79179 5	801311455F1 NIH_MGC_44 Homo suptems aDNA done IMAGE:3833204 5	Homo sepiens thimet oligopeptidase 1 (THOP1) mRNA	Homo sapiens thimet oflgopeptidese 1 (THOP1) mRNA	Homo saplens EWS, gar22, mp22 and bam22 genes	wb51e07.x1 NCI_CQAP_QC9 Homo sapkens dDNA done IMAGE:2309220 3' similar to gb:M15182 BETA- GLUCURONIDASE PRECURSOR (HUMAN);	wb51e07.x1 NCI_CGAP_GC8 Homo sepiens cDNA done IMAGE:2308220 3' shriler to gb:M15182 BETA-	GLUCURONIDASE PRECURSOR (HUMAN);	wr13e03.x1 NO_CGAP_Bm23 Hamo sepiens cDNA clane IMAGE:2529436 3'	wv13e03.x1 NCL_CGAP_Bm23 Hamo sepiens oDNA clane IMAGE:25294353'	Homo explans MCP-1 gene and enhancer region	Homo septens MCP-1 gene and enhancer region	Homo sepiens protein kinase C beta-li type (PRKCB1) mRNA, complete cds
Jie Exon Proc	Top Hit Database Source	NT	EST_HUMAN	NT	LN.	NT.	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	LN	EST_HUMAN	EST_HUMAN	EST_HUMAN	TN	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	LN.	EST_HUMAN	EST HUMAN	LN	IN	IN	EST HUMAN		EST HUMAN	EST HUMAN	EST HUMAN	IN	NT	뉟
SID	Top Hit Acession No.	2.0E-63 AL 163218'2	2.0E-63 N78945.1	2.0E-63 AF099610.1	2.0E-63 AF099810.1	11418185 NT	-08485.1	-08485.1	-08485.1	1.0E-63 F08485.1	J271736.1	1.0E-63 AW 582266.1	4W451950.1	4W451950.1	1.0E-63 AL.163247.2	1.0E-63 AL163207.2	9.0E-64 A1478186.1	3E280796.1	3E885755.1	11418177 NT	T80651.1	123	4507490 NT	4507490 NT	707848.1	6.0E-64 Al661992.1		6.0E-64 AI051992.1	6.0E-64 AW026445.1	6.0E-64 AW028445.1	6.0E-64 Y18933.1	/18933.1	6.0E-64 M13975.1
	Most Similar (Top) Hit BLAST E Value	2.0E-63	2.0E-63	2.0E-83	2.0E-63	2.0E-83	1.0E-63 F08485.1	1.0E-63 F08485	1.0E-63 F08485.1	1.0E-83	1.0E-63 AJ2717	1.0E-83	1.0E-83 AW451	1.0E-63 AW 451	1.0E-63	1.0E-63	9.0E-64	8.0E-64 BE2807	8.0E-64 BE8857	8.0E-64	8.0E-64 T60651	7.0E-64 BE3943	7.0E-64	7.0E-64	7.0E-64 Y07848.1	6.0E-64		6.0E-64	6.0E-64	6.0E-84	6.0E-84	6.0E-64 Y18933.1	6.0E-64
	Expression Signal	1.12	6.43	2.98	2.98	26.9	1.28	1.28	2.82	2,92	8.0	1.4	0.68	0.08	2.68	4:04	4.36	6.16	3.88	7.34	1.6	1.13	2.73	273	3.43	1.63		1.63	4.39	4.39	2.46	2.46	4.08
	ORF SEQ ID NO:	35691	36577	36904	38805	30807	20934	26935	29672	29673	30703	31394	32055	32056			33586		31792					30053	35779	27156		27157	28524	28525	31237	. 31238	31281
	Exan SEQ ID NO:	22490	23338	23363		25177	14248		17047	17047	18074	18476	19071	19071	21064	25288	20462		18829	24479	24518	16276	17417	17417	22581	14450	L	14459	15885	15885	18332		18352
	Probe SEQ ID NO:	8836	10647	10672	10672	12098	1502	1502	4308	4308	8979	5883	6238	6298	8371	12737	7768	1024	9049	11918	11970	3520	899	4683	8833	1716		1718	3120	3120	5534	5534	9999

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Single Exert 10bes Expressed in Dian	Top Hit Database Source	NT Homo sapiens golgi matrix protein GM130 (GOLGA2) mRNA, complete cds	bb72h12y1 NIH_MGC_12 Home septens cDNA done IMAGE:3047975 5' similar to gb:L08069 DNAJ EST_HUMAN PROTEIN HOMOLOG 2 (HUMAN);	bb72h12.y1 NIH_MGC_12 Home septens cDNA clone IMAGE:3047975 5' stimited to gb:L08069 DNAJ EST_HUMAN PROTEIN HOMOLOG 2 (HUMAN);	П	NT Hamp saplens chromosome 21 segment HS21C046	EST_HUMAN EST389463 MAGE resequences, MAGO Homo saplens cDNA	T HUMAN	NT Homo seplens chromosome 21 segment HS21C027	EST_HUMAN art09d08.s1 Scenes_testis_NHT Homo septens cDNA clone IMAGE:1031151 31		we97501.x1 NCI_CGAP_Kid11 Homo sepiens cDNA clone IMAGE:2462281 3' similar to contains element EST HUMAN L1 repetitive element;				T_HUMAN	П	T HUMAN	NT Homo septens englopoletin 4 (ANG4) mitting parties cos	HUMAN			EST_HUMAIN QV1-HT0413-010200-059-h12 HT0413 Homo septens dDNA	NT Homo septiens lymphocyte cytosolic protein 1 (L-plastin) (LCP1), mRNA			EST HUMAN AU132570 NT2RP4 Homo septems cDNA clone NT2RP4000109 5'	EST_HUMAN		EST_HUMAN 602042882F1 NC CGAP_Bm67 Homo sepiens cun cione IMAGE: 4180556 5
	ost Similar (Top) Hit Top Hit Acession BLAST E No.	3.0E-64 AF248953.1	3.0E-64 BE206521.1 E		3.0E-64 AL163246.2						2.0E-64 4757701 NT	2.0E-64 Al927030.1	T	2.0E-64 AL163246.2 NT	2.0E-64 4504088 NT	AW858145.1			2.0E-64 AF113708.1 N	T	_	2.0E-84 11431054 NT	2.0E-64 AW606785.1	2.0E-64 11434008 NT	2.0E-84 11434008 NT	2.0E-84 1.1423508 NT	2.0E-64 AU132570.1	2.0E-64 T06397.1	2.0E-84 T06397.1	20E-64 BF528114.1
	200 200 200 200 200 200 200 200 200 200		1.1	3.0E-84 BE208521.1	3.0E-64 AL163246.2						1.54 2.0E-64 4757701 N	2.0E-64 AI927030.1	2.0E-64 AL163248.2		2.0E-64	2.0E-64 AW858145.1	2.0E-64 AW958145.1	2.0E-64 AU124387.1	2.0E-64 AF113708.1	T	2.0E-64 M77185.1		85.1	2.0E-64	,	2.0E-84	20E-64 AU1325		0.59 2.0E-64 T06397.1	20E-84 BF52811
	Most Similar (Top) Hit Top Hit/ BLASTE N	34100 1.93 3.0E-64 AF248953.1	34220 3.69 3.0E-64 BE208521.1	34221 3.69 3.0E-64 BE206521.1	35165 1.54 3.0E-64 AL163246.2	35166 1.54 3.0E-64 AL163246.2	35263 0.6 3.0E-64 AW977384.1	35284 0.8 3.0E-84 AW977384.1	37608 1.8 3.0E-64 AL163227.2	28484 1.64 2.0E-64 AA609040.1	26799 1.54 2.05-64	1.82 2.0E-64 A 1927030.1	27987 2.05 2.0E-64 AL163248.2	27988 2.05 2.0E-64 AL163246.2	28546 1.42 2.0E-84	29157 0.78 2.0E-64 AW858145.1	29158 0.78 2.0E-64 AW958145.1	31655 2.78 2.0E-64 AU124387.1	31895 1.47 2.0E-64 AF113708.1	32784 148 2.0E-84.AI078387.1	32378 4.54 2.0E-64 M77185.1	33484 0.7 2.0E-84	33510 0.65 2.0E-64 AW606785.1	34395 0.73 2.0E-64	34396 0.73 2.0E-64	34882 0.56 2.0E-84	34984 0.97 2.0E-64 AU1325	35726 0.59	35727 0.59 2.0E-84 T06397.	36592 3.72 2.0E-64 BF52811
	Most Similar Expression (Top) Hit Top Hit L Signal BLASTE N	1.93 3.0E-64 AF248953.1	21086 34220 3.69 3.0E-64 BE206521.1	21086 34221 3.69 3.0E-64 BE206521.1	21994 35165 1.54 3.0E-84 AL163246.2	35166 1.54 3.0E-64 AL163246.2	22092 35263 0.6 3.0E-84 AW977384.1	22092 35284 0.6 3.0E-64 AW977384.1	24286 37608 1.8 3.0E-64 AL163227.2	1.64 2.0E-64 AA609940.1	14125 26799 1.54 2.0E-64	1.82 2.0E-64 A 1927030.1	15248 27987 2.05 2.0E-64 AL163246.2	27988 2.05 2.0E-64 AL163246.2	15901 28548 1.42 2.0E-64	16519 29157 0.78 2.0E-04 AW858145.1	16519 29158 0.78 2.0E-64 AW958145.1	18701 31665 2.78 2.0E-64 AU124387.1	18925 31895 1.47 2.0E-04 AF113708.1	1 48 2 0E-84 AI078387.1	19364 32378 4.54 2.0E-64 M77185.1	0.7 2.0E-84	20396 33510 0.65 2.0E-64 AW606785.1	21259 34395 0.73 2.0E-64	21259 34396 0.73 2.0E-64	21728 34882 0.56 2.0E-84	21818 34984 0.97 2.0E-64 AU1325	22529 35726 0.59	22529 35727 0.69 2.0E-64 T06397.	3.72 2.0E-64 BF52811

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	Top Hit Descriptor	wm81b06.xt NCI_CGAP_Utf Homo saplens cDNA clone IMAGE:2452211 3'	wn81608x1 NCL_CGAP_Ut1 Hama sapiens aDNA done IMAGE:2452211 3'	PM2-SN0018-220300-002-e12 SN0018 Homo sepiens cDNA	Homo sepiens period (Drosophila) homolog 3 (PER3), mRNA	CHR220101 Chromosome 22 exan Hamo seplens cDNA clane C22_132 5	Homo seplens chromosome 21 unknown mRNA	au00c01xt1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519136 3' similar to ab:L21696_cds1 PROTHYMOSIN ALPHA (HUMAN);contains element MSR1 repetitive element ;	Homo septens synaptojenin 1 (SYNJ1), mRNA	Homo sepiens transcription factor IGHIM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein,	JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes,	complete cds; and L-type calcium channel a>	Homo sepiens TRIAD3 mRNA, pertiel cds	Homo sapiens TRIAD3 mRNA, partiel cds	Homo septems hypothetical protein FLJ11028 (FLJ11028), mRNA	zk3108.s1 Soares pregnant uterus NbHPU Homo septens cDNA clone IMAGE:486667 3"	Homo seplens chromosome 21 segment HS21C046	H.sapiens DNA for endogenous retroviral like element	H.saplens DNA for endogenous retrovinal like element	QV4-BT0257-081189-017-e03 BT0257 Homo septens oDNA	eu68h07x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519005 3' similar to SW-Rt 21 HI IMAN P46778 eoS RIBOSOMAL PROTEIN L21	QV2-BT0635-240400-162-c02 BT0635 Homo septens cDNA	HSAAAEAWO TEST1, Human actuit Testis tissue Homo sapiens CDNA clone cam test346 (b)	AV721898 HTB Homo septems dDNA clone HTBBZC06 5"	nj86d10.s1 NCL_CGAP_Pri1 Homo sepiens cDNA clone IMAGE:989379 similar to gb:K03002.60S RIBOSOMAL PROTEN 132 (HUMAN):	nh37b07.e1 NCI_CGAP_Pr5 Homo septens cDNA clone IMAGE:954517	xx07b09.x1 NCI_CGAP_Cc21 Homo sepiens cDNA clone IMAGE:2583545 3' similar to TR:Q63306 Q63306 LONG INTERSPERSED REPETITIVE DNA CONTAINING 7 ORF'S, ;contains L1.b2 L1 repetitive element;	zw53b06.s1 Soares_total_fetus_Nb2HF8_9w Homo septems cDNA clone IMAGE:773747 3'	zw63b06,s1 Soares_bdai_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773747 3*	qf18h05xt NCL_CGAP_Bm25 Homo saplens cDNA clone IMAGE:1750425 3'
Solidie LAUIT 1950 Solidies	Top Hit Database Source	EST HUMAN WM	EST HUMAN wm	EST HUMAN PN		T_HUMAN		. SET HIMAN OD			<u>≥</u>	NT NT	NT IN	어 IN		T_HUMAN	H		'H IN	EST_HUMAN Q	UN NAMIN TEST	Т	Г	HUMAN	AVEL TOO	T	EST_HUMAN LC			EST HUMAN of
2 IS	Top Hit Acession No.	-	.1	3.1	8567387		1.1	1 0F-64 A1929419 1	07334				7.1	7.1	B922829 NT	5.1	82			8.1	•	3.1		6.1		T			8.1	-
	Most Similar (Top) Hit BLAST E Valte	2.0E-64 AI922911	2.0E-64 AI922911	2.0E-64 AW86477	2.0E-64	2.0E-64 H55162.1	1.0E-64 AF23191	4 OF A4	1.0E-04			1.0E-64/	1.0E-64 AF22852	1.0E-64 AF22852	1.0E-04	1.0E-64 AA04297	1.0E-64 AL16324	9.0E-65 X89211.1	9.0E-65 X89211.1	9.0E-85	ALCOCOLA RA SO 8	7.05-65	7.0E-85 Z21378.1	6.0E-65	# DC #	8.0E-85	6.0E-85/	6.0E-65 AA42787	8.0E-65	6.0E-65 A1085314
	Signal	28.9	5.97	1.78	1.65	4.85	2.94	10.45	0.79			5.74	1.27	1.27	0.79	1.07	1.81	1.53	1.53	10.43	40.07	201	127	3.59	2	0.62	23	3.46	3.48	0.81
	ORF SEQ ID NO:	36909	30910	37149	31114		25698	27244		L		28912	28974	28975	29270	35816		27738	27739		97406		37731	28454		32242	34481	34742	Н	34814
	Exen SEQ ID NO:	23656	23656	23863	l	24834	13060	14514		į		16257	16327	16327		22812	24545	15000	15000		24004		1_	L	44050	1	21337	<u>L</u> .	21600	21063
	Probe SEQ ID NO:	10981	10981	11198	12039	12468	251	Î.	3010			3501	3572	3572	3881	888	12012	2274	2274	11523	44.60	10055	11807	1034	4	0475	86 848	8008	8909	5268

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8973 21663 3 10763 2346 3 10868 23644 3 11480 24081 3 1331 14080 2 2157 14881 2 2157 14881 2 2157 1481 2 3250 16012 2 10364 23011 3 2250 13801 2 1469 14216 2 2336 15060 2 2336 15060 2 5124 17842 3 6063 18842 3 6063 18842 3 6063 18842 3 7017 1970 3 7119 18907 3	26642 2098 26642 1098 26642 1098 26642 200 26642 200 26642 200 26642 200 26642 200 27786 13 28675 13 28675 13 28675 13 28675 13 28675 13 28675 13 28675 13 28677 13 2		4.0E-65 4.0E-65 4.0E-65 6.0E-6	Top Hit Acession No. No. No. Aloes214.1 BE567816.1 BF340825.1 AL153210.2 AL153210.2 AL153210.2 AL153210.2 AL153210.2 AL15348.1 AL20418.1 AL20418.1 AL20418.1 AL2040.1 BE271469.1 BE271469.1 AW963185.1 G055269 G055269 G055269 AB033063.1 AN96372.1 M19879.1	Pulman H HUMAN T HUMAN T HUMAN T HUMAN T HUMAN	qf18165.x1 NCI_CGAP_Bra26 Harto septens cDNA dane IMAGE:1750425 3° 601340483F1 NIH_MGC_53 Harto septens cDNA dane IMAGE:1750425 3° 60203727215 INIH_MGC_53 Harto septens cDNA dane IMAGE:185677 5° Harto septens diraction septens cDNA dane IMAGE:185677 5° Harto septens diraction septens cDNA dane IMAGE:185677 5° Harto septens (IMA0166 gene product (KIAA0169), mRNA Harto septens (IMA0166 gene product (KIAA0169), mRNA Harto septens (IMA0166 gene product (KIAA0169), mRNA Harto septens (IMA0166 gene product (KIAA0169), mRNA Harto septens (IMA0166 gene product (KIAA0169), mRNA Harto septens (IMA0166 gene product (KIAA0169), mRNA Harto septens (IMA01166 gene product (KIAA0169), mRNA Harto septens (IMA01169 gene product (KIAA0169), mRNA Multiple scherokis associated retroitus polyprotein (pol) mRNA, partial cds DKFZp761G108_17 761 (synonym: harry2) Harro septens cDNA clone DKFZp761G108 5° qm46e01.x1 Scenes_placenta_8toSweaks_2NbHP8tx0W Harro septens cDNA clone IMAGE:1891800 3° qm46e01.x1 Scenes_placenta_8toSweaks_2NbHP8tx0W Harro septens cDNA clone IMAGE:1891800 3° Harro septens fragle X mental retardation, subsomal hornolog 1 (FXR1), mRNA Harro septens fragle X mental retardation, subsomal hornolog 1 (FXR1), mRNA Harro septens fragle X mental retardation, subsomal hornolog 1 (FXR1), mRNA Harro septens fow density (poprotein receptor related protein-deleted in tumor (LRPDIT), mRNA Harro septens mRNA for KIAA1287 protein, partial cds Harron septens mRNA for KIAA1287 protein, partial cds Harron septens mRNA for KIAA1287 protein, partial cds Harron septens mRNA for KIAA1287 protein, partial cds Harron septens mRNA sor kia 287 protein, partial cds Harron septens mRNA contracted protein (11, and L1 and Au reposite Harron septens mRNA contracted protein FLI22087 (FLI22087), mRNA
		78.0	4.0E-85	U403721	5	Human 3,5 cyclic nucleotide phosphodiesterase (HSPDE1C3A) mRNA, peritel cds
		0.97	4.0E-65		左左	Human 3,5 cyclic nucleotide phosphodiesterase (HSPDE1C3A) mRNA, pertial cds Himan 3,5 cyclic nucleotide phosphodiesterase (HSPDE1C3A) mRNA, pertial cds
		1.86	4.0E-65	U40372.1 5453765	Z Z	Human 3,5 cyclic nucleotide phosphodiesterase (HSPDE1C3A) mRNA, partial cds Homo seciens nel (chicken Hite 2 (NELL2), mRNA
20437	33559	86 - 1.86	4.0E-85 4.0E-85		ZZ	Homo sapiens het (chicken)-like 2 (NELL2), mRNA Homo sapiens het (chicken)-like 2 (NELL2), mRNA
	34888	8.0	4.0E-65		۲	Homo sapiens Janus kinase 2 (a probein tyrosine kinase) (JAK2), mRNA
23128		2.04	4.0E-85	4.0E-85 AJ277548.2	도	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor

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	Top Hit Descriptor	Societa 124F1 NIH MGC 21 Homo septens cDNA clone IMAGE:3841012 5	601568124F1 NIH MGC 21 Home sapiens CDNA done THYRO1000356 5 601568124F1 NIH MGC 21 Home sapiens CDNA done THYRO1000356 5	AU14/295 INTRO I Hamo sepiens aDNA done THYRO 1905-4283313 5	AU141289 TITLE MGC 56 Hamo septems CLINA GARD TITLE STATES AND MGC 56 Hamo septems CLINA GARD TITLE STATES AND TITLE STATES A	00212000 NT2RP2 Homo septens CDNA GARS NT2RP2004714 5	AU129040 NT2RP2 Hamo saplens curve, type 1 (ITPR1), mRNA	Homo sepiens mostro 1,4,0-m moduci (KIAA0656), mRNA	Homo sepiens KilAnucoo san Homo sepiens cDNA clone innovative element;	9456802.X1 Source (HUMAN), contains MER19.71 MEX16 3	THINGEN STATES Hamo septens conditions agains conditions liMAGE:382/34 3	ACTORON TO Source, pineel gland North ording ods	Homo septiens mRNA for KIAA1411 process complete cds	Human platelet factor 4 varation 1 (1 1 2 1 2 4 2 2 4 2 2 4 2 2 4 2 4 2 4 2	Hono septens ribosoma in action septens conditions and action in the condition of the condi	602126239F1 NIH MGC 30 Home septens cDNA dane IMAGE:2237173	Markenos Mulcour			Homo saplens sulfotrensing about the choriceante 22	Nove human gara mandra to chamosome 22	Nove human gare many associated pad homorou (1011)	Homo services 26S protestione essociated petal inches	Harman transposon-like element, partial	+	+	1		Ī	1
Single Exoll Floor	***		EST HUMAN OF	П	-	١.	TOMOR	NAME -			-1	- 1	TOWAR	1		4506880 INT		FST HUMAN	418041 NT	1418322 NI	TV L		198	5031980 NT	Į.	TEST HUMAIN	1	FST HUMAN		
Sing		Top Hit Acession No.	1.0E-65 BE732118.1	1.0E-65 BE 732118.1	1.0E-66 AU141280.1	1.0E-65 A014140	1.0F-85 AU129040.1	1.0E-65 AU129040.1	11431994111		1,404718.1	1.0E-00 AUT 53793.1	4 DE 45 AAOG9559.1	1.0E-65 AB037832.1	4 NF-85 MZ6187.1	450	1.0E-65 BF698707.1		A1621017.		1.0E-85	9.0E-86 AL160311.1	1002	9.0E-00	W87299.	8 0F-86 AA424304.1	7.0E-66 BE064410.1	-	6.0E-06 AI924653.1	6.0E-86 AI924653.1
	1	Most Similar (Top) Hit BLAST E Value	0.58 1.0E-65					105-05		1.96 1.0E-65				1.06	L	1.58 8 F3 1.0E-05				4 92 1.0E-05			1.31 9.0		1		17 000		1.15	1.15
		Q Expression Signal			34047				34753	24048		35124		36064	36346	30477	38610	37018	37122		31086	26531	28532	26756	26757		30008	+	29698	29696
		Exan ORF SEQ SEQ ID ID NO:	_		1	20912				١	21687	3				Ш	23367	١.	22839	1	24604	Ш	_1	1280	\perp	L	1_	10 24010		1
		Probe Exan SEQ 10	ÖN	8178 2	8178	1	١.	8/38	L		2006		8877	40200		10470	10878	11075		12013	12108	12519	8	8	1332	1332	4842	11310	}	3

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	Top Hit Descriptor	wn57h07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similer to Wir.indice CE18595 ;	PM2-HT0604-030300-001-b08 HT0604 Homo septens curva	H. sepiens mRNA for ribosomal protein L31	RC4-BT0311-141199-011-00-01-00-01-00-00-00-00-00-00-00-00	BOTOR1662-1 NIT MICC. STRUID SEPARA CONT.	60106106ZF1 NRT MCC_F1XIID SEPTEMBER (AIBS), mRNA	India saprats upod namero cooperation syndrame 1 homolog (Fmr1), mRNA	Mus finasculus Inglie Amonto Mannes Home septens CDNA	ACTIVITIES TO CONTRACT AND THE SECOND TO CONTRAC	The agriculture of the Control of Regions Doubs	Homo eaplens garitreis Disk upserden is diskipled	Human and oggenous real owners, continued and an analysis (NAD+ dependent), methery/tetrahydrofolets	Homo sapients mentyrene reusary under the second processor (MTHFD2), mRNA cyclohydrotase (MTHFD2), mRNA	QVI-DT0069-110200-067-910 U L0009 from september China	ED 1977 OHO MAIOE I peroductions, the Control of th	Homo sepiens cAMP-regulated guerrine nucleotide exchange factor I (cAMP-GEFI) mRNA, complete cds	Homo sepiens menyene transfere transference de l'yacogo mos (15 t.c.). Gwatahudralese (MTHFD2), mRNA	Homo sanians hypothetical protein FLJ20116 (FLJ20116), mRNA	Himan and months retrovirus pHE 1 (ERV9)	III H. RW1-enr-a-10-0-ULS1 NCI CGAP Sub7 Homo explens cDNA clone IMAGE:3070747 3'	Home services mRNA for KIAA0998 protein, partial cds	Long sections solide perrier family 25 (mitochandrial carrier, adentire nucleatide translocator), member 5	riono sepretis sous carios immis y (Homo eaplens solute carrier family 25 (mitochondrial carrier; adenine nucleodos uninscouru.), membra carrier family se rosa, s. purchan cana encoding mitochondrial protein, mRNA	10502070), income multiple adjentistic 2NIDHMSP Homo septens cDNA clone IMAGE:284326 5' stmiller to	SW:H281_TIGCA P35068 HISTONE H28.1/H28.2 [2] PIR:B56612; SW:H281_TIGCA P35068 HISTONE H28.1/H28D Home serions cDNA clone IMAGE:284326 5 similar to	yZZ7g1Zr1 Sogres_mutiple_general_znummer: [2] PIR:B56612; SW:H2B1_TIGCA P36068 HISTONE HZB.1/HZB.2 [2] PIR:B56612;
	Top Hit Database Source	EST_HUMAN		П	Т	Т	HUMAN			HUMAN	NT NT	LN L	Į.		EST HUMAN	EST HOMAN	Ę	Ŀ	1	2	NAME TO T	TOWOU TO LE	Z	F		IN.	EST HUMAN	EST HUMAN
	Top Hit Acession No.	_	<u>~</u>		5.1	Ξ	-	11420557 NT	6879816 NT	8.1		\J223364.1	9635487 NT	11428643 NT	4.0E-86 AW939119.1	AW965473.1	U78168.1	TIM 01400111	2402411	INI OCOLZALI	4.0E-86 X5/14/.1	4.0E-86 BF50/463.1	4.0E-86 AB0Z3Z15.1	4502098 NT		4502098 N	3.0E-66 N55323.1	3.0E- 66 N55323.1
	Most Similar (Top) Hit BLAST E Value	6.0E-66 Al924653	6,0E-86 BE178563	6.0E-86 X69181.1	5.0E-88 BE064410	5.0E-88 BE89864	5.0E-06 BE89864	5.0E-66	4.0E-86	4.0E-06 AW89779	4.0E-06 X89211.1	4.0E-66 AJ22336	4.0E-66	4.0E-66	4.0E-68	4.0E-88 AW9854	4.05-66 U78168.		4.0E-66	4.05-98	4.0E-86	4.0E-06	4.0E-86	3.0E-88		3.0E-86		
-	Expression Signal	1 4	0.48	3.14	1.45	0.74	0.74	16.11	96.0	1.14	1.83	3.02	10.89	3.73	1.15	4.83	7.93		0.72	6.63			1.28	40.95		10.96	1.18	1.18
	ORF SEQ ID NO:	2070	2012	37062	28769	30382	<u> </u>	35028	26206	27170				31153			32779	1_				36489				20830	27429] .
	Exan SEQ ID NO:	12.00	202	23778	14004	17765	17765	21864	13545	14471	15004	١.	1_	1		L	L	1	18262	20671	20729	23252	24041	L		14154	14711	11
	Probe SEQ ID NO:	9	7555	145	136	86	8 8	218	13	1720	2278	2477	4733	27.5	2999	6757	7034		7529	7976	8034	10556	11351		1407	1407	1975	1975

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Single Exon Probes Expressed in Brain	Exam ORF SEQ Expression ID NO: Crop Hit Acession Signel Top Hit Acession No: Top Hit Acession Signel Top Hit Acession Signel Top Hit Desoribion Source	1.16 3.0E-66 N55323.1 EST HUMAN SW:HZB1 TIGCA P35068 HSTONE HZB.1.1/HZB 2.12) PR:-B5863.5 6' similer to	28156 3.54 3.0E-68 11141880 NT	15890 28520 6.3 3.0E-86 7002223 NT Homo sapiens KIAA0649 gene product (KIAA0649), mRNA	30870 1.14 3.0E-68 AB020699.1 NT	31186 0.73 3.0E-68 M13975.1 NT	31397 1.92 3.0E-88 11417946 NT	31398 1.92 3.0E-98 11417946 NT	0.62 3.0E-68 AK024453.1 NT	35459 0.52 3.0E-86 11417118 NT	35826 0.8 3.0E-36 7019480 NT		3.0E-96 5453949 NT	1.57 3.0E-98 AF223391.1 NT	2.15 2.0E-88 7857334INT	2.15 2.0E-68 7857334 NT		Homo seplens origin recognition complex, aubunit 5 (yeast homolog)-like (ORCSL) mRNA, and translated	27272 2.05 2.0E-69/AL163301.2 NT	0.77 2.0E-66 8923290 NT	AL117233.1 NT	29417 0.8 2.0E-08 AF108389.1 NT	29973 9.48 2.0E-66 A.1133267.2 NT	¥	31439 1.3 2.0E-08 AW908854.1 EST HUMAN	31440 1.3 2.0E-66 AW968854.1 EST HUMAN	34585 2.28 2.0E-88 N45480.1 EST HUMAN	П	1.15 1.0E-66 BE887173.1 EST HUMAN	28309 1.36 1.0E-68 AV717817.1 EST HUMAN
-				Ш																								0.		
-		1975 147									_				50 1287		413 1282	413 1282		L						[5 15662
	Probe SEQ ID NO:	19	2711	3115	2380	2	5686	2686	8	9619	8973	10420	11494	11806			4		1819	3510	3747	4044	490	4807	5726	572	8746	12320	1678	2895

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						gle Exon Pro	Single Exon Probes Expressed in Brain
Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2895	15682	28310	1.36	1.0E-68 AV7178	AV717817.1	EST HUMAN	AV717817 DCB Homo seniens cDNA clear DCBADC07 5"
4352	15662		3.81	1.0E-66	1.0E-66 AV717817.1		AV717817 DCB Home sensions china china DCB ADCh7 6:
4362	16682	28310	3.81	1.0E-08	1.0E-88 AV717817.1	¥.	AV717817 DCB Home seniens con a close DCB ADONZ &
5297		30761	5.96	1.0E-88	1.0E-66 BF673088.1	EST HUMAN	602152908F1 NIH MGC 81 Homo seniene cinva close (1204752)
2685			0.77	1.0E-66 BE7662	BE786232.1	EST HUMAN	IL2-NT0101-280700-116-E04 NT0101 Homo sapiens cDNA
2682			0.77	1.0E-86 BE7652	BE765232.1	EST HUMAN	IL2-NT0101-280700-116-E04 NT0101 Homo seniens cDNA
8836	_	32526	1.57	1.05-88	1.0E-88 BF328623.1	EST HUMAN	RCS-BN0193-010900-034-006 BN0192 Homo sandons china
8357		34189	1.19	1.0E-66 AA6688	AA668858.1	EST HUMAN	BBB0e04 81 NCI CGAP GCB4 Home services Characteristics (1977) 20
9328	21903	35164	0.84	1.0E-86	1.0E-86 AA018828.1	EST HUMAN	2857612.11 Southe militar NAMHR Home envises CONS Acres 144 ACRES 244 21
10270		36129	0.92	1.0E-86	Γ	EST HUMAN	AV748749 NPC Home september CDINA close NBCBVANE ET
10270	22918	36130	0.92	1.0E-86	Γ	EST HUMAN	AV748749 NPC Homo seplens cDNA clone NPCBVA05 55
10862	23542	36789	2.48	1 0F-65 AF11116	1,	Į.	Livro contact in discontaction
11509	24109	37422	8.	1.0E-68 AW9687	14	EST HIMAN	EST 300820 MACE make union and an analysis of the partial cust cross gards, complete cots; and unknown gene
12113	24608		2.51	9.0E-67	1418177	.1	Homo sablens Ran GTPsee activating northern 1/PANGAB1 DNA
424	13108	75042					8175002.x1 Schneider fetal brain 00004 Homo septiens cONA clone IMAGE:2782083 3' similar to gb:M37104
	08150	14007	7.52	7.0E-57,	7.0E-67 AW162232.1	EST HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
1361	14109	28784	2.89	7.0E-67 AA38341	6	FST HIMAN	EST98812 Tests (Homo seplens cDNA 5' end similar to similar to C. elegans hypothetical protein, cosmid 7X333
1547	14283	20979	1.38	7.0E-67 W85947		Т	205806 of Source field live exteen AND C S4 Lives and a Live of Lives and Live of Lives of Li
1547	14293	26980	1.38	7.0E-67 W85947		Т	ZHOROOST Source field live enlace AND S. S. Lives co. Lives Co. Li
2028		27480	2.06	7.0E-67	7857243		Homo septens mostral 1.3 4-trichescharte Sik kinese (TTDK1) m.DNA
2028	14781	27490	2.06	7.0E-87	7857243 NT		Homo sepiens incettal 1,3,4-triphosphate 5/6 kinase (TTPK1), mRNA
2813	13196	25841	3.4	7.0E-67 AW1622	32.1	EST HUMAN	eu/5d02x1 Schneider fetal brein 00004 Homo septems cDNA clone IMAGE:2782083 3' similar to gb:M37104 ATP SYNTHASE COVIETING FACTION A MITTOCHORING TO BE ALLIANDED ALLIAND TO BE ALLIANDED ALLIAND TO BE ALLIANDED ALLIAND TO BE AL
2969	18770	31733	0.78	7.0E-67	0190695		Homo secients zinc finder crossin 2014 (7NE2014) DNA
6177	18954	31927	2.02	7.0E-67	11425572 NT		OMO services adentive-relative inches complex 2 peaks 4 asternity 2000 24
6177	18954	31928	2.02	7.0E-67	11425572 NT		Homo sepiens edector-releted protein complex 2 here 1 enturing (AP 201), minNA
9623	10385	32300	2	7 00	7		Homo septems ATPasse, H+ transporting, hysosomet (vacuoler proton pump) non-catalytic accessory protein
15.5	20204	33.306	1	1000	N 4900094		14 (110/1184) (AIPSNIA), mRNA
753	2000	22207	-	7.05-67	11419212 NT		Homo sepiens mitochondrial carrier femily protein (LOC55972), mRNA
3 6	1000	18086		/.0E-8/	11419212 NT		Homo saplens mitochondrial carrier family protein (LOC56972), mRNA
77 8	OLEN2	34052	0.59	7.0E-87	4557732 NT		Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
l gestor	71822	34660	0.58	7.0E-67	10835044 NT		Homo sepiens retinaldetryde dehydrogenase 2 (RALDH2), mRNA

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Table 4
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4340 17078 1806 14646 1802 14660 2056 14788 4199 16940 5395 18195 5395 18195 5395 18195 6828 19487 8830 21023 8830 21023 8830 21023 8830 21023 8830 21023 8830 20406 8835 20406 8836 20406 8836 20406 8836 20406 8837 20431 11010 23682 11010 23682 11597 24198	SEQ ID NO: 10 NO	Signal Signal Signal Signal Signal Signal 1.01 1.01 1.01 1.00 1.00 1.00 1.00 1.0	(Top) HR BLAST E Value 8.0E-70 7.0E-70	99) HR Top HR Acession AST E No. AST E No. AST E No. AST E No. AST E No. AST E S. 0E-70 AA230303.1 ES T. 0E-70 AA497807.1 ES 7. 0E-70 AA497807.1 ES 7. 0E-70 AA497807.1 ES 7. 0E-70 AA23036.1 NT 7. 0E-70 AB032369.1 NT 7. 0E-70 AB032369.1 NT 7. 0E-70 AB032369.1 NT 7. 0E-70 AB032369.1 NT 7. 0E-70 AB032369.1 NT 7. 0E-70 AB032369.1 NT 7. 0E-70 AB032369.1 NT 7. 0E-70 AB038429.1 NT 7. 0E-70 AB03	Detabase Source Source T HUMAN T HUMAN T HUMAN	Top Hit Describtor First 3d 12,r1 NCI_CGAP_Pri Homo sepiens cDNA clone IMAGE:1008023 Homo sepiens DGSH_MRNA, 3' and Homo sepiens DGSH_MRNA, 3' and Homo sepiens DGSH_MRNA, 3' and Homo sepiens DGSH_MRNA, 3' and Homo sepiens ACI_CGAP_BRNS Homo sepiens cDNA clone IMAGE:2165305 3' ### The sepiens attend stappressor deleted in crail cancer-related 1 (DOC-IR) mRNA Homo sepiens MISIT mRNA, partial cds Homo sepiens MISIT mRNA, partial cds Homo sepiens MISIT mRNA, partial cds Homo sepiens MISIT mRNA, partial cds Homo sepiens mRNA for KIAA/1284 protein, partial cds Homo sepiens mRNA for KIAA/1284 protein, partial cds Homo sepiens mRNA for KIAA/1284 protein, partial cds Homo sepiens mRNA for KIAA/1284 protein, partial cds Homo sepiens protein (CCAAT) mRNA Homo sepiens protein (CCAAT) mRNA Homo sepiens phospholipul scrembiase 1 gene, exon 1 and 6' flanking region Homo sepiens phospholipul scrembiase 1 gene, exon 1 and 6' flanking region Homo sepiens phospholipul scrembiase 1 gene, exon 1 and 6' flanking region Homo sepiens phospholipul scrembiase 1 gene, exon 1 and 6' flanking region Homo sepiens phospholipul scrembiase 1 gene, exon 1 and 6' flanking region Homo sepiens phospholipul scrembiase 1 gene, exon 1 and 6' flanking region Homo sepiens phospholipul scrembiase 1 gene, exon 1 and 6' flanking Regolation (TRN2), mRNA Homo sepiens phospholipul scrembiase 1 gene, exon 1 and 6' flanking Regolation (TRN2), mRNA Homo sepiens phospholipul scrembiase 1 gene, exon 1 and 6' flanking (SPG4), mRNA Homo sepiens phospholipul scrembiase 2 general distributed and continuent, spessin) (SPG4, mRNA Homo sepiens spessic preraplegia 4 (autocomel dominant, spessin) (SPG4, mRNA Homo sepiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA Homo sepiens and the spession sepiens (SPG4, mRNA) Homo sepiens phospholipul scrembia (A.) precinence protein (protein protein --	--	--	---	--	--	--
Ш		121	8.0E-70 M30938.1			Human Ku (p70/p80) subunit mRNA, complete cds						
2513 15230		1.22	8.0E-70	TN 68823889 NT		Homo sapiens CMP-14-acetylneuraminic acid synthase (LOC55807), mRNA						
2555 15598		2.18	5 0F-70	TARTANT		Party & contains Elik ACTYS and a second of Elik ACTYS and ACTYS and ACTYS and ACTYS and ACTYS and ACTYS and ACTYS and ACTYS ACTIS A						
		2.18	5.0E-70	TR82307 INT		Home series KIAA0782 rems product (KIAA0702) mRNA						

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Cingle Lybiassed III Digiti	Top Mit Descriptor	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA	MR3-HT0487-150200-115-406 HT0487 Homo sapiens cDNA	EST03028 Fetal brain, Strategene (cett838208) Homo eaplens cDNA clone HFBDN25	CM4-UM0003-010300-105-008 UM0003 Homo septens cDNA	CM4-UM0003-010300-105-g08 UM0003 Homo septens cDNA	RC0-BT0522-071299-011-e12 BT0522 Homo sepiens cDNA	RC0-BT0522-071289-011-e12 BT0522 Homo septens cDNA	Homo saplens plakophilin 4 (PKP4), mRNA	Homo saplens plakophilin 4 (PKP4), mRNA	wh90d03.xf NCI_CGAP_CLL1 Hano septens cDNA clane IMAGE:2388005.3	802141581F1 NIH MGC 48 Hamo septens cDNA clane IMAGE:4302806 5'	602141561F1 NIH MGC 46 Homo sapiens cDNA clone IMAGE:4302806 51	hz81h02x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:32144193	Homo seplens phosphetidyfinosital 4-kinase 230 (pJ4K230) mRNA, complete cds	yy07a10.r1 Sogres melanocyte 2NbHM Homo sablens cDNA clone IMAGE:270522 6' similar to	SW.D3HI JRAT P29288 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR;	9907a10.r1 Sogres melemotyle 2NbHM Homo saplens CDNA clone IMAGE:270522 5' similer to SW:D3HI RAT P29266 3-HYDROXYISOBUTYRATE DEHYTROGENASE PRECY ISSOR	0051h01x1 NOI CGAP Pent Homo sepiens cDNA clone IMAGE:20049133'	Homo septens hypothetical protein FLJ20758 (FLJ20758), mRNA	Homo saplens KIAA0183 gene product (KIAA0183), mRNA	Homo sepiens KIAA0193 gene product (KIAA0193), mRNA	Homo seplens chromosome 21 segment HS210002	248g04.11 Soares retine NZD4HR Homo septens cDNA clone IMAGE:380214.5' similar to SW:GAG_HTL1A	vo68b04rf Sorres fetal liver splean 1NFI S Homo senions cDNA clara (MAGE-104509 At	Human normuscle myosin heavy chain-B (MYH10) mRNA translations	H. sapiens gene for schwanzomin (CS8)	H.eapiens gene for schwarmornin (CSS)	Homo sepiens NALP1 mRNA, complete cds	Human mRNA for NF1 protein isoform (neurofibromin isoform), complete cds	Homo sapiens cytoplasmio dynein intermediate chain 1 mRNA, complete cds	Homo septems cytoplesmic dynein intermediate chain 1 mRNA, complete cds
	Top Hit Database Source		EST HUMAN	Г	EST HUMAN	EST_HUMAN (Г	EST HUMAN			T HUMAN	EST HUMAN	Г	Т	Т		EST_HUMAN S	EST HUMAN	Т	8923689 NT			INT TN	Z Z MINIMA	Т	Т						T.
	Top Hit Acession No.	7662307 NT	-	_	4.0E-70 AW 793226.1	4.0E-70 AW 793226.1	3.0E-70 BE071798.1	3.0E-70 BE071796.1	888	11430988 NT	5.1	3.1	3.1	3.1	21				1246899.1	8823689	7861983 NT	7861983 NT	2.2	0.4					5.1		4.1	1
	Most Similar (Top) Hit BLAST E Value	6.0E-70	5.0E-70 BE10003	4.0E-70 T06037.	4.0E-70	4.0E-70	3.0E-70	3.0E-70	3.0E-70	3.0E-70	3.0E-70 AI83197	3.0E-70 BF68523	3.0E-70 BF68523	3.0E-70 BE50297	2.0E-70 AF01287		2.0E-70 N42161.1	2.0E-70 N42161.	2.0E-70 A1248899	2.0E-70	2.0E-70	2.0E-70	20E-70 AL16320;	2 OF-70 AA05404	2.0E-70 H37988	2.0E-70 M69181.1	2.0E-70 X72862.1	20E-70 X72882.1	2.0E-70	2.0E-70 D12625.1	2.0E-70	20E-70 AF12307
	Expression Signal	2.18	2.75	1.03	1.78	1.78	1.23	1.23	0.65	0.65	1.6	1.85	1.65	0.58	1.2		14.09	14.09	1.7	1.56	3.05	3.05	1.08	28	0.78	5.06	8.7	8.7	127	1.75	12.14	12.14
	ORF SEQ ID NO:	28004		32431	32653	32654	27016	27017	31234	31235	31581	32031	32032	35860	25484	-	26080	26080	26113	26421	26578	28579	27177		28011	29404	30839	30040	31857	32307	32342	32343
	Exan SEQ ID NO:	15598	24519	19417	19613	19613	14330	14330	18330	18330	18642	19053	19053	22858	12865		13440	13440	13464	13760	13915	13915	14478	15043	16368	16772	18227	18227	18888	18303	19333	19333
	Probe SEQ ID NO:	2555	11974	9656	9699	9699	1584	1584	5532	5532	5855	6280	0829	10008	37		8	£	888	1000	1161	1161	1736	2318	3615	4027	5428	5428	6111	96338	88	6269

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CONTROL TO THE PROPERTY OF THE
19405 32420 1.07 1.0E-71 11426182 NT
19879 32726 1.39 1.0E-71 AB011131.1 NT
7211 19896 32071 43.38 4.08.2411180789.4 IAT

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Single Exon Probes Expressed in Brain

					Ö	gie Exori Pro	Single Exon Propes Expressed in Brain
Probe SEQ ID NO:	SEQ ID	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
				Value			
8048		1	0.00	1.0E-71	AF105267.1	Ł	Homo sapiens glypican-8 (GPC8) mRNA, complete cds
8069			2.28	1.0E-71	11425430 NT	N-	Homo saplens mycmesin (M-protein) 2 (185tD) (MYOM2) mRNA
8345		34174	4.09	1.0E-71	B922811 NT	Į.	Homo saplens hypothetical protein FLJ10998 (FLJ10998), mRNA
8345			4.09	1.0E-71	8922811 NT	NT	Homo saplens hypothetical protein FLJ10908 (FLJ10908), mRNA
9128		34982	82'0	1.0E-71 S72393	572393.1	TN	CSNK2A1=casein kinase II (CKII) subunit abha Ihuman. Genomic. 18862 nfl
8008	3 22557		08.7	1.0E-71	1.0E-71 AYD07643.1	Į.	Homo sebiens evidefinane c addese subunit VIII-rejaker makin nane manifes ade
8968	22818		2.05	1.0E-71		EST HUMAN	AV761217 MDS Homo sepiens cDNA clone MDSEIA03 5
10436		60898	1.45	1.0E-71	1433142	N.	Homo saplans activated beuccode cell adhesion molecule (A) CAM) mRNA
10684	23375		2.58	1.0E-71 AV7612		EST HUMAN	AV761217 MDS Homo eaciens cDNA clone MDSFAns of
10796	23479	36720	2.19	1.0E-71	11418903 NT	Į.	Homo saplens coadulation factor XIII A1 polynophite (F13A1) mPNA
11093	23763	37037	1.73	1.0E-71	114171911NT	Į.	Homo sablens lexcvi/cvafink eminovarificae (1 NDED)DNA
11003	23763		1.73	10F-74	1141710H NT	L'A	Home serious learning and proportion of the Company
12401	L	l	188	4 OF 74	4 0E-74 AB011300 4	E L	THE CONTROL OF THE CO
	L				T		Total advanta gale (a. 1c), cutilized cas
88	13183	25830	1.72	9.0E-72	9.0E-72 AI857835.1	EST HIMAN	WROOGUST NCI_CASAP_Lu19 Homo septems aDNA dane IMAGE:2423188 3' similier to TR:088705 086705 HYPOTHETICAL 38 6 KD PROTEIN TOTAINS Als septembers Als septemb
							W65003 x1 NCI CGAP 1119 Home seriors colors from INA Circums INACE 3423489 21 11 1- TD CREATE COLORS
88		25831	1.72	9.0E-72	9.0E-72 AI857635.1	EST HUMAN	HYPOTHETICAL 38.6 KD PROTEIN, contains Au repetitive element
8020	18801	31762	76.0	8.0E-72		EST HUMAN	601458747F1 NIH MGC 66 Homo sapiens cDNA clone IMAGE-3862454 5
4092	16834	20458	2.89	7 05 70	75070	ŀ	
			3	1:00-12	N 000100%		num suprem accrimate 2, minorionera (ACO2), nuclear gene encoding mitocondrial protein, mRNA
4092	16834	29450	2.63	7.0E-72	4501888 NT	¥	Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gane encoding mitocondral protein mRNA
4082	16834	29460	283	7.0E-72	4501898 N		Homo seniene synthese 2 mthybouthal (ACCs)
7024	19716	32773	280	7.0E-72 S41694.1	341694.1		(begudodene) PTMAP2-profitymostin styte filiumen. Carocatio 4402 de 2012 de 2012
12520	24968		1.8	7.0E-72 F26259.1		T HUMAN	HSPD13870 HMS Home septeme CDNA chose actions (100 H) and the chose actions (100 H)
8283			4.14	6.0E-72 AL 16324	22	Т	Hamo saplens chromosome 21 segment HS210048
8		25621	1.06	5.0E-72 BF33370	7.1	EST HUMAN	QV0-CS0010-150900-369-e11 CS0010 Homo seciens cDNA
8		25622	1.06	6.0E-72 BF33370	7.1	EST HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo segiens cDNA
2	12889	25521	3.47	5.0E-72(BF33370)	2	EST_HUMAN	QV0-CS0010-150600-388-e11 CS0010 Homo sepiens cDNA
ठॅ		25622	3.47	5.0E-72 BF33370	7.1	Г	QV0-CS0010-150900-398-e11 CS0010 Homo sepiens cDNA
1117	_		3.62	5.0E-72 L11645.1		Г	Homo sepiens alpha-tubulin mRNA, complete cds
6851	19651	32581	1.59	5.0E-72 AU12858	7.	EST_HUMAN	AU126584 NT2RP2 Homo sepiens aDNA done NT2RP2003761 5

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Top Hit Detablese Source	EST188312 HCC cell line (metastasis to liver in mouse) Il Homo sapiens cDNA 5' end similar to similar to FAC1	au80c03.y1 Schmelder fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782564 5' similar to TR:089785 099785 HYPOTHETICAL 3.2 4 KD PROTEIN 'contests alarment MSD4' supplies alarment MSD4' supplies.	AV724632 HTB Hamo septens CDNA clone HTBAKB01 5	MR 4-BT0598-010600-005-d05 BT0608 Homo sepiens cDNA	MR4-BT0598-010600-005-d05 BT0598 Hamo seplens cDNA	be08g08.y1 NIH_MGC_7 Hamp septens cDNA clone IMAGE:2823806.5"	be08g08.y1 NIH MGC 7 Home sablens cDNA clone IMAGE:2823808 5	QV1-BT0632-280800-342-a10 BT0632 Home septems cDNA	Homo saplens zinc finder protein ZFP-85 (ZFP95) mRNA alternatively spiliped complete onte	ydd3a01.r1 Soeres fetal liver spleen 1NFLS Home sepiens cDNA clone IMAGE:115762.5' similar to SP:A44282 A44282 RETROVIRUS-REI ATED PO: PO:YPROTEN - HINAAN	Homo sablens hect domain and RLD 2 (HFRC2) mRNA	Hamo saciens hypothetical protein FL (20758 (FL 120758) mRNA	RC3-LT0023-200100-012-d11 LT0023 Horro smokens cDNA	RC3-LT0023-200100-012-d11 LT0023 Homo septems cDNA	qh67c02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849730 3' similar to TR:014408 Q14408 SPLICING FACTOR. [1] ;contains Alu repetitive element;contains element.contains	element;	ee23f09.s1 NG_CGAP_GCB1 Homo septens cDNA clone INACE:814121 3' similer to SW:CPTR_FLAPR P49131 CHI.OROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR.:	Re23f08.s1 NG_CGAP_GC81 Homo septens oDNA clone INAGE:814121 3' stimilar to SW:CPTR_FLAPR	Sent of the control of the subsection and Sent of the control of the subsection of t	Publication 1 Code to leave lives before I INTLO FIGURE SUPPLY CONTROL OF THE STATE	Homo explores curse your translation interest included to scious a feet of the country of the co	TOOLOGY Specific And Its Comment of State of Specific Annual Comments of Specific Annu	Accessed Course lead into spices I INTL'S Traing sapiens CLINA GIONE IMA CE: 109649 3	Homo sapiens WEE1 gene for protein kinase and pertial ZNF143 gene for zinc finger transcription factor	Homo saplens pre-B-cell colony-enhancing factor (PBEF) mRNA	eth03a06.s1 Soares_testis_NHT Homo septems aDNA clone 1310290 3"
Top Hit Detabase Source	EST HUMAN	EST HUMAN	Γ	EST HUMAN N	EST_HUMAN N	EST HUMAN	EST HUMAN	EST HUMAN	Т	EST HUMAN			T HUMAN	Г		EST_HUMAN	EST_HUMAN P	EST HIMAN	Т	- ICINOIS		T LIBIAN	NOMO:	H		EST_HUMAN_B
Top Hit Acession No.	AA316632.1	5.0E-72 AW 161274.1	12.1		6.0E-72 BF331671.1	3E208545.1	5.0E-72 BE208545.1		4.0E-72 AF170025.1		5729867	8923669 NT	5	30.1		4.0E-72 AI248796.1	4.0E-72 AA465388.1	4.0E-72 AA465388 1		7857057	7857057 NT			3.2	5031976 NT	3.1
Most Similar (Top) Hit BLAST E Value	5.0E-72 AA31683	5.0E-72	5.0E-72 AV7246	5.0E-72 BF33157	5.0E-72	6.0E-72 BE20854	5.0E-72	5.0E-72	4.0E-72 /	4.0E-72 T87947.1	4.0E-72	4.0E-72	4.0E-72 AW 8362	4.0E-72		4.0E-72	4.0E-72	4.0E-72	4 0F-72 H79421	4 0E-72	4 0E-72	4 0E.70 TR1010 1		4.0E-72 AJ27754	3.0E-72	3.0E-72 AA72382
Expression Signer	67.0	3.71	0.80	3.45	3.45	1.01	1.61	2.82	0.62	88:0	2,03	1,3	0.48	0.48		0.92	1.57	1.57	7.78	1,75	192	2.18		8.92	0.69	1.52
ORF SEQ ID NO:	33509	34514	35708	37157	37158	37563	37564		30868	32230	33069	35531	36152	36153		36186	37210	37211	37424	37555	37556	37597		31020	25459	1
Exan SEQ ID NO:	20394	21367	22511	23871	23871	24240	24240	25358	18178	19229	19992	22336	22939	22839		72007	23917	23917	24114	24234	24234	24275	000,0	770	12846	13652
Probe SEQ ID NO:	7731	8675	1986	1208	1288	168	11643	12107	5378	6462	7309	9684	10292	10292		10320	11255	11256	11514	11637	11637	11680	3,	12400	2	883

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SCD (2000) Expr. (FC) HR (To)								
19473 31390 3.63 1.0E-72 7657676 NT 19231 32231 1.31 1.0E-72 11321578 NT 19231 32232 1.31 1.0E-72 11321578 NT 25083 32305 3.7 1.0E-72 11321578 NT 20207 33306 3.7 1.0E-72 E17544.1 EST_HUMAN 22144 35324 1.0.25 1.0E-72 AV751818.1 EST_HUMAN 22144 35326 1.0.25 1.0E-72 AV75188.1 EST_HUMAN 22144 35326 1.0.25 1.0E-73 AV374988.1 EST_HUMAN 22144 35326 1.0.25 1.0E-73 AV374988.1 EST_HUMAN 22144 35326 1.0.25 1.0E-73 AV374988.1 EST_HUMAN 22245 32245 6.16 8.0E-73 AV371204.8 NT 22282 35496 1.82 8.0E-73 AV47180480 NT 22282 35496 1.22 <	Probe SEQ ID NO:		ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value		Top Hit Database Source	Top Hit Descriptor
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	8656	21348	34403	0.65	3.0E-73/		EST_HUMAN	AV729428 HTC Hamo sepiens cDNA clane HTCAAF071 5

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ORF SEQ Expression (Top) Hit Top Hit Acession ID NO: Signal BLASTE No. Source	30E-73 A1004040.1 EST_HUMAN out1d02xt Scares_NFL_T_GBC_St Homo septens cDNA clone IMAGE:16259553'	1.6 3.0E-73 AL.163246.2 NT Homo sapiens chromosome 21 segment HS21C046	3.0E-73 AW 898081.1 EST_HUMAN RC3-NN0068-270400-011-c04 NN0068 Homo sepiens cDNA	21 26271 1.43 2.0E-73 AF139897.1 NT Homo septems BASS1 (BASS1) mRNA, pertied cds	1.78 2.0E-73 AW 898081.1 EST HUMAN	1.3 2.0E-73 U01317.1	40 28690 3.99 2.0E-73 4502582 NT Homo saplens caspess 8, epoplosis-related cysteins protease (CASP8) mRNA	Homo saplens Parkinson disease (autosomal recessive, Liverille) 2, parkin (PARK2), transcript vertiant 3, mRNA	Homo sepiens Perkinson disease (autosomei rocessive, Juvenile) 2, perkin (PARK2), transcript verient 3, mRNA	1.03	32102 0.89 2.0E-73 AF086824.1 NT	32103 0.89 2.0E-73 AF086824.1 NT	32159 6.27 2.0E-73 AB048811.1 NT	32376 1.27 2.0E-73 11431471 NT	32377 1.27 2.0E-73 11431471 NT	33476 0.09 2.0E-73 M94048.1 NT	33478 0.73 2.0E-73 AB037750.1 INT	36284 0.52 2.0E-73 AF198349.1 NT	35285 0.52 2.0E-73 AF19634	36189 1.21 2.0E-73 4504168 NT	36267 1.31 2.0E-73 1	36258 1.31 2.0E-73 11496980 NT	36917 3.37 2.0E-73 4557612 NT	36018 3.37 2.0E-73 4557812 NT	36955 1.82 2.0E-73 AB028982.1 NT	1.83 2.0E-73 AW 898081.1 [EST_HUMAN	8 27221 1.71 1.0E-73 AU121585.1 [EST_HUMAN AU121585 MAMMA1 Homo sapiens cDNA clone MAMMA1000460 5	6 27946 1.12 1.0E-73 AF198349.1 NT Gellus gellus Dech2 protein (Dech2) mRNA, complete ods	9 32015 1.07 1.0E-73 BE151283,1 EST_HUMAN CM1+HT0282-111198-042-h10 HT0282 Homo septens cDNA	35230 1.37 1.0E-73 A147427.1 EST HUMAN	38426 2.95 1.0E-73 BE385477.1
ORF SEQ ID NO:				28271			28690	28943	28944	-	32102	32103	32159	32376	32377	33476	33478	35284	35285	36189	36257	36258	36917	36918	30955		27221	27946	32015	35230	38426
- 8		4 25003	8 25005	13601		15021	7 15940	16294	16294	17138	4 19114	19114	19158		1						_!					14674		15205	19039	22061	23195
Probe SEQ ID NO:	11611	12734	12738	831	1939	2296	3177	3538	3538	4401	6344	6344	6389	9800	980	7699	79	9432	9432	10322	10394	10394	10987	10987	11020	12283	1778	2488	.6286	8399	11428

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חושים דייניים בערופי בערופי בערופי בייניים ביינים ביינים בייניים בייניים בייניים ביינים ביינים ביינים ביינים ביינים ביינים ביינים ביינים בייני	Top Hit Descriptor	Homo sapiens CD39-like 4 (CD39L4) mRNA	Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rats, brain, mRNA, 3429 nt]	Ca2+/calmodulin-dependent protein Idnase IV kinase Isoform (rats, brain, mRNA, 3429 nt)	yv48g10.s1 Scares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:245826 3'	Homo sepiens NKG2D gane, exan 10	Homo saplens chromosome 21 segment HS21C046	801640284F1 NIH_MGC_73 Homo septiens cDNA clane IMAGE:3632997 6	601191927F1 NIH_MGC_7 Homo septens cDNA clone IMAGE:3535855 5	Homo sepiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds.	801283621F1 NIH MGC 44 Homo septems cDNA clams IMAGE-3605453 5	801283521F1 NIH MGC 44 Homo services (DNA close IMAGE SERVICES ET	H-BIO-earth-03-0-U. st NCI CGAP Sub1 Homo seriens cDNA clone MAGE: 27003853	ULH-Bi0-earth-03-0-Ul.s1 NCI CGAP Sub1 Homo serviers aDNA done IMAGE:2708385 3'	h54e11.x1 NCI CGAP Kid11 Hamo sapiens cDNA clone IMAGE 3132332 3'	hr54e11.x1 NCI_CGAP_Kid11 Hamo sepiens cDNA clone IMAGE:3132332.31	Homo sapiens actin filament associated protein (AFAP), mRNA	df17c09.y1 Mortan Fetal Cootilea Homo sapiens cDNA clane IMAGE:2483704 5	PM0-CT0289-271099-001-h07 CT0289 Homo septens cDNA	Homo saplens phosphatidylinositid glycan, class L (PIGL), mRNA	H.saplens mRNA for TPCR18 protein	Homo saplens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA,	and translated products	Homo sepiens interleukin 4 receptor (IL4R), mRNA	Homo saplens Interfeukin 4 receptor (IL4R), mRNA	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA	Homo saplens hypothetical protein FLJ13222 (FLJ13222), mRNA	H.sapiens mRNA for HIP-	H.sepiens mRNA for HIP-I	Homo sepiens cell adhesion molecule with homotocy to L1CAM (close homotocus of 11) (CHI 1) mRNA	Homo sapiens DNA for amyloid precursor protein, complete cds	Homo saplens mRNA for KIAA1019 protein, partial cds
	Top Hit Defeabese Source		N	N	EST_HUMAN	Г		EST_HUMAN	EST_HUMAN		T HUMAN	Т	Т-	EST HUMAN	Т	Г		EST_HUMAN	EST_HUMAN										-	FN			
	Top Hit Acession No.	4557426 NT	1	1	_	100		7.0E-74 BE987432.1		R DE-74 AE400007 4		Ī	İ	6.0E-74 AW014039.1		8.1	1058013	1.0	58.1	1425417	1		45078 08 NT	11431471 NT	11431471 NT	7862283 NT	7682283 NT	11345483 NT			5729768/NT	_	2.1
	Most Similar (Top) Hit BLAST E Value	8.0E-74	8.0E-74 S83194.	8.0E-74 S83194.	8.0E-74 N52239.	7.0E-74	7.0E-74 /	7.0E-74	7.0E-74	8 OF 74 /	6.0E-74	6 0F-74 F	6.0E-74	6.0E-74	6.0E-74 BE04884	6.0E-74 BE04884	6.0E-74	5.0E-74 AW0209	5.0E-74 AW3627	5.0E-74	5.0E-74 XB9670.		6.0E-74	5.0E-74	5.0E-74	5.0E-74	5.0E-74	5.0E-74	6.0E-74 Y09420.1	5.0E-74 Y09420.1	5.0E-74	4.0E-74 D87875.	4.0E-74 AB02894
	Expression Signal	1.88	22	22	1.36	2.59	1.08	2.83	5.51	76	11.78	17	1.32	1.32	1.3	1.34	3.02	7.33	262	1.86	12.98		7.41	1.84	1.84	96'9	0.0	2.78	2.58	2.56	2.68	1.79	5.15
	ORF SEQ ID NO:	28150	31544	31545		27390		35038	31011	26518	27778	277777	28279	28280	28082	29093	30744	26322			31419		31462	31536	31537	32567	32567	33758	38585	36586	36687	26723	26272
$\left[\right]$	SEQ ID	13407	18613	18613	23474	14677	16082	21873	24858	13858	15039	15039	15834	15634	16453	16453	18086	13654	15413	18125	18497		18540	19908	18608	19539	19539	20631	23328	23328	23442	13080	13002
	Probe SEQ ID NO:	723	5824	5824	10791	1942	3322	9142	12505	1100	2314	2314	2867	2867	3700	3700	5281	885	2706	6322	6703		5748	5819	5819	6795	7569	7836	10636	10636	10757	273	832

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Table 4
Single Exon Probes Expressed in Brain

Top Hit Descriptor	Homo septens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)	Homo septens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete ods)	Homo septens probassame (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA	Homo sapiens protessome (prosome, macropain) subunit, beta type, 1 (PS/NB1) mRNA	Homo eaplens mRNA for KIAA1168 protein, pertial cds	Homo saplens PLP gene	Homo septens PLP gene	Homo sepiens chromosome 21 segment HS21C010	Hamo septens chromosome 21 segment HS210047	Homo saplens KIAA0569 dens product (KIAA0568), mRNA	Homo sapiens mRNA for transmebrane receptor protein	Homo septens hydroxyscyl-Coenzyme A dehydrogenese/3-ledoscyl-Coenzyme A thiolese/enoyl-Coenzyme A hydratese (trifunctional protein), beta sethanti (14.0-18) mRNA	Homo sapiens hydroxyacyl-Coenzyme A dehydrogenses/3-lestoscyl-Coenzyme A thiolese/encyl-Coenzyme A hydroxyacyl-Coenzyme A	FST4344 Them is throw III Home earlies a challe if the challe to challe to the challe	Homo sapiens antitutated review 2546 (ADDODCTA) INDIA	EST01132 Subtracted Hippocentous. Strategies (cet #200005) Home services ANA services	nol 7005 st NCI CGAP Phat Home serviers CDNA does BAACE-1400084 2"	Homo saplens gives addended 3 choschate dehicingeness (CAPIT) mRNA	Homo septens giyosraldehyde 3-phoachate dehydrocenase (GAPD), mRNA	Human endogenous retrowns HERV-K-T47D	ww61e07.xf NCI_CGAP_Lu28 Home septens cDNA clone IMAGE:2547204.3' similar to SW:GG95_HUMAN D08379 GOI GIN-05 "contrates element NEE222 mounts, along a similar to SW:GG95_HUMAN	Homo saplens epidermal growth factor receptor (arian erythroblastic leukemia viral (v-erb-b) oncogene homoloo) (FGFR) mRNA	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukernia viral (v-erb-b) oncogene homoton) (FGRF) mRNA	PT2.1 15 G11.r tumor2 Homo sepiens cDNA 3'	Novel human gene mepoing to champeagne 22	Novel human gene mapping to chanceame 22
Top Hit Detabase Source	± o	<u> </u>			±		Į.	토	F					Т	PD666012 NT		Т	*			W WANTE			T HUMAN	Ž L	\top
Top Hit Acessian No.	4.0E-74 AB020898.1	4.0E-74 AB028898.1	4506192 NT	4506192 NT	4.0E-74 AB032994.1	8.1	8.1	0.2	AL163247.2	7682183 NT	217227.1	4504326 NT	TU SCALASE NT	AA300378.1	9069012	478984.1	3.1	7869491	7669491 NT	7.	•	4885198	4885198 NT	-		
Most Similar (Top) Hit BLAST E Value	4.0E-74	4.0E-74	4.0E-74	4.0E-74	4.0E-74	4.0E-74 AJ00697	4.0E-74 AJ00697	4.0E-74 AL16324	4.0E-74	4.0E-74	4.0E-74 Z17227.1	4.0E-74	4 OF-74	3.0E-74 AA30037	3.0E-74	3.0E-74 M78984.	3.0E-74 AA60149	2.0E-74	2.0E-74	2.0E-74 AF02009;	2.0E-74 A1950528	2.0E-74	20E-74	2.0E-74 AI557280	2.0E-74	2.0E-74
Expression Signal	2.02	2.02	2.75	2.75	1.90	27.23	52	0.82	1.03	2.23	0.88	0.96	800	8.45	0	2.99	2.08	175.01	175.01	1.11	1.36	3.70	3.79	18.0	2.44	244
ORF SEQ ID NO:	27403	27404	27523	27524	27580	27882	28495	28028	29414	29889	29937	30343	30344		34309	35196	36098	26370	26371	26570	26644	27024	27025	28063	30281	30282
Econ SEQ ID NO:	14690	14690	14797		14859	15148	15853	16274	16786	17255	17308	17738	17736	2140	2165	22028	22885	13705	13705	13907	13972	14336	14336	15321	17872	17672
Probe SEQ ID NO:	1955	1955	2065	2065	2128	2427	3088	3518	4041	4520	4573	5015	5015	8448	8473	9272	10237	828	938	152	23	1590	1590	2609	4945	4945

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SEQ ID NO: NO: 10140 10140

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Probe SEQ ID SEQ		Expression Most Similar Top Hit Acession Top Hit Acession Top Hit Acession Top Hit Acession Top Hit Acession Top Hit Descriptor Top Hit Desc	37800			8 OE 75 AE478228 4 NE	1.86 8.0E-75 AL 163202.2	27781 1.47 6.0E-75 A1817415 1 EST LEIMAN	33468 0.61 5.0E-75/AA5734461 FET HIMAN	33467 0.61 5.0E-75 AA573446.1	34643 0.94 5.0E-75 BE272325.1 EST HUMAN	34855 0.8 6.0E-75 AA132811.1 EST HUMAN	34946 0.78 5.0E-75 BE501655.1 EST HUMAN	34947 0.78 5.0E-75 BE581655.1 EST HUMAN	35197 1.53 6.0E-75 BF890254.1 EST HUMAN	35983 2.39 5.0E-75 Al638823 1 EST HIMAN	25568 2.16 4.0E-75 BE081333 1 FET HIMJAN	1.02 4.0E-75 N36757.1	27202 1.5 4.0E-75 AW897230.1 EST HUMAN	28266 4.89 4.0E-75 BE409464.1 EST HUMAN	28902 0.94 4.0E-75 8922637]NT	31128 0.56 4.0E-75 11417946 NT	31129 0.56 4.0E-75 11417946 NT	31926 6.78 4.0E-75 5579467 NT	32436 2.26 4.0E-75 11417948 NT	32437 2.26 4.0E-75 11417946 NT	36517 18.12 4.0E-75 7669505 NT	28409 3.72 3.0E-75 AF157623.1 NT	26409 2.41 3.0E-75/AF157623.1 NT	27279 2.76 3.0E-75 AB011153.1 NT	27570 1.11 3.0E-75 4507334 NT	5.86 3.0F-75 4750459 NIT
0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1				3		 																_							26409			27R7R
T D & IMMALE GIBLES ENIMINACIONES MINISTRIBUMI	-	o,			[IJ	15044	88 20352	1_1						72782		13232									1					

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Table 4
Single Exon Probes Expressed in Brain

will be a second of the second	Top Hit Descriptor	Homo saplens chromosome 21 semment HS21Cnn1	Homo seriens mRNA for KIAANSA nominal cal	Human calcium-denendant phoentolistic binding metals (DI Ap) DNA	Human calcium denonder bioscholicki, kieden ender (DI An) - BATA	Homo services DNA for emulation processors and the contract of	Homo eaplens KIAA0971 profein (KIAA0971) mRNA	Homo seciens adector-related purples of comment of comment (Abson) 10114	HOMO Sections administrational protein complex 4 plans 2 millions (AP 132), metal	Homo eaclers HR (hatrae call nation references to second in (Ar. 102), michael	form service HID (history and service).	Long contract (1) A Appendix cent cycle regulation defective, S. defension) homolog A (HIRA), mRNA	Harrie expense nuchabates gene product (NJAAU623), mRNA	righto sapiens KiAAU023 gene product (KIAA0623), mRNA	Homo sapiens Oncogene TIM (TIM) mRNA	Homo sapiens Oncogene TIM (TIM) mRNA	Homo sepiens sneil 1 (drosophila homolog), zinc finast protein (SNA11), mRNA	Homo saplens Drosophila Kelch like protein (DKELCH) mRNA	Homo septens synuclein, alpha (non A4 commonant of amindad graces and A10 A10 A10 A10 A10 A10 A10 A10 A10 A10	AV734680 cdA Homo sepiens cDNA clone cdABED02 5	9091602.x1 NCI_CGAP_KId5 Hamo sepiens oDNA clone IMAGE:1915898 3' similar to TR:Q66386 Q69386 POLJENY (25NF:	Homo sapiens profesh forest preschates recently has not as a forest of the same of the sam	Homo septens protein tyrosine physicians, received the control of	200002X1 NCI_CGAP_UM Homo septens cDNA done IMAGE:2632707 3' similar to contains PTR7.ft	Heading FROM some arms 18 3 / mmin.	257703.81 Soares, testis. NHT Homo sepiens cDNA done IMAGE:726485 3' similar to gb:M13932.40S	KIBUSUMAL PROTEIN ST7 (HUMAN);	SOTIWAZENTI NIFT MIGG_19 Hamo suplens cONA clane IMAGE:4129678 5'	20 120228-H 1 Nn JMGC_19 Flored Sapiens CLAVA Gotte (MAGE:4129678 57	Homo septens calcium charmel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, atternatively spliced
	Top Hit Defabase Source	LN L																		T_HUMAN	EST HUMAN			ENT HIMAN	Т		T	EST LINAAN	Т	
	Top Hit Acession No.	3.0E-75 AL163201.2		Π	-	-	7682421			11528319 NT	1152631DINT	TMGCCART	Townson.	IN STREET	ZYDANA	LN COORT	1142004 NT	11438222 NT	11436430 NT	2.0E-75 AV734680.1	2.0E-75 Al311783.1 E	1506328	4506328 NT	1.0E-75 AW168135.1 F	T	,		T	Ī	-
	Most Similar (Top) Hit BLAST E Value	3.0E-75	3.0E-75	3.0E-75	3.0E-75	3.0E-75	3.0E-75	3.0E-75	3.0E-75	3.0E-75	3.0E-75	3 0F-75	3 OF 75	2 PE 75	0.0E-70	3.0E-75	3.0E-75	3.0E-75	3.0E-75	2.0E-75	2.0E-75	1.0E-75	1.0E-75	1.0E-75	1.0E-75 X52221.1	i i	1.0E-75	1 OF 75 F	1.0E-75 AA664377	1.0E-75 AF223391
	Expression	0.97	1.32	0.75	0.75	3.27	0.73	0.83	0.83	1.68	8.	4.56	8	200	3 2	7.57	127	0.77	228	1.41	2.45	1.12	1.12	6.68	3.27	* 7	27.5	3.75	10.83	2.56
	ORF SEQ ID NO:	28434	28597	28757	28758	29521	29769	30493	30494	32623	32624	32783	32784	33284	2220	2777	12.8	35414	36314		34484	27539	27540	27772	28368		35167	35168		36672
	Exan SEQ ID NO:							17980	17980	19588	19588	19727	19727	8483	3	3 2	4/017	888	23088	18384	21340	14808	14808	15026	15713	21006	21905	21995	23480	23704
	Probe SEQ ID NO:	3021	3184	3345	3345	4147	<u>\$</u>	5171	5171	0671	6671	7035	7035	7622	75.22	2000	8	1/98 88	<u>\$</u>	2587	8648	2078	828	2301	2947	8313	8328	8282	10797	11033

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Probe SEQ ID NO.: NO.: NO.: NO.: NO.: NO.: NO.: NO.:	SEO ID NO: NO: NO: NO: NO: NO: NO: NO: NO: NO:	ORF SEQ ID NO: 26027 27023 270	Signal Si	Moet Similar (Top) Hiff BLAST E Natue (Top) Hiff BLAST E Natue (A.OE-76 BF91625. 3.0E-76 BF91625. 3.0E-76 BF37586 3.0E-76 BF37586 3.0E-76 BF37586 3.0E-76 AA10001 3.0E-76 AA4230 3.0E-76 AA4330 3.0E-76 A	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Top Hit Source Source Source Source Source ST HUMAN ST HUMAN ST HUMAN TH	Top Hit Descriptor Top Hit Descriptor Source Source EST HUMANN HUM/TSGO1B Human fetal brain (TF-tijkwara) Homo saplens a CNA cione IMAGE-3082982 3' EST HUMANN UI-HSW1-4arz-b-04-0-UI-st NGT GOAP_Staft Homo saplens a CNA cione IMAGE-3082982 3' EST HUMANN UI-HSW1-4arz-b-04-0-UI-st NGT GOAP_Staft Homo saplens a CNA cione IMAGE-3082982 3' Homo saplens exteryobb translation adorgation factor 1 beta 2 (EEF-RB2) mRNA EST HUMANN RCA-ST3000-180100-053-403 510300 Homo saplens a CNA EST HUMANN RCA-ST3000-180100-053-403 510300 Homo saplens a CNA EST HUMANN RCA-ST3000-180100-053-403 510300 Homo saplens a CNA clone IMAGE-31925 5' similar to TR::Ocksse CNA EST HUMANN RCA-ST3000-180100-053-403 510300 Homo saplens a CNA clone IMAGE-31925 5' similar to TR::Ocksse CNA EST HUMANN RCA-ST3000-180100-053-403 510300 Homo saplens a CNA clone IMAGE-31925 5' similar to TR::Ocksse CNA EST HUMANN RCA-ST3000-180100-053-403 510300 Homo saplens a CNA clone IMAGE-31925 5' similar to TR::Ocksse CNA EST HUMANN RCA-ST3000-180100-053-403 510300 Homo saplens a CNA clone IMAGE-3194 5' EST HUMANN RCA-ST3000-180100-053-403 510300 Homo saplens a CNA clone IMAGE-3194 5' EST HUMANN RCA-ST3000-180100-053-403 510300 Homo saplens a CNA clone IMAGE-3194 5' EST HUMANN RCA-ST3000-180100-053-403 5' EST HUMANN RCA-ST3000-180100-053-403 5' EST HUMANN RCA-ST3000-180100-053-403 5' EST HUMANN RCA-ST3000-180100-053-403 5' EST HUMANN RCA-ST3000-180100-053-403 5' EST HUMANN RCA-ST3000-180100-053-403 5' EST HUMANN RCA-ST3000-180100-053-403 5' EST HUMANN RCA-ST3000-180100-053-403 5' EST HUMANN RCA-ST3000-180100-053-403 5' EST HUMANN RCA-ST3000-18010-053-403 5' EST HUMANN RCA-ST3000-053-403 5
3291	15614	28261	3.34	2.0E-76 P23.266 2.0E-76 AA445992	7		280UTT1.51 Streaggne schizo brain S11 Homo septens cDNA done IMAGE:701925 3' OLFACTORY RECEPTOR-LIKE PROTEIN F5 zw64e02.s1 Sceree_testis_NFT Homo septens cDNA done IMAGE:780986 3' similar to SW;TTB5_HUMAN P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR.
3281	16062	28702	2.06	2.0E-76	2.0E-76 AA445992.1	EST_HUMAN	2w64e02.s1 Sogree_lestis_NHT Homo sepiens cDNA clone IMAGE:780988 3' similer to SW:1TB6_HUMAN P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR;

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						200	Chighe Lacit Flower Expressed in Brain
SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Vatue	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3469	16225	28879	0.97	2.0E-76	2.0E-76 AI821149.1	EST HUMAN	ac83b02.y5 Strategene lung (#637210) Homo sapiens cDNA clone IMAGE:869163 5' similar to TR:014591 014591 SIMII ARITY TO P22099.
4114	13082	25725	1.23	2.0E-76	2.0E-76 D84295.1	NT	Human mRNA for bossible prohein TPRDII communicate cyle
4895	17622	30240	6.21	2.0E-78	2.0E-76 AW879618.1	EST HUMAN	QV3-OT0028-220300-132-511 OT0028 Home services chiva
5055			1.49	2.0E-78	5031660 NT	I.N	Homo septems EGF-like repeats and discovinin Lillia domains 3 (EDII 2) mDMA
6226			1.6	2.0E-76	AF127845.1	Ę	Gorlla gorilla difactory receptor (GGO18) gene partial cole
5531		31233	6.47	2.0E-78	4.1	Ę	Homo saplens mRNA for KIAA 1081 profein martial role
7334	20016	33094	0.75	2.0E-76	11426908	¥	Hamo seciens A kinese (PRKA) ancher purale 10 (AKAD40)
7560		33333	1.91	2.0E-76		Ę	Homo sepiens TPCR86 protein /HSTPCR849) mRNA
10182	22830	36045	3.53	2.0E-78		Ę	Homo saplens similar to riboarmal protein 226 (H. emisses // O. 283450)
10839	23521	36763	3.58	2.0E-78		5	Homo septens Hill A Interacting protein 4 (dna Lika) (HIRIDA) mRNA
4285	17006	29638	2.38	1.05-76	D63874.1	¥	Human mRNA for HMC-1 complete ode
4265		29639	2.38	1.0E-78		7	Human mRNA for HMG-1, complete cds
5362	18164	30849	6.12	1.0E-78	17.1	EST HUMAN	801559896F1 NIH MGC 7 Home sarders o'DNA closs BAADE:3044303.57
6150		 	0.72	1.0E-78	7.1	EST HUMAN	EST37301 Embryo. 8 week I Homo senions of INA 5' and
6825	19486	32508	4.53	9.0E-77	5.1	Т	8015/2435F1 NIH MGC 71 Home servines CDNA close NACE:3012727 F
1284	24041		1.4	9.0E-77	9.0E-77 BE410364.1	П	601302333F1 NIH MGC 21 Homo saciens cDNA done IMAGE acceptes 5
182	12894	25633	0.92	8.0E-77	8.0E-77.883144.1	1	yp11h02.r1 Soares breast 3NbHBst Homo sepiens cDNA clone IMAGE:187155 5' similar to SP-ANKR HIMAN OPASA ANKODIN DDAIN YADAART
4486	17221	29849	1.09	8.0E-77	Ξ.	Т	801868026F1 NIH MGC 17 Hamp septemb alone IMAGE 4105573 F
53.00	18168	30854	1 74	8 0E 77	4804000		Homo sepiens protessome (proecme, macropain) 26S subunit, non-ATPase, 7 (Mov34 homolog) (PSMD7)
11360		37351	181	8 0E-77	8 0E-77 AA019770 1 ES	T HI MAN	TOURS TO THE TANK I THE TOUR OF THE TANK I T
11380	24048	37352	19.	8.0E-77	-	Т	285262-1 South ruline NOMALIE Home services CONA April 114 APRIL 2002 1
12620	24925	31008	4 73	8 OF 77			ye09f04.s1 Source fetal fiver spicen 1NFLS Homo septens cDNA clone IMAGE:123007.3' similar to contains
1922	14659	27370	2.4	7.0E-77	Ţ.		MENTO INDICATOR CONTROL IN THE PROPERTY OF THE
2411	15132	27868	2.52	7.0E-77	1505044	No.	Home sentions achieve the Indian septents Culty Achieve Indian In
2411	15132	27869	252	7.0E-77	4505944INT		Homo septimes columnase (RNA) II (DIAA diseased) purpopular E (2500) (POLYZE) MRNA
256	13064	25703	8.53	.6.0E-77	4504600 NT		Homo sapiens interferon (slohe hete and ornane) bounder 2 (INIADO) (FOLKE) MRNA
1534	14281	26969	3.22	8.0E-77	6.0E-77 AI204086.1	T HUMAN	GOTTHICK Scenes fetal lung NEHL 19W Homo seniens COMA Accom MARCE 1745069 21
1214	13964	28631	211	5.0E-77	5.0E-77 AF041015.1		7 Homo sepiens glucoldnase (GCK) gene, excn 2
1339	14087	26763	1.77	5.0E-77	557250		Homo saplens distribution and metalloprotease domain 10 (ADAM10) mRNA
2601	15400	28139	0.98	5.0E-77	5.0E-77 AF162666.1		Homo sepiens tousied-like kinese 1 (TLK1) mRNA, complete cds

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Single Exon Probes Expressed in Brain	ORF SEQ Expression (Top) Hit Acession (Top) Hit Acession (Top) Hit Descriptor Signal No. Signal Value		28923 0.89 5.0E-77 8394518 NT	30022 2.47 5.0E-77 5031680 NT	30023 2.47 5.0E-77 5031880 NT	30231 2.96 5.0E-77 ALD43853.1 EST HUMAN	32642 0.57 5.0E-77 M13975.1 NT	33508 0.59 6.0E-77 8923319 NT	34099 1.28 5.0E-77 11428849 NT	34100 1.28 5.0E-77 11428849 NT	35249 2.48 5.0E-77 11421928 NT	35250 2.48 5.0E-77 11421928 NT	36249 1.22 5.0E-77 AB002297.1 NT	36250 1.22 6.0E-77 AB002297.1 NT	37716 3.12 5.0E-77 U37194.1 NT	37717 3.12 5.0E-77 U37194.1	27417 1.00 3.0E-77 6720038 NIT	27418 1.09 3.0F-77 F730038 NT	36050 0.79 3.0E-77 H651671 FCT HIMAN		36051 0.79 3.0E-77 H65167.1 EST HUMAN	36709 3.58 3.0E-77 BF350917.1 EST HUMAN	26763 1.4 2.0E-77 AV764617.1 EST HUMAN	26844 1.91 2.0E-77 AW 997712.1 EST HUMAN	27548 1.13 2.0E-77 L41825.1 NT	27560 5.28 2.0E-77 7706315 NT	28053 1.92 2.0E-77 AB037836.1 NT	28054 1.92 2.0E-77 AB037836.1 NT	28396 1.96 2.0E-77 BE044316.1 EST_HUMAN	29749 0.74 2.0E-77 AIB13519.1 EST HUMAN	29750 0.74 2.0E-77 A1613519.1 EST_HUMAN
																	Ĺ	L												ĺ	
-	SEQ ID NO:	J						. 1	- 1		ı			3 23034	24384	24384	14701		3 22836	<u> </u>		_1	l	- 1		- 1	_ [15599	16758	17116	17116
	Probe SEQ ID NO:	2767	3512	4655	4655	\$	9899	3	828	8266	2	2	10388	10388	1179	11794	1965	1965	10188		10188	10785	1330	1412	2084	8	2802	2002	4012	4370	4379

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Table 4
Single Exon Probes Expressed in Brain

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	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similer (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5839	18627	31582	246	1.0E-77 AF08694	AF086944.1	¥	Homo sapiens dynactin 1 (DCTN1) cana service 27 and 28
9	18738	31697	4.1	1.0E-77 M25844.	M25844.1	Z	Human von Willebrand factor same arm 20
6356	19126	32120	0.82	1.06-77	4885182 NT	Z	Homo saplens discharicus (Directhils homoloc) / (DIADLA) mDNA
6953	19436	32450	24.7	1.0E-77	5881412 NT	Ę	Homo sepiers election (supremely for every extra character Williams Downs and 1771).
	20234	33338	1.05	1.0E-77	11420159 NT	Þ	Homo septens cultin 1 (Cli 1) mRNA
	20327	33437	0.69	1.0E-77 X04571.	_	F	Human mRNA for kidney ecidermal growth factor (FGE) press reco
l	21835	35000	0.62	1.0E-77 X94354.1		노	H. Seplens DNA for Cone cGMP-DDE ones
	21835	35001	0.62	1.0E-77 X94354.1	104354.1	Ę	H. seroiens DNA for Come cGMP_PDF wave
	23067	36288	3.1	1.0E-77	1.5	Ę	Homo sablens hu-GicAT-P mRNA for nitremend/maneference commisse of
10421	23067	36280	3.1	1.0E-77		¥	Homo sepiens hu-GicAT-P mRNA for nitra monultane faces a complete cut.
l	23095	36326	2.55	9.0E-78 AW7533(12.1	EST HUMAN	RC3-CT0254-280909-011-b05 CT0254 Home seniors chas
6354	19124	32117	3.11	8.0E-78	8.0E-78 AW947061.1	EST HUMAN	RC2-E10023-080500-012-405 ET0023 Home earlone ANIA
6354	19124	32118	3.11	8.0E-78	8.0E-78 AW947061.1	EST HUMAN	RC2-FT0023-080-60-012-005 FT00-23 Hours emission and A
	12910	25548	1.87	6.0E-78	6.0E-78 AU118789.1	Т	AU18789 HEMBA1 Homo sembers CDNA close HEMBA4000224 ET
	12910	25549	1.87	6.0E-78	Γ	Г	AU118789 HEMBA1 Homo series CDNA close HEMBA1004354 6
	19232		2.54	8.0E-78	11432710 NT		Homo saplens GDNF family receptor sinha 1 (GFRA1) mRNA
212	13024	25963	0.72	5.0E-78	11422486 NT	Ę	Homo saplens hypothetical protein FLJ11316 (FLJ11316), mRNA
2567	15281	28019	5.53	5.0E-78	5.0E-78 AW673424.1	TSH TENT	be54h03.y3 NIH_MGC_10 Horno septens cDNA clone IMAGE:2800405 5' similar to WP:Y48B6A.6 CF22431
	16139	28797	3.81	5.0E-78 M55586.1		Т	Human collegeness two IV (C) C4) was arm 8
	18130	30789	2.33	5.0E-78 A	5.0E-78 AF038536.1		Homo sapiens Best's merular distributivalent protein mDNA merital colo
	18287	31183	11.12	5.0E-78	6585		Homo sapiens transforming growth factor between 88kD (TOED) DAIA
	19745	32808	223	5.0E-78 A	5.0E-78 AW963120.1	HUMAN	EST386190 MAGE resocuences, MAGB Homo saciena chala
	21671	34821	6.78	5.0E-78 U60889.1			Human Neosomal alpha-marmosidase (manB) gene. Eron 7
:	21672	34822	3.31	5.0E-78 BE960836	1.1	EST HUMAN	601648061F1 NIH MGC 62 Homo septems cDNA clame IMAGE 3031887 F
	13872	26531	1.07	4.0E-78 AL043314	2	Т	DKFZp434N0323 r1 434 (avnonum: hiera) Homo sanione china chos DKEZ-494N0323 r1
568	14264	28940	1.78	4.0E-78 A	-	LN.	Novel human gene mapping to champeome 22
1644	14390	27079	1.09	4.0E-78 AISB5094	ļ .		WIB7D12X1 NCI_CGAP_KId11 Home septens cDNA clone IMAGE:2495615 3' similar to SW:WAP_PIG
	15041	27779	2.08	4.0E-78 AF107405	-	Т	Homo seniene memBNA entirine feath (SIDS3) DNA
	17027	29852	5.	4.0E-78	056876		Homo series swords () OC20816 mRNA
	17454	30088	2.61	4.0E-78	4505806INT		Homo secient phoenhalfolding of these sections able to the secient of the secine of the secient of the secient of the secient of the secient
	17454	30080	2.61	4.0E-78	4505806 NT		Homo septions phosphetically a trices petablish sight and properties (Pirketh) mixing
5681 1	18474	31391	1.41	4.0E-78	11420732 NT		Homo eaciens SFRS protein traces 2 (SRPKs) mRNA

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					,														_														
Only Charles Expressed in Diani	Top Hit Descriptor	Homo expiens ribosomal protein S6 kinase, 70kD, potypeptide 1 (RPS6KB1) mRNA	Homo sepiens phosphatidylinosital 4-kinase 230 (p4K230) mRNA, complete cds	Homo sepiens phosphatidylinositol 4-Kinase 230 (p/4K230) mRNA, complete cds	Homo serolens X-ray repair complementing defective repair in Chinese homester and 4770 CVA	Homo saplens twoothetical C2H2 zinc finder protein FI (22504 (FI (22504) mBNA	Homo explens hypothetical C2H2 zinc finger protein P 122504 (FL 122504) mRNA	Homo saplens a-CaBP1 (CABP1) mRNA, complete cds	Human transforming growth factor-beta precursor gene exons 4-5 (and loned mature peoplids)	Homo sepiens gene for AF-8, complete ods	Homo sepions eRF1 gene, complete cds	Homo saplens eRF1 gene, complete cds	AU140804 PLACE3 Homo seplens cDNA clane PLACE3000373 61	Homo septens synaptolanin 1 (SYNJ1), mRNA	Homo septens synapolojenin 1 (SYNJ1), mRNA	Homo septems protein tyrosine phosphatase, receptor-type, zata polypeotide 1 (PTPRZ1) mRNA	CMC-HT0180-041099-065-007 HT0180 Homo serbiens cDNA	QV0-HT0367-150200-114-009 HT0367 Homo sabiens cDNA	Homo saplens type IV collegen aiche 5 chain (COL4A5) gene, excn 20	EST182583 Jurket T-cells VI Homo explens cDNA 5' end	UHHF-BKO-eat-g-10-0-Ul.r1 NIH MGC 36 Hamp septems cDNA clone IMAGE:3054139 5	UHF-BK0-eet-g-10-0-Ul.rl NIH, MGC 36 Hamo sablens cDNA done MAGE:3054139 67	602186529F1 NIH_MGC_49 Hamp sepiens oDNA clone IMAGE:4298589 5	AV714177 DCB Hamo sepiens aDNA clane DCBAW F09 5'	Pt2.1_16_B07.r tumor2 Homo sepiens cONA 3'	Pt2.1_16_B07.r tumor2 Homo sepiens cDNA 3'	qi50h05.x1 NCI_CGAP_Bm25 Homo septens cDNA clone IMAGE:1859961 3' similar to WP:R90.1 CE06325 PROTEIN KINASE:	2948112.s1 Source fetal Iver spleen 1NFLS Homo serviens cDNA clone INAGE-205823.31	Homo explens synaptosomel-essociated protein, 25tD (SNAP25) mRNA	Homo saplens synaptosomel-associated protein, 25(O) (SNAP25) mRNA	Homo sepiens GAP-like protein (LOC5/306), mRNA	AV648699 GLC Homo sepiens cDNA clone GLCBMCo1 3'	AU122163 MAMMA1 Homo saplens cDNA clone MAMMA1001785 61
מום האסיו בונו	Top Hit Detebase Source	F	Į.	NT	5	Þ	Ę	F	¥	Ę	Ę	¥	EST HUMAN	F	F	E	EST HUMAN	EST HUMAN	Ę	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	Ę	¥	Ę	T_HUMAN	EST_HUMAN
, in the second	Top Hit Acession No.	4506736 NT	4.0E-78 AF012872.1	4.0E-78 AF012872.1	11417251 NT	11580151 NT	11560151 NT	4.0E-78 AF169148.1		4.0E-78 AB011399.1	VF095901.1	-	7	4507334 NT	TN 4507334	4506328 NT	-	-		2.0E-78 AA311872.1	5	2.0E-78 AW402306.1	-	Ţ.					4507098 NT	4507098 NT	11417304 NT	1	
	Most Similar (Top) Hit BLAST E Value	4.0E-78	4.0E-78	4.0E-78	4.06-78	4.0E-78	4.0E-78	4.0E-78	4.0E-78 X05844.1	4.0E-78	3.0E-78 AF095901	3.0E-78 AF095901	3.0E-78/	3.0E-78	3.0E-78	3.0E-78	3.0E-78 BE144758	3.0E-78 BE156318	2.0E-78 U04489.1	2.0E-78	2.0E-78	2.0E-78	2.0E-78 BF689800	2.0E-78 AV714177	2.0E-78 AI557509.	2.0E-78 AI557509.1	2.0E-78 A1197837.1	2.0E-78 N68951.1	1.0E-78	1.0E-78	1.0E-78	1.0E-78 AV648699.	1.0E-78 AU122163
	Expression Signal	0.58	2.86	286	9.0	1.96	1.96	5.18	2.15	3.57	1.39	1.39	90.0	0.72	96.0	56.0	5.14	1.97	2.17	1.87	1.54	1.54	3.99	2.33	1.4	1.4	3.27	3.80	3.07	3.07	2.03	0.78	0.65
	ORF SEQ ID NO:	33148	34591	34592	35192	36208	36207	37305	37456	31018	25610	25611	-	29181	29181	30430		36832		-	33126	33127	33405	33762	34180	34181	36952	37012	29481	29492	30655	30570	33517
	SEQ ID NO:	20069	21444	21444	22022	22989	22080	24002	24148	24868	12972	12972	16499	16548	16548	17813	22834	23582	15884	16743	20047	20047	20297	20635	21044	21044	23689	23738	16865	16865	18029	17834	20401
	Probe SEQ ID NO:	7390	8752	8752	9268	10342	10342	11396	11547	12517	157	157	3746	3796	4084	5004	10186	10902	3119	3886	7367	7367	7631	7940	8351	8351	11017	11068	4123	4123	6222	6857	7736

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Most Similar ORF SEQ Expression (Tex) Hit Anseston	ID NO: Signal BLASTE Value	0753 3.28 1.0E-78 U52373.1 INT Human serine/threonine kinase MNB (mrb) mRNA, comolete cds	31117 1.39 1.0E-78 11430490 NT	30718 1.55 1.0E-78 AI650919.1 EST HUMAN	30016 4.05 9.0E-79 11526891 NT	30166 8.05 9.0E-79 BE000837.1 (EST HUMAN	30829 16.87 9.0E-79 AB028070.1 NT	31994 2.38 9.0E-79 5454145NT	0.99 9.0E-79 11424427 NT	33239 0.79 9.0E-79 1142/735 NT	33240 0.79 9.0E-79 11421735 NT	34074 0.49 9.0E-79 11417260 NT	34075 0.49 9.0E-79 11417280 NT	34802 5.1 9.0E-79 J02853.1 NT	34803 5.1 9.0E-79 J02853.1 NT	35206 0.58 9.0E-79 D87675.1 NT	36121 0.82 9.0E-79 11438643 NT	36182 1.73 9.0E-79 AF062346.1 NT	36183 1.73 9.0E-79 AF062346.1 NT	36930 3.13 9.0E-79 AY008273.1 NT	37410 3.55 9.0E-79 11423827 NT	37411 3.55 9.0E-79 11423827 NT	29115 0.91 8.0E-79 AL163210.2 NT	30596 1.82 8.0E-79 8567387 NT	28680 28.39 7.0E-79 BE619648.1 EST_HUMAN	T COUNTY Y CAL JOY OF TO	37300 2.52 F.DE.70 A 148282.2 NT	IN 7.202.00 P. 10.20.20.20.20.20.20.20.20.20.20.20.20.20	1.49 4.0E-79 8922325 NT	25/49 1.28 3.0E-79 AF114488.1 (NT	28388 3.85 3.0E-79 AF232708.1 NT	28501 1.51 3.0E-79 U09410.1 NT	30738 5.24 3.0E-79 AF110322.1 NT	31345 1.24 3.0E-79 AB020699.1 NT
ORF SEQ	Ö Ö Ö			30718	30016	30166		31994		33230	33240	34074	34075	34802	34803	35206	36121	36182	36183	36930	37410	37411	29115	30596	28680		37390		100	25/48	26388	28501	30738	31345
	NO.		24585	7 25244	17384	17542	18149	19022	25108			- 1							╝			_1		_ [18009	24400	L			_		_1	18082	18432
Property	8 8 8 9 9 9 1 1 1 1 1 1 1 1 1 1 1 1 1 1	8050	12045	12477	4650	4811	5346	6248	7251	7473	7473	8244	8244	8981	8961	9280	10263	10318	10318	138	11497	11407	3725	11996	3247	11800	11478	24.72	206	3	ŝ	3005	5277	5637

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Table 4
Xon Probase Expressed in

					Sin	gle Exon Pro	Single Exon Probes Expressed in Brain
SEQ ID	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E	Top Hit Acession No.	Top Hit Detebase Source	Top Hit Descriptor
				Value			
5862	18457	31371	0.93	3.0E-79	3.0E-79 BE789470.1	EST HUMAN	801487143ET NIH MGC AS Homo conjusc a DNA Jan 1944 Charles
5862	18457	31372	0.93	3.0E-79	3.0E-79 BE789470.1	EST HIMAN	R014R2147E4 NIH MOO R8 HOUSE COUNT GROWN IN THE COUNTY GROWN IN TH
5882	18475	31392	3.56	3.0E-79		Į.	Homo serience noting a (NTNA)
5682	18475	31393	3.56	3.0E-79		Į	Homo series north 4 (NTM) - India
5646		32422	0.67	3.0E-79	BE256803.1	EST HUMAN	80112055F1 NIH MAC 16 Home section CALA Line MACE comment
9990	19442	32457	3.35	3.0E-79	2	Į.	Homo seniers mRNA for KIAAAso profile
90		32458	3.35	3.0E-79	Π	Į	Homo saplens mRNA for KIAAARSD models and all
7726		33503	0.78	3.0E-79	8012455	5	Homo penients another with the first for the
8064		33887	1.61	3.0E-79	AF249273.1	¥	Homo seriene Brit 2 secondate transmission of Rapi (KIAA0277), mRNA
5003	21970	35144	1.33	3.0E-79	5036	5	Home earlies extend the second of the second
10245	22893		1.24	3.0E-79 AV6081	2	EST HUMAN	AV698116 CKC Home seniors about Almo OK ALLESS :
10768	23452	36694	1.62	3.0E-79	1.5	LX	Horne series BH2 accordand a Curva Chile
10768	23452	38895	1.52	3.0E-79	3.1	LN	Homo saniene Bol 2 sesociated transfer from michael Complete cds
281	13088		080	2.0E-79		HIMAN	Ve48f03 at Some field lives and a state of the complete cds
619	13398	26033	1.8	2.0E-79	6.1	Т	80159415F2 NIH MCC 83 Home emisse DNA 114 OF SECTION 100 DNA 114
200	13674	26339	228	2.0E-79	4757841	Į.	Homo sablems BCI 2-line 2/BCI of 3/m-DNA
1012	13772		2.09	2.0E-79	2.0E-79 AJ523747.1	T HUMAN	MISHOT Y NO COAD POR HOME
1781	14522	27228	1.12	2.0E-79	57024		Home services Dickloud name & Mark A
178/	14622	72272	1.12	2.0E-79	7657024 NT		Homo sablene Dickowy gare 4 (Dick 4) Duly
2144	14874	27607	5.93	2.0E-79	4585863 NT		Homo senions physochopies & A. Charles
2144	14874	27608	5,83	2.0E-79	4585863 NT		Homo segiens phosphodisedness & CAID shows . J. L.L. (1955), This
28 28 28	4918	27652	1.07	2.0E-79 AJ271408	AJ271408.1		Homo sapiens mRNA for Fas-associated factor EAEA / End.
2721	15428	28106	1.09	2.0E-79			Homo eaplens mRNA for KIAA0627 profess netter Ale
2888	16843	20283	0.83	2.0E-79	2.0E-79 AF170492.1	Į.	Homo seplens channe C C4 (CICA) mentata and
4144	888	29517	1.09	2.0E-79 AJ271408	ŀ	¥	Homo septens mRNA for Fast-associated factor FAET (Faft Ages)
5885	18382		122	2 0E-70 A A 312222		TOT CHIMAN	EST182926 Jurket T-cells VI Homo septens cDNA 5 end similar to similar to C. elegens hypothetical protein.
5840	18435	31348	0.8	20E-79	81789	NO.	Homo sariane Y femanoshos and 1 0 (VTo) 1011
9149	18926	31896	1.14	2.0E-79 AB020637	_		Hamo saplens mRNA for KIAA0830 profinin partial pole
2884	17041	30577	0.80	2.0E-79	2.0E-79 AF263613.1	<u> </u>	form sarrians manufactures associated as in the control of the con
7087	19758	32822	1.7	20E-79	2479		Homo seniore Rhy CTDees and with a serial in the Parish of the serial of
7067	19758	32823	1.7	2.0E-79	7382479INT		Homo sections Rho GTDees and the control of ARTHON transcript vertent 4, mRNA
7900	20694	33821	1.08	2.0E-79	4506442 NT		Homo sections retiroble sections like 4 (AAAA) (DDI 4), DAIA
							To the separate redictions such that I will be a separate reduction of the separate reduction of

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ſ							
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8415	21108	34247	225	2.0E-79	11427428 NT	Ę	Homo saplens hypothetical protein F. 111006 (F. 111008) m.BNA
8664		34503	0.58	2.0E-79		¥	Homo saplens Probled and Problem F1 (20275/F1)20275/ mDNA
8884	21358	34504	0.58	2.0E-79		F	Homo saplens hypothetical protein FL/20275 (FL/20275), mRNA
8902		34734	1.85	2.0E-79	11432184 NT	<u> </u>	Homo saptens similar to ATP ase, H+ transporting, lysosomal (vacuolar proton pump) membrane sector associated protein MA.0 (H. emiens) (I. Operada I
9992	22640	35850	4.	2.0E-79 S72869	S72869.1	Ę	H-KD10S170)=putative cytostoletel protein [human flyand mpn.k. 2014
9002	22840	35851	1.4	2.0E-79 S72869	S72869.1	F	H4(D10S170) outsides cytoskeletel prodein Prumen Sharid mRNA 3011 m
10696	23389	36627	12.34	2.0E-79	2.0E-79 U07819.1	Į.	Human contactin 1 precursor (CNTN1) mRNA complete cde
10936		36880	4.05	2.0E-79	$]^{-}$	EST HUMAN	RC4-BT0310-110300-015-f10 BT0310 Home serviews cDNA
10056		36881	4.05	2.0E-79	2.0E-79 BE064386.1	EST HUMAN	RC4-BT0310-110300-015-f10 BT0310 Home servious c-DNA
8	- 1	30594	2,18	2.0E-79	7062357 NT	L LX	Homo sapiens KIAA0879 protein (KIAA0879), mRNA
12018	. [31108	5.19	2.0E-79	2.0E-79 AB020640.1	ĮN.	Homo septens mRNA for KIAA0833 protein, partial cals
12238		31075	280	2.0E-79	11418322 NT	PA PA	Homo sapiens cadharin EGFLAG seven-ceas G-hora recentor 1 (CEI SR1) mBNA
8			3.78	1.0E-79 BF3630	BF363071.1	EST HUMAN	MRO-NN0087-280600-017-510 NN0087 Home series CDNA
8143	20837	33909	0.78	1.0E-79	1.0E-79 BE394211.1	EST HUMAN	801311517F1 NIH MGC 44 Homo sepiens CDNA clara IMAGE: 3R320no F
<u> </u>	24220	37543	2.05	1.0E-79	1.0E-79 BF087405.1	EST HUMAN	QV2-HT0640-120500-368-e06 HT0640 Homo septems cDNA
2 <u>8</u>	25333		1.8	1.0E-79 AI46011	Al460115.1	EST_HUMAN	ar 79a04 x1 Barstoad colon HPLRB7 Homo saciens cONA clone INAGE 2151438 31
3143	15907	28551	2.35	9.0E-80	9.0E-80 AA725848.1	EST HUMAN	at 23e05.s1 Soares testis NHT Homo sapiens cDNA clone 1343648.3
3143	15907	28552	235	D.0E-80		EST HUMAN	8123406.81 Sogres tests NHT Home sexions china chana 1343848 9
8912	22561	35757	1.14	9.0E-80	Γ	EST HUMAN	601581662F1 NIH MGC 7 Homo sapiens cDNA clone IMAGE: 3339061 5
11245	23907	37100	8.88	9.0E-80	11433924 NT	Ę	Homo sepiens solute carrier family 7 (calionic amino acid transporter, y+ system), member 8 (SLC7A8), mRNA
11245	23907	37200	8.00	9.0E-80	11433924 NT	5	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 8 (SLC7A8), mRNA
3588	16342		1.31	8.0E-80 U94387.		L	form sanians V chromosome successive state of the state o
ğ	20175	33268	3.07	8.0E-80	11422647		Homo septeme KIAA0724 name sendina RKIAA0723 - Distribute House (NDM) pseudogene mKNA, parbel cds
7504	20175	33269	3.07	8.0E-80	11422847 NT		Homo saplens KIA A0724 pers product (NAA07.24), mKNA
8302	21989	35142	1.13	8.0E-80	6005921 NT		Homo sanians trials fractional domain (DTDDE International ATDDA)
2302	21989	35143	1.13	8.0E-80	9005921 NT		Homo sabiens trible functional domain (PTPRE interestina) (TRIO), many
88	13640	26318	1.12	6.0E-80 A 422197	2	. II	#58402.xf NCI_CGAP_Bm23 Home septens cDNA clone IMAGE:2103459 3' similar to SW:NUEM_HUMAN
1638	14384	27071	222	6.0E-80 U64898.		Т	Homo seniens NRD convertes mRNA complete At
							To the opposite that the control section in t

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					,	121 - 1120- 218	Chighe Excit Flobes Expressed III Brain
Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acessian No.	Top Hit Database Source	Top Hit Descriptor
4252		29620	1.08	6.0E-80	6.0E-80 AB032981.1	N	Homo supleme mRNA for KIAA1155 protein, pertial cds
4252		29621	1.08	6.0E-80	6.0E-80 AB032981.1	N	Homo septens mRNA for KIAA 1155 protein partial cds
5712		31427	1.79	6.0E-80	11421482 NT	Ę	Homo seplens malate defrictiogeness 2 NAD (mitrodicinal) (MIDH2) mRNA
5984	18766	31729	3.37	6.0E-80	6.0E-80 AJ404468.1	¥	Homo seplens mRNA for dynam heavy chain (DNAHO nows)
6135	18913	31882	4.69	6.0E-80	11436736	Ę	Homo sepiens tubov like projen 3 (TLII P3) mRNA
6179			1.17	6.0E-80		Z	Homo esplays KIAA0941 probe (KIAA0941) mRNA
6230	19004	31980	96.0	6.0E-80	6.0E-80 M18533.1	Z	Homo espleys dystrophin (DMD) mRNA complete cits
8723		34558	3.22	6.0E-80	11528464	Ę	Homo saplens G protein-coupled receiper 51 (GPR51) mRNA
8723		34559	3.22	8.0E-80		Z	Homo espiene G protein-coupled receptor 61 (GPR61) mRNA
8917		34761	1.61	6.0E-80	AL163301.2	Į.	Homo saplens chromosome 21 segment HS21C101
8228		35113	0.83	6.0E-80	5.1	N	Homo saplens HSPC148 mRNA, complete oda
9761	22412	35619	1.48	8.0E-80		Z	Human cone photonocentor cGMP-phosphodisebrase slinks, seleunik zene.
10861	23541	36788	2.83	6.0E-80	1427368	Z.	Homo septens brefeldin A-habitine duantine michanistaamhama anna 1,010.4 / 1010.4
11187	23862	37138	28.56	6.0E-90	6.0E-80 AF228730.1	Į.	Homo septens CM19 mRNA complete ede.
11702	24297	37623	1.59	6.0E-80		Σ	Human percedame largeting state 2 months Pex77 mRNA complete Ada
11756	24347	37877	1.5	6.0E-80	6.0E-80 AF102265.1	Σ	Homo explere N-acet/ducosamine-phosphate mittees mRNA complete colo
11802	24392	37725	2.28	6.0E-80	Γ	N	Homo septens mRNA for KIAA0717 protein martial orts
11802	24392	37726	2.26	6.0E-80		N.	Homo sepiens mRNA for KIAA0717 protein, partial cds
11906	13849	26318	88:	6.05-80	6.0E-80 Al422197.1	FST	#38402.x1 NCI_CGAP_Bm23 Homo sepiens cDNA done IMAGE:2103459 3' similar to SW:NUEM_HUMAN 016726 NATHUI IRIOI IINONIE OXINODERII IOTA 6E 30 KB SK RA RA RA RA RA RA RA RA RA RA RA RA RA
12028	26217		64.6	8.05.80		T^{-}	Homo septions S-transferase their 2 (GSTT2) and glubathione S-transferase their 1 (GSTT1)
12219	ĺ		5.78	6.0E-80			Homo saniens CST name for combined as information
12707	25341		4.	8.0E-80	-	L'N	Homo eaglens mRNA for addition-discover contravenories (SCI T2 news)
1300,4	76064	-	,				Homo saplens glubathione S-transferase thete 2 (GSTT2) and glubathione S-transferase theta 1 (GSTT1)
1	1000	OCANS OCANS	1.35	6.0E-80.	6.0E-80 AF240786.1		genes, complete cds
5 2	3 3	70802	0.74	5.0E-80	6228		Homo septens protessome (procome, mecropain) 26S subunit, non-ATPese, 3 (PSMD3) mRNA
CLS L	9865	28253	1.97	6.0E-80/			Homo sapiens serine-threonine probein kinase (MNBH) mRNA, complete cos
010	2000	20204	1.97	5.0E-80,	-		Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
B .	13920	1	239	5.0E-80 X91647.1			H.saplens next gene (exen 12)
200	8 2		228	5.0E-80,	2		Hamo septens ahranceane 21 segment HS210083
	15083	27821	8.	5.0E-80 (5.0E-80 U89358.1		Human (3) mbt protein homolog mRNA, complete cds
2431	15152	27886	1.65	5.0E-807	-	I.N	Homo saplens mRNA for KIAA1434 protein, partial cds

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ſ		_	Т	Т	_	Т	т-	Т	т-	т-	,	_	_	_	_	_	т-	_	_	_	_	_	Tac	_	_	_		_	7	 -
	Top Hit Descriptor	Homo sapiens H3 histone family, member J (H3FJ) mRNA	Homo sepiens HMT-1 mRNA for beta-1.4 mannosytransferase, complete cds	Homo sapiens HMT-1 mRNA for beta-1,4 mannosytransferase, complete cds	Homo saplens chromosome 21 segment HS21C088	Mus musculus leratin complex 2, gene 6g (Krt2-6g), mRNA	HSPD13155 HM3 Homo espiens cDNA clone \$4000045F03	Homo sapiens chromosome 21 segment HS21C010	PMO-GN0018-040900-002-E03 GN0018 Homo sapiens cDNA	QV4-BN0263-040600-241-g10 BN0263 Homo septens cDNA	0023912.x1 Soeres, NSF_F8_9W_OT_PA_P_S1 Homo sapiens oDNA done IMAGE:1567054 3' similar to TR:035790 035790 PIG-L.	V085a08.rf Soares Infant brain (NIB Homo saciens cDNA clone IMAGE:38000 5:	RET4B7 subtracted refine cDNA-library Homo sapiens cDNA clone RET4B7	DKFZp434D1323 r1 434 (swonym: https://dww.aeplens.cDNA.clove.DKFZp434D1323 5	Im80d01.s1 NCI_CGAP_Co9 Hamo saplens cDNA clone IMAGE:10901773	Homo septens Golgi transport complex protein (90 kDs) (GTC90), mRNA	1986/12.rt Source Infant brain 1NIB Homo septems CDNA clone IMAGE 22851 5' similar to SP:K1CR XENLA P08802 KERATIN, TYPE I CYTOSKELETAL ENDO B.	EST376343 MAGE resequences, MAGH Homo sepiens cDNA	Homo sapiens GGT gene, excm 6	2/2011.2.1 Soares, tests, NHT Homo septens cDNA dane IMAGE:72/727 5' similar to TR:G191315 (G191315 ANDROGEN-DEPENDENT EXPRESSED PROTEN.:	Homo sapiens chromosome 21 segment HS21C103	Homo sepiens chromosome 21 unknown mRNA	m01f12.55 NCL_CGAP_Coe Homo sepiens cDNA clone IMAGE:1078495 3' similar to contains OFR.t1 OFR necessitive element;	Homo sepiens gamma-aminobuharic acid (GABA) A neceptor, gamma 2 (GABBG2) mRNA	801274305F1 NIH MGC 20 Homo septens cDNA clone IMAGE:3615433 5	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds	Homo saptens matete dehydrogenase 2, NAD (mitochondrial) (MDH2), nuclear gene encoding mitochondrial protein, mRNA	Homo sapiens mRNA for lipophilin B	wq25006.x1 NCI_CGAP_Kid11 Hamo sepiens oDNA done (MAGE:2472298 3)	wq25c05x1 NCI_CGAP_Kid11 Hamo seplens cDNA clone IMAGE:24722963
	Top Hit Datebase Source	N.	IN	N N	NT	NT.	EST_HUMAN	NT	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	N	EST HUMAN	EST HUMAN	NT	EST HUMAN	N.	IN	EST HUMAN	Z	EST HUMAN	NT	I.	NT	EST_HUMAN	EST HUMAN
	Top Hit Acession No.	4504292 NT	AB019038.1	AB019038.1	5.0E-80 AL163268.2	9910283 NT	-25915.1	AL163210.2	3.0E-80 BF085009.1	3.0E-80 BE817465.1	A1091675.1		N444821.1	L043116.2	A582952.1	11421930 NT	75215.1	2.0E-80 AW964270.1		2.0E-80 AA303362.1	1.0E-80 AL163303.2		-	4557810	5.1		5174540 NT	1.0E-80 AJ224172.1	-	÷.
	Most Similar (Top) Hit BLAST E Value	6.0E-80	5.0E-80 AB01903	5.0E-80 AB0190	6.0E-80	5.0E-90	4.05-80	3.0E-80 AL16321	3.0E-90	3.0E-80	3.0E-80 Ai08167	2.0E-80 R35321	2.0E-80 AI44482	20E-80 AL04311	2.0E-80 AA58295	2.0E-80	2.0E-80 T75215.1	2.0E-80 /	2.0E-80/	2.0E-80	1.0E-80/	1.0E-80	1.0E-80 A 732866	1.0E-80	1.0E-80 BE38061	1.0E-80 L10347.1	1.0E-80	1.0E-80 A	1.0E-80 AIS48731	1.0E-80 A194873
	Expression Signal	1.67	1.37	1.37	1.28	1.04	8.77	8.98	1.7	3.77	2.68	5.08	1.10	5.82	0.83	1.71	1.46	1.41	1	4.40	2.25	1.37	244	0.99	6.43	6.58	1.36	0.95	2.53	2.53
	ORF SEQ ID NO:	28242	28383	29394	30244	34086			30030		31443	27238	27307	27509	32067	32406	32908	34905	35518	36705	-	28215		30397		31608	32174	32850	33237	33238
	Econ SEQ ID NO:	15502	16764	18764	17627			13023	17395	17580	18522	14530	14591	14782	19623	19474	19638	21748	22320	23463	13132	13554	14082	1778	18050	18967	19175	19794	20145	20145
	Probe SEQ ID NO:	2797	4018	4018	4900	8255	9157	211	4661	4850	6730	1790	1853	2046	6708	6813	7151	29057	8998	10780	331	82	194	2060	5244	5881	9050	7108	7472	7472

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	Top Hit Descriptor	Homo sapiens protein tyrosine phosphatase, receptor type, A (PTPRA), mRNA	Homo sapiens protein tyrosine phosphetase, receptor type, A (PTPRA), mRNA	Homo sepiens protein tyrosine phosphatase, receptor type, A (PTPRA), mRNA	Homo eapiens probable mannose binding C-type lectin DC-SIGNR mRNA, complete cds	Homo saplens probable memose binding C-type lectin DC-SIGNR mRNA, complete cds	Homo sepiens mRNA for KIAA0145 protein, partiel ods	Homo expiene eimilar to rat myomegalin (LOC84182), mRNA	Homo sepiens similar to ret myomegalin (LOC84182), mRNA	Homo sepiens meningiome (disrupted in balanced transfocation) 1 (MN1), mRNA	Homo sepiens mRNA for KIAA0833 protein, pertial cds	qh80g05x1 Soeres_NFL_T_GBC_S1 Homo septens cDNA clone IMAGE:1854296 3'	qh90g05.x1 Sogres_NFL_T_GBC_S1 Homo septens cDNA clone IMAGE:1864296 31	601310531F1 NIH_MGC_44 Home saplens cDNA clone IMAGE:3632070 5	2891c08x5 Soures_fetal_lung_NbHL19W Homo sapiens cDNA clone (MAGE:299918 3'	601111970F1 NIH_MGC_16 Hamo septens cDNA clone IMAGE:3352840 5	601111970F1 NIH_MGC_16 Homo septiens cDNA clone IMAGE:3352840 5	Homo sepiens ATP-binding cessetts, sub-family A (ABC1), member 3 (ABCA3), mRNA	Homo sepiens ATP-binding cessetts, sub-family A (ABC1), member 3 (ABCA3), mRNA	Homo sapiens chromosome 1p33-p34 beta-1,4-galactosytransferase mRNA, complete cds	EST60129 Fetal king II Homo septens cDNA 6' end	312522F1 NIH_MGC_44 Homo septens cDNA done IMAGE:3659284 5	802153888F1 NIH_MGC_83 Hamo sapiens cDNA done IMAGE:4294801 5	602163666F1 NIH_MGC_83 Homo sapiens cDNA done IMAGE:4294601 5	601125505F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE;3345480 5	Homo sapiens mRNA for KIAA0454 protein, pertial cds	Homo sapiens mRNA for KIAA0454 protein, pertial cds	Human transforming growth factor-beta (tgf-beta) mRNA, complete cds	Human transforming growth factor-beta (tgf-beta) mRNA, complete cds	Homo saplens hypothetical protein (FLJ11045), mRNA	Homo septens armadillo repeat gene deletes in velocardiofacial syndrome (ARVCF), mRNA	th60e12.x1 NCI_CGAP_Ov23 Homo septens cDNA clone IMAGE:2122702 3' stmilar to TR:Q85660 Q85560	hn98d02x1 NCI_CGAP_Co14 Hamo septens cDNA clane IMAGE:3035907 3' similar to SW:COPG_BOVIN P53620 COATOMER GAMMA SUBUNIT;
-	Top Hit Detabese Source				와 N	¥ FN	N FN				N IN	EST_HUMAN qh	EST_HUMAN qh	Г	EST_HUMAN Zan	EST HUMAN 60	EST_HUMAN 60			NT H	EST_HUMAN ES	HUMAN	EST_HUMAN 803	EST_HUMAN 603	EST_HUMAN 60	OH. IN	오	王	문			T_HUMAN	
	Top Hit Acessian No.	11421211 NT	11421211 NT	11421211 NT	1.0E-80 AF246219.1	19.1	2	11841276 NT	11841278 NT	11417901 NT	1.0E-80 AB020840.1	8.0E-81 AI251752.1			7.0E-81 AI822115.1	29.1	23.4	4501848 NT	4501848 NT						5.0E-81 BE268042.1		5.0E-81 AB007923.1	-	-	9506634 NT	11626341 NT	4.0E-81 AI521435.1	12.1
	Most Similar (Top) Hit BLAST E Value	1.0E-80	1.0E-80	1.0E-80	1.0E-80	1.0E-80	1.0E-80 D63479	1.0E-80	1.0E-80	1.0E-80	1.0E-80	8.0E-81	8.0E-81	8.0E-81 BE39452	7.0E-81	6.0E-81 BE25682	6.0E-81 BE2568;	6.0E-81	6.0E-81	6.0E-81	6.0E-81	6.0E-81	6.0E-81	6.0E-81	5.0E-81	5.0E-81	5.0E-81	5.0E-81 M90316.	5.0E-81 M60316.	5.0E-81	5.0E-81	4.0E-81	4.0E-81 AW7796
	Expression Signal	2.84	1.72	1.72	1.21	1.21	0.95	525	5.25	1.57	3.08	1.46	1.46	8.46	3.58	5.26	5.26	2.1	2.1	78.0	1.36	1.61	2.29	229	2.8	1.83	1.83	77.0	0.77	2.23	1.3	2.03	1.31
	ORF SEQ ID NO:	09628	34435	34438	36019	35020		38479	36480	31051	31034	36515	36516	37048	32909	29726	29727	30630	30631	33253	34989	37723	31041	31042	27682	34143	34144	35383	35384	37491	37764	26109	27270
	SEQ ID		21293	21293	21855		22972	23244	23244	24719	24853	23278	23278	23772	19839	17092	17092	18009	18009	20161	21824	24390	24803	24803	14942	21005	21005	22201	22201	24176	24423	13461	14565
	Probe SEQ ID NO:	8130	9601	8801	9185	9185	10325	10548	10548	12289	12408	10583	10583	11102	7162	4354	4354	5201	5201	7489	9136	11800	12430	12430	2214	8311	8311	9548	9548	11577	11839	989	1815

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Single Exon Probes Expressed in Brain	Top Hit Top Hit Detablese Top Hit Descriptor	198.1 INT Homo sapiens mRNA for KIAA1345 protein, pertial cds	EST HUMAN	¥	Ę	3209 NT	4757863 NT Homo sapiens caldum channel, voltace-decendent. Litze, alcha 2/delta subunit (CACNA2) mRNA		TN L	- N	F	1.1 N	11425281 NT Homo saplens ligase I, DNA, ATP-dependent (LIG1), mRNA	11439065 NT Homo sepiens acyt-Coerzyne A dehydrogenase family, member 8 (ACAD8), mRNA			4759085 NT Homo seplena vesicle trafficking protein sec.22b (SEC22B) mRNA	11417862 NT Homo sepiens calcineurin binding protein 1 (KiAA0330), mRNA	11417852 NT Homo saplens calcineurin binding protein 1 (KIAA0330), mRNA		11417871 NT Homo sepiens bets-ureldoproplonase (LOC51733), mRNA	11417974 NT Homo sapiens transcobalamin II; macrocydc anemia (TCN2), mRNA	ķ	Ż	38.1 INT Hamo sapiens cullin 4A (CULAA) mRNA, complete cds	4506280 NT Homo sepiens pielotrophin (heperin binding growth factor 8, neurits growth-promoting factor 1) (PTN) mRNA	Assessed NTCI/() which analysis and an artical threath binding productions and the manufacture of the North Assessment (NTCI/() and the second of the North Assessment (NTCI/() and the second of the North Assessment (NTCI/() and the second of the North Assessment (NTCI/() and the second of the North Assessment (NTCI/() and the second of the North Assessment (NTCI/() and the second of the North Assessment (NTCI/() and the second of the North Assessment (NTCI/() and the second of the North Assessment (NTCI/() and the second of the North Assessment (NTCI/() and the second of the North Assessment (NTCI/() and the second of the North Assessment (NTCI/() and the second of the North Assessment (NTCI/() and the second of the North Assessment (NTCI/() and the North Assessment (NTCI/() an	EST HUMAN	EST HUMAN	EST HUMAN
Single Exon Probes Ex	Acession lo.	38.1 NT	EST HUMAN	¥	Ę	3209 NT			TN L	- NT	F	1.1 N											ķ	Ż	NT			EST HUMAN	EST HUMAN	EST HUMAN
	Most Similar frop Hit BLAST E Netue	3.58 4.0E-81 AB0377	0.98 4.0E-81 AW004608.1	2.26 4.0E-81 AF263306.1	2.28 4.0E-81 AF283308.1		1.11 4.0E-81	0.57 4.0E-81	3.59 4.0E-81 X06989	3.43 4.0E-81 U20197.	3.43 4.0E-81 U20197	6.1 4.0E-81 AB01800	1.53 4.0E-81	0.71 4.0E-81		3.2 4.0E-81	3.2 4.0E-81	3.63 4.0E-81	3.63 4.0E-81	1.63 4.0E-81		4.82 4.0E-81	12.36 3.0E-81 Y18000.	12.36 3.0E-81 Y18000.1	1.23 3.0E-81 AF077188.1	5.83 3.0E-81	5.83 3.0E-81		2.97 2.0E-81 BE784636.1	0.71 2.0E-81 AW611542.1
	ORF SEQ Expression ID NO: Signal	28580	28013	29509	29510	29733	32034	33058	34016	34271	34272		35861	35635	35836			30731	30732	31030	31031	31004	26658	20059	27832	28400	28401	28254	28255	28144
	Probe Exon SEQ ID SEQ ID NO: NO:	3168 15931	3619 16372	4139 16881		4360 17098	7177 19863	7299 19982				_						_	11928 25280		_1		_ 1	1244 13993	2371 15093	2989 15755	2989 15755			3755 16507

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Table 4
Single Exon Probes Expressed in Brain

zr85d06.r1 Soares_NhHMPu_S1 Homo septems cDNA clone IMAGE:082475 5" similar to SW;PRI2_HUMAN Homo saplens caveolin-1/-2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2/4/5/109.11 Scares_pregnant_uterus_NbHPU Homo sepiens cONA clone IMAGE:485825 5' similar to SW:YB36_YEAST P38/28 HYPOTHETICAL 60.5 KD PROTEIN IN RPS/101-RPS/13 INTERGENIC ac14d06.s1 Stratagene HeLa cell s3 937216 Homo septens cDNA clone IMAGE:858427 3' similar to Homo sapiens phorbolin (similar to apolipoprotein B mRNA editing protein) (DJ742C19.2), mRNA Homo sepiens phosphodiesterase 1C, calmodulin-dependent (70kD) (PDE1C), mRNA Homo sepiens phosphodiesterase 1C, calmodulin-dependent (70kD) (PDE1C), mRNA Homo sepiens erm-repeat protein NPRAP/neurojungin (CTNND2) mRNA, pertiel ods Homo sapiens arm-repeat protein NPRAP/neurojungin (CTNND2) mRNA, partial cds 245c04.y1 NCI_CGAP_Bm52 Homo sepiens cDNA clone IMAGE:2291526 5 802137864F1 NIH_MGC_83 Homo septens aDNA done IMAGE:4274535 5 601645051F1 NIH_MGC_56 Homo septens cDNA clone IMAGE:3830228 57 801645051F1 NIH_MGC_58 Homo septens cDNA clone IMAGE:3830228 67 801343180F1 NIH_MGC_53 Homo septens cDNA dane IMAGE:3685483 5' 601867714F1 NIH_MGC_17 Homo seplens cDNA clone IMAGE:4110459 5 601577339F1 NIH_MGC_9 Hamo sepiens aDNA done IMAGE:3838280 5 801577339F1 NIH_MGC_9 Homo septems cDNA clone IMAGE:3838280 5 33f3 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA Homo sepiens polymerase (DNA directed), gamma (POLG), mRNA Homo sepiens polymerase (DNA directed), gamma (POLG), mRNA Top Hit Descriptor EST372729 MAGE resequences, MAGF Homo saptens cDNA EST372729 MAGE resequences, MAGF Homo sapiens cDNA CM3-NN0059-140400-147-812 NN0059 Homo sepiens cDNA PIR:S52437 S52437 CDP-diacylglycerol synthese - fruit fly; MR0-CT0006-250589-019 CT0006 Homo sapiens cDNA MR0-CT0006-250599-019 CT0006 Homo sapiens cDNA Human aconitate hydratase (ACO2) gene, exon 3 Homo sepiens golgin-like protein (GLP), mRNA Homo sapiens HSPC288 mRNA, pertial cds P49643 DNA PRIMASE 58 KD SUBUNIT REGION. ন EST_HUMAN EST_HUMAN EST HUMAN EST HUMAN EST HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN **EST HUMAN** EST_HUMAN HUMAN EST HUMAN HUMAN EST_HUMAN Database Source 불용 EST EST 눛 11432966INT 눋 눋 눋 눋 11420965|NT 눋 11418138 NT ¥ Top Hit Acession 11432966 11432966 8923696 1.0E-81 AW960658.1 AW844986.1 AW990658.1 1.0E-81 AW844986.1 AA255569.1 BE968278.1 1.0E-81 AA040370.1 BE047996.1 1.0E-81 BE958278.1 1.0E-81 BE744545.1 AW897550. 1.0E-81 BF674841.1 AA630784.1 I.0E-81 BE744545.1 1.0E-81 AJ133269.1 8.0E-82 AF161406.1 BE564367. 1.0E-81 BF204253.1 W 26539.1 U87928.1 1.0E-81 U52351.1 U52351.1 1.0E-81 1,0E-81 1.0E-81 1.0E-81 1.0E-81 1.0E-81 1.0E-81 1.0E-81 1.0E-81 1.0E-81 1.0E-81 1,0E-81 1.0E-81 .0E-81 .OE-81 1.0E-81 1.08.4 BLASTE **Jost Simils** 至(金) Value 6.99 4.69 0.69 8.45 5.00 1.07 3.56 3.47 0.87 <u>8</u> 8 2 3.47 0.59 3.27 3.27 1.97 1.97 1.99 Expression Signal 26829 29037 29964 37785 30704 31796 32416 ORF SEO 830 30705 32218 32219 35524 35715 31274 35523 35866 36260 36787 36966 36967 25452 29037 37421 ÖN 14149 16397 17335 17890 18075 18365 SEQ ID 17214 18214 18365 18834 20333 22328 22328 22519 22853 23540 23700 23,700 12839 1922 19221 22651 24622 18076 23051 24108 16397 ÿ <u>(5</u>) SEQ ID 3644 £17 4600 5157 5269 5415 **2268** 5568 6054 10860 6269 6453 6839 7669 9676 6986 <u>8</u>8 10005 1020 1402 6453 9496 1005 505 11240 10405 11029 12132 11507 ġ

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Exan OR; 12839 10 D D D D D D D D D D D D D D D D D D	SEQ Expression (Top) Hit Acession Detablese No. Signal BLASTE No. Source	5452 2.45 8.0E-82 AF161406.1 INT Homo sepiens HSPC288 mRNA, pertial cds	1.1 8.0E-82 U08988.1 NT	2.83 8.0E-82 U08988.1 NT	0.84 8.0E-82 U08988.1 NT	1.42 8.0E-82 ABG37748.1 NT	1.43 8.0E-82 6715801 NT	0.9 8.0E-82 8923432 NT	BF035327.1 EST HUMAN	1.2 7.0E-82 AU144050.1 EST HUMAN	1.71 7.0E-82 AA863747.1 EST HUMAN	0.71 5.0E-82 AA515512.1 EST_HUMAN	49.82 4.0E-82 AF081484.1 NT	0.8 4.0E-82 BF351691.1 EST HUMAN	0.8 4.0E-82 BF351691.1 EST HUMAN	0.65 4.0E-82 M25833.1 NT	11.61 4.0E-82 A1837300.1 EST HUMAN	Т	21.65 3.0E-82 4502188 NT	3.11 3.0E-82 BE005705.1 EST_HUMAN	5.7 3.0E-82 5174702 NT	10.65 3.0E-82 4502186 NT	AA725848.1 EST HUMAN	1.25 3.0E-82 AW875073.1 EST HUMAN	3.44 3.0E-82 AL163285.2 NT	1.91 3.0E-62 BE813232.1 EST_HUMAN	1.63 3.0E-82 466/922/NT	
Even OR SEQ ID NO: 12839 13065 13065 13065 13065 13065 13065 13065 14412 14400 15400 15400 13070			1.1						1.7							0.65	11.61	5.05				10.65	18.58	155	3.44	1.91	8	
				:					80									73					8				36 27459	
	Probe Exer SEQ ID SEQ I NO: NO:	104 128	257 1306	795 1350	867 1363	1474 142	1654 1440	4219 1696	1433 1418				_1				11716 2431	12374 2477	271 1307	687 1346	770 1354	850 1362	1039 1379	1333 1408	1450 1419	1894 1463	2000 1473	

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					Sin	gle Exon Prot	Single Exon Probes Expressed in Brain
Probe SEQ ID NO:	SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E.	Top Hit Acession No.	Top Hit Detabase Source	Top Hit Descriptor
4864	17583	30216	96.0		3.0E-82 AA135979.1	EST HUMAN	2082b04.r1 Stratagene lung carchioma 937218 Homo sapiens cDNA clone IMAGE;565711 5' stinifar to SW:PAGT BOYIN 007537 POLYPEPTIDE N-AGETYI GAI ACTOSAMINY TRANSFERASE:
8052	20746	33878	3.14		11425206 NT	N-	Homo seplens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
8454	21148	34287	0.88		11432889 NT	Z	Homo septens contactin 6 (CNTN6), mRNA
8454		34288	0.88			¥	Homo saplens contactin 6 (CNTN6), mRNA
9724	22375	35575	3.23		3.0E-82 AB029000.1	Z	Homo septens mRNA for KIAA1077 protein, pertial cds
9724	22375	35576	3.23		3.0E-82 AB029000.1	¥	Homo seplens mRNA for KIAA1077 protein, partial cds
583	13363	25990	2.55		6.1	Ę	Homo sepiens mRNA for KIAA0999 protein, pertial cds
583	13363	25991	2.55		2.0E-82 AB023216.1	E	Homo sepiens mRNA for KIAA0999 protein, partial cds
1681	14425	27121	1.21	2.0E-82	2.0E-82 AL046390.1	EST_HUMAN	DKFZp434M117_r1 434 (synonym: htes3) Hamo saplens cDNA clane DKFZb434M117 5
3827	16578	29210	1.25		2.0E-82 D87675.1	Z	Homo sapiens DNA for amyloid precursor protein, complete cds
4208	16949	28575	1.17		4504116	F	Homo sepiens glutamate receptor, ionotropio, kainate 1 (GRIK1) mRNA
4521	17256	29890	1.01	2.0E-82	2.0E-82 AB029019.1	F	Homo expiene mRNA for KIAA1098 protein, pertial cds
4521	17258	29891	1.01	2.0E-82	2.0E-82 AB029019.1	Ę	Homo sapiens mRNA for KIAA 1096 protein, partial cds
4816	17547	30172	285		O DE BOLDERERE 1	5	Homo septients wheart (WBSCR1) and whearts (WBSCR5) genes, complete cds, elternatively spliced and
5021	17742	30352	1.46		4507580	Ž	Homo services times necessis factor recents a perfectly member 5 (TNEDAER) money
5021	17742	30353	1.48			Ę	One sarians hims nature factor recents enseteming member 6 (TAIEDSES MEMA
5384	18184	30874	5.65		2.0E-82 AB018270.1	LZ.	Homo sapients mRNA for KQA0727 protein, partial cds.
6082	18861	31827	4.73	2.0E-82		F	Homo septens FAM4A1 splice varient a (FAM4A1) mRNA, complete cds
7581	25426		0.91	2.0E-82	-	EST_HUMAN	tm21g05.x1 Soeres NFL_T GBC S1 Hamo sepiens cDNA clone IMAGE:2157272 3
7705	20369	33482	0.85		8023130	Ę	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
8204	20898	34035	2.16		11321570 NT	Þ	Homo sepiens sit (Drosophile) homolog 3 (SLIT3), mRNA
8208	21280	34397	0.45		7657340 NT	IN	Homo sepiens microrchidis (mouse) homolog (MORC), mRNA
8268	21280	34398	0.45		7657340 NT	¥	Homo sapiens microrchidia (mouse) homolog (MORC), mRNA
1000	22657	35870	1.84	2.0E-82		N.	Human endogenous retrovirus-K, LTR U6 and gag gene
- 000 000	22657	35871	1.84	2.0E-82	2.0E-82 Y08032.1	Ξ	Human endogenous retrovirus-K, LTR U5 and gag gene
11237	23900	37187	1.27	2.0E-82	11417191 NT	<u> </u>	Homo saplens leucy//cystmy/ eminopeptidese (LNPEP), mRNA
11237	23900	37188	127	2.0E-82	11417191 NT	¥	Homo sapiens ieucy//cystinyl eminopeptidase (LNPEP), mRNA
11279	23940	37233	4.45	2.0E-82	2.0E-82 U80736.1	NT	Homo sepiens CAGF9 mRNA, pertiel cds
11279	2882	37234	4.45	2.0E-82		N	Homo sapiens CAGF9 mRNA, pertiel cds
11750	2834	37670	1.91	2.0E-82	2.0E-82 5031660 NT		Homo sepiens EGF-like repeats and discoldin I-like domains 3 (EDIL3), mRNA
11957	24508		1.88	2.0E-82		THUMAN	2531d10.s1 Soeres_perathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:305203 3'

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Onligie Exter Expressed III District	Most Similar (Top) Hit Accession (Top) Hit Accession (Top) Hit Accession (Top) Hit Accession Signal BLASTE No. Source Source	44 3.47 2.0E-82 AA011278.1 EST_HUMAN Z01g09.r1 Soares_fold liver_spicen_1NRLS_S1 Homo sepiens cDNA clone IMAGE:429588 5	1.95 2.0E-82 11418097 NT	25985 1.14 1.0E-82 11545921 NT	0.77 1.0E-82 BE885106.1 EST_HUMAN	28679 3.1 1.0E-82 BE064386.1 EST_HUMAN	28880 1.26 1.0E-82 AB011110.2	34678 1.13 1.0E-82 AB037838.1 NT	35390 0.59 1.0E-82 AB014562.1 NT	1.17	36576 2.34 1.0E-82 AL163209.2 NT	34449 4.51	36039 0.53 0.0E-83 BE253347.1 EST_HUMAN	28816 3.33 8.0E-83 BE383973.1 EST_HUMAN	27115 5.63 8.0E-83 N68951.1 EST_HUMAN	28759 0.97 7.0E-83 AW385529.1 EST_HUMAN	- NOTE SEC. 10 10 10 10 10 10 10 1		6.68 7.0E-83 BF221813.1 EST_HUMAN	31702 0.58 7.0E-83 11428657 NT	37834 1.4 7.0E-83		79 25828 1.98 6.0E-83 M33320.1 INT Human platelet Glycoprotein IIb (GPIIb) gene, exons 2-29	hr31h03.xt Sogres_NFL_T_GBC_S1 Home sepiens cDNA clone IMAGE:2833525.3' similar to 27224 1.6 6.0E-83 AW673088.1 EST HUMAN SW:YBEB HAEIN P44471 HYPOTHETICAL PROTEIN HI0034.:	28432 0.71 6.0E-83 AW818405.1 EST HUMAN	1.08 6.0E-83 AF231919.1 NT	30641 2.02 6.0E-83 4507866 NT	31674 1.52 6.0E-83 AJ010770.1 INT	33160 2.27 6.0E-83 11422024 NT	35413 2.85 6.0E-83 4505314 NT	35517 2.34 6.0E-83 11430647 NT	35518 2.34
				26985		20679	26880	34678	35390		36576	34449	36039	28816	27115	26759				31702	37834	37835	25826	27224	28432		30641	31674	33160	35413	35517	35518
	B Exon D SEQ ID NO:	35 24844	75 25029	78 13358	36 13938	3 14012	14013					5 21307	74 22822	14139	6 15623	14084	15835	1	17497	18742		7 24311	13179	9 14520		15812	18019	3 18716	1 20079			0 22321
	Probe SEQ ID NO:	12485	12775	678	1186	1263	1284	8841	9553	10145	10646	8615	10174	1392	1676	1335	2888		4765	2960	11717	11717	394	1779	3017	3048	5211	5933	7401	8575	8	0996

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	Top Hit Descriptor	ab14e10.s1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:840810 3' similar to contains THR.t2 THR repetitive element;	Homo septiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cits	Human succinate dehydrogenase (ron-protein subunit (sdhB) gene, exon 5	Homo sepiens 26S proteasome regulatory subunit (SUG2) mRNA, complete cds	Novel human gene mapping to chamosame X	Homo sepiens decrynibanuclesse I (DNASE1), mRNA	Homo sapiens catalase (CAT) mRNA	Homo sapiens catalase (CAT) mRNA	Homo seplens EGF-the repeats and discoldin Hike domains 3 (EDII 3), mRNA	Homo sepiens EGF-like repeats and discoldin Filke domains 3 (EDIL3), mRNA	Homo sapiens mannosidase, beta A, Iysosomal (MANBA) gene, and ublquitin-conjugating enzyme E2D 3 (UBE2D3) ceres, complete eda.	EST79542 Placenta I Homo sapiens cDNA similar to similar to endocencus natrovinus ERV9	np87c07.st NCI_CGAP_Thy1 Homo sepiens cDNA clone IMAGE:1133292 similar to contains THR.t2 THR recettive element:	973908x1 Soares teads NHT Homo septens CDNA clone IMAGE:17556823	o064g05.81 Soeres_testis_NHT Homo sepiens CDNA clone IMAGE:1621692.31 strillar to TR:092814 Q92614 MYELOBLAST KIAA0216.;	ot64g05.s1 Soeres_bastis_NHT Homo sepiens cDNA clone IMAGE:1621592.3' similar to TR:Q92614 Q92614 MYELOBLAST KIAA0216.	2948(12.s1 Soares fetal Iver spiesn 1NFLS Homo seciens cDNA clone IMAGE: 205823.3	RC8-ET0046-280600-013-H12 ET0046 Homo serviens cDNA	Homo sepiens sel (Drosophile-like 1 (SALL1), mRNA	Homo sapiens chromosome 21 segment HS21C002	Homo sapiens hematopoletic progenitor cell antigen CD34 precursor (CD34) mRNA, partiel cds	Homo eaplens enlyrin repeat-containing protein ASB-2 (LOC51678), mRNA	Homo sepiens ankyrin repeat-containing protein ASB-2 (LOC51678), mRNA	Human carcinoembryonic antigen gene family member 18 (CGM18) gene, excus A1 and B1	Homo sapiens membrane protein CH1 (CH1), mRNA	601507482F1 NIH_MGC_71 Homo sepiens cDNA clone IMAGE:3809068 5	Homo saplens F-box protein FbI3b (FBL3B) mRNA, partial cds	Homo sapiens F-box protein Fbt3b (FBL3B) mRNA, partial cds
	Top Hit Detabase Source	EST_HUMAN	Ę	N-	TN	Z	Ę	Þ	5	Ę	5	5	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	 	NT	NT	T.	11	LN	F	EST_HUMAN	NT	NT
	Top Hit Acession No.	6.0E-83 AA486105.1	6.0E-83 AF240786.1	-		5.0E-83 AL133207.2	4885190 NT	4557013 NT	4557013 NT	5031680 NT	5031690 NT	4.0E-83 AF224860.1	1.1	3.0E-83 AA632654.1	2	2.0E-83 AA993492.1	2.0E-83 AA983492.1		1.4	11430834 NT	4L163202.2	2.1	7706398 NT	7706398 NT		11428081 NT	1.1	3.1	3.1
	Most Similar (Top) Hit BLAST E Value	6.0E-83	6.0E-83	5.0E-83 U17883.	5.0E-83	5.0E-83	5.0E-83	5.0E-83	5.0E-83	€.0E-83	5.0E-83	4.05-83	3.0E-83 AA36831	3.05-83	3.0E-83 AI217223	2.0E-83	2.0E-83	2.0E-83 N 98 951.1	2.0E-83	2.0E-83	2.0E-83 AL16320;	2.0E-83 AF202871	2.0E-83	2.0E-83	2.0E-83 U06679.1	2.0E-83	2.0E-83 BE88540	2.0E-83 AF12953	2.0E-83 AF12953
	Expression Signal	2.53	4.27	2.03	1.55	1.18	0.77	11.53	11.53	1.07	1.07	1.72	4.9	1.33	0.62	1.86	1.86	4.07	1.1	1.80	0.7	4.11	6.14	6.14	6.0	0.85	1.31	1.12	6.36
	ORF SEQ ID NO:						29275	30350	30351	30428	30429	26039				27240	27241	27365	28288			29868	20068	20069	30620	31468	31603	32423	33005
	SEQ ID NO:	24117	24472	13692		- 1				17812	17812	13404	13742	15485	19250	.14532	14632	14655	15624	16025	16508	1704	17330	1733	17897	18547	18662	19408	20017
	Probe SEQ ID NO:	11517	11908	925	2043	3629	3886	2050	2020	5093	5083	\$25	225	2780	6483	1782	1792	1918	2856	3263	3756	4302	4804	\$	5189	5755	6876	8	7335

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	601822080F1 NIH_MGC_75 Hamo septions cDNA clone IMAGE:4042318 5	Homo sapiens mRNA for brain ryanodine receptor, complete cots	Homo sapiens mRNA for brain ryanodine receptor, complete cds	Rattus norvegicus densin-180 mRNA, complete cds	Homo sepiens protein kinase CX2 catalytic subunit alpha gene, excn 1	Homo sepiens protein kinese CK2 catalytic subunit alpha gene, exon 1	Homo septens phosphorylese idnase, gamma 1 (muscle) (PHKG1) mRNA	Homo saplens phosphorylase litnese, gamma 1 (muscle) (PHKG1) mRNA	Human neural cell adheelon malecule (N-CAM) secreted teoform mRNA, 3' and	Human neural cell adhesion molecule (N-CAM) secreted isoform mRNA, 3' and	AU117659 HEMBA1 Homo septens cDNA clone HEMBA1001910 5'	UI-HF-BNO-emd-h-07-0-UI.r1 NIH_MGC_50 Hamo sepiens aDNA dane IMAGE:3081862 6	Homo sepiens KIAA0995 protein (KIAA0985), mRNA	DKFZp647J135_71 547 (synonym: hfbr1) Homo saplens oDNA clone DKFZp647J135 5'	DKFZp547J135_r1 547 (synanym: htfbr1) Hamo sapiens cDNA clone DKFZp547J135 51	Homo explems gene for AF-8, complete ods	Homo sepiens hydrocyscyl-Coenzyme A dehydrogenese/3-ketoecyl-Coenzyme A thickse/encyl-Coenzyme A	hydratase (tritinodional protein), beta subunit (HADHB) mRNA	Homo sepiens hydroxyacyl-Coenzyme A dehydrogenase/3-keboscyl-Coenzyme A thickse/encyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA	Homo sepiens (popolysechande-binding protein (LBP) mRNA, complete cds	Homo sapiens lipopolyseccheride-binding protein (LBP) mRNA, complete ods	Homo sepiens cell recognition molecule Cespr2 (KIAA0868), mRNA	Rattus norvegious brain specific cortactin-binding protein CBP90 mRNA, pertiel cds	H.saplens gene for mitochondrial dodecencyl-CoA delta-isomerase, expn 3	Homo saplens amyold beta (A4) precursor protein (protesse nextr-4, Alzheimer disease) (APP). mRNA	0000008xt Scenes testis_NHT Homo sepiens CDNA clone IMAGE:1646431 3' similer to gb:M84241 QM	PROTEIN (MUMAN);	601678023F1 NIH_MGC_21 Hamp septems aDNA dane IMAGE:3858853 5	RC2-FN0119-200800-011-g05 FN0119 Homo sapiens cDNA	RC2-FN0119-200600-011-g05 FN0119 Homo sepiens dDNA	ae68a03.s1 Stratagene actizo brain S11 Homo sapiens cDNA clone IMAGE:971020 31	DKFZp434H0322_r1 434 (synonym: hises) Homo septens cDNA clone DKFZp434H0322 5	
gie Exon Pro	Top Hit Detabase Source	EST HUMAN	E	Z	Z	Ę	닐	N	Ł	۲	N	EST_HUMAN	EST_HUMAN	Ę	EST_HUMAN	EST HUMAN	Σ		¥	둗	5	Ę	NĪ	IN	NT	Ę		EST HOMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	
uio	Top Hit Acession No.	2.0E-83 BF105097.1	AB001025.1	AB001025.1	J66707.1	2.0E-83 AF011920.1	2.0E-83 AF011920.1	5453881 NT	5453881 NT	W22094.1	V22094.1	2.0E-83 AU117559.1	4W505600.1	11436448 NT			2.0E-83 AB011399.1		4504328 NT	4504326 NT	AF105067.1	1.0E-83 AF105067.1	. 7862349 NT	1.0E-83 AF053768.1	25822.1	4502166 NT		1.0E-83 AR02/614.1	7.0E-84 BE901209.1	6.0E-84 BE838864.1	6.0E-84 BE838864.1	A776574.1	1.042863.2	
	Most Stratler (Top) Hit BLAST E. Value	2.05-83	2.0E-83 AB00102	2.0E-83 AB00102	2.0E-83 U66707.	2.05-83	2.0E-83	2.05-83	2.0E-83	2.0E-83 M22094.	2.0E-83 M22094.	2.0E-83	2.0E-83 AW5058	2.0E-83	2.0E-83	2.0E-83	2.0E-83 /		1.05-83	1.05-83	1.0E-83/	1.0E-83 /	1.0E-83	1.0E-83	1.0E-83 Z25822.1	1.0E-83	10,	1.05-83	7.0E-84	6.0E-84	6.0E-84	6.0E-84 AA77657	6.0E-84	·
	Expression Signal	0.64	0.78	0.78	1.79	2.05	2.05	0.48	0.48	4.01	4.01	1.39	0.77	6.64	2.19	2.19	3.85	3	2.18	2.18	96.0	96'0	1.18	3.83	1.99	3.36	,	8 ;	3.8	3.5	3.5	8.28	3.33	
•	ORF SEQ ID NO:	33480			33710	34042	34043	35328	35329	35780	35781	35881	35952	36682	36770	36771		-	20813	26814	26873	26874	28593	29237	29588	30184	21.00 0	5/57/5	28167	26687	26688	27854		
	Exen SEQ ID NO:	20367	20438	20438	20581	20907	20802	22147	22147	22582	22582	22664	22737	23438	23527	23527	24869	7777	213	14137	14189	14180	15942	10000	16961	17562	5	2	876	14021	14021	15117	17892	
	Probe SEQ ID NO:	†0 //	7742	7742	9882	8213	8213	9404	9494	9934	9834	10016	10089	10753	10845	10845	12522		200	1390	1442	1442	3179	3850	4220	4831	PEDP	2	2//2	1272	1272	2398	5160	

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origie Exori Probes Expressed in Brain	Top Hit Descriptor	a47g03.s1 Sogres_NRT_GBC_S1 Hamo sepiens cDNA done IMAGE:1460500 3' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);	Homo sapiens acetyl LDL receptor; SREC=scavenger receptor expressed by endothelial cells (SREC), mRNA	Homo saplens acetyl LDL receptor; SREC=scavenger receptor expressed by endothelial cells (SREC), mRNA	PM0-LT0019-190900-004-F02 LT0019 Homo sepiens cDNA	Homo sapiens pre-mRNA splicing factor (PRP16) mRNA, complete ods	PM4-FT0054-180800-004-e10 FT0054 Homo sepiens cDNA	EST98094 Teetis I Homo sapiens aDNA 5' end	Homo sapiens chromosome 3 subblomeric region	2499e07.r1 Strategene HNT neuron (#637233) Homo saplens cDNA clone IMAGE:632100 5' similar to TR:0483915 G483915 RETROTRANSPOSABLE L1 ELEMENT LRE2 FROM CHROMOSOME 10	Homo saplens regulatory factor X, 3 (influences HLA class II expression) (RFX3), mRNA	Homo sapiens mRNA for KIAA1131 protein, partial cds	Homo saplens mRNA for KIAA1131 protein, pertial ods	Homo sapiens tropomodulin 2 (neuronal) (TMOD2), mRNA	wa78c04.x1 Soares, NPL_T_GBC_S1 Homo saplens cDNA clone IMAGE:2302086 3' similar to SW:NRDC_HUMAN 043847 NARDILYSIN PRECURSOR:	Homo sepiens mycein light chain kinase Isoform 2 (MLCK) mRNA, complete cds	Homo sapiens problem tyrosine phosphatase, receptor type, G (PTPRG), mRNA	Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA	Homo sapiens histone descetylase 3 (HDAC3) gene, complete cds	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA	Homo sapiens disce, large (Drosophile) homolog 2 (chapsyn-110) (DLG2) mRNA	Hamo sepiens discs, large (Droscphila) hamalog 2 (chapsyn-110) (DLG2) mRNA	Homo saplens mRNA for KIAA1130 protein, partial cds	Homo sepiens Bacht protein homolog mRNA, partial cds	Homo saplens pericentrioler meterial 1 (PCM1) mRNA	Novel human mRNA containing Zinc finger C2H2 type domains	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes,	complete cds)	Homo septens X-finked juveralle retinoschists precursor protein (XLRS1) mRNA, complete cds	
פופ באסוו היוסד	Top Hit Database Source	EST_HUMAN	Ę	Į.	EST HUMAN	Þ	EST_HUMAN	EST_HUMAN	TN	EST HUMAN	LN L	F	۲	TN	EST HUMAN	LN LN	Z.	MT	IN	NT	NT	NT	NT	L	Į.N	NT			NT	
בוה 	Top Hit Acession No.	AA897339.1	11426718 NT	11426718INT	6.0E-84 BE810371.1	6.0E-84 AF038391.1	BE770199.1	AA382811.1	5.0E-84 AF109718.1	5.0E-84 AA167678.1	11428740 NT	5.0E-84 AB032957.1	AB032957.1	5.0E-84 11433550 NT	4.0E-84 AI685321.1	4.0E-84 AF069601.2	11386168 NT	11386168 NT	50.1	11421328 NT	4557528 NT	4557526 NT	58.1	20.1	5453855 NT	90.1		3.0E-84 AB026898.1	7	
	Most Similar (Top) Hit BLASTE Value	6.0E-84 AA8973	6.0E-84	6.DE-84	6.0E-84	6.0E-84	6.0E-84 BE7701	5.0E-84	5.0E-84	5.0E-84	5.0E-84	5.0E-84	5.0E-84	5.0E-84	4.0E-84	4.0E-84	4.0E-84	4.0E-84	4.0E-84 AF0596	4.0E-84	4.0E-84	4.0E-84	4.0E-84	3.0E-84 AF0282	3.0E-84	3.0E-84 AL0968	-	3.0E-84/	3.0E-84	
	Expression Signal	1.87	1.04	10,0	2.94	28'0	2.37	0.71	1.82	0.59	3.17	1.77	1.77	1.44	2.19	1.79	1.36	1.36	1.88	14.38	121	121	4.51	1.24	1.15	2.41	!	1.07	5.2	
	ORF SEQ ID NO:	30943	31282	31283	33134	33367	33789	26121		31758	37438	37570	37571-	37738	26812	30242	31168	31169	31925	33319	34647	34648	36759	26752	27401	27460		28977	28121	
	Exen SEQ ID NO:	18230	18371	18371	20053	20259	20687	13472	15779	18796	24133	24240	24240	24401	14138	17624	18274	18274	18952	20217	21501	21501	23517	13112	14688	14736		6833	- - - - - - - - - - - - - - - - - - -	
	Probe SEQ ID NO:	5431	5574	5574	7373	7591	7872	269	3013	9015	11533	11652	11652	11813	1389	4897	9442	9476	6175	7547	8808	888	10835	808	1953	2001		3578	3731	

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Top Hit Detactions of the Control of
Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Top Hit Descriptor Toras-Labosou, 272-b08 BT0755 Homo seplens cDNA chore IMAGE:2520565 3° similates cost RIBOSOUMAL PROTEIN L18A (HUMAN); To726-190600-272-b08 BT0755 Homo seplens cDNA Begiens profession and the seplens cDNA chore IMAGE:3084663 3° H-ect e-02-0-UL s1 NG_CGAP_Sub8 Homo seplens cDNA clone IMAGE:3084663 3° H-ect e-02-0-UL s1 NG_CGAP_Sub8 Homo seplens cDNA clone IMAGE:3084663 3° H-ect e-02-0-UL s1 NG_CGAP_Sub8 Homo seplens cDNA clone IMAGE:3084663 3° H-ect e-02-0-UL s1 NG_CGAP_Sub8 Homo seplens cDNA clone IMAGE:3084663 3° H-ect e-02-0-UL s1 NG_CGAP_Sub8 Homo seplens cDNA clone IMAGE:308243 3° Dax IN CT_CGAP_Lub Homo seplens cDNA clone IMAGE:1865728 3° Seplens that the seplent the seplens cDNA clone IMAGE:4080251 3° similar to 200 HEMBEI Homo seplens cDNA clone IMAGE:4080251 3° similar to 201 HEMBEI Homo seplens cDNA clone IMAGE:4080251 3° similar to 201 HEMBEI Homo seplens cDNA clone IMAGE:4080251 3° similar to 201 HEMBEI Homo seplens cDNA clone IMAGE:4080251 3° similar to 201 HEMBEI Homo seplens cDNA clone IMAGE:4080251 3° similar to 201 Seplens Intersectin short territorin (TSN) mRNA, complete cds seplens cDNA clone IMAGE:4080251 3° similar to 202 to 1080 209 UCSS DL7560223 1° Zoxx I Lupeki sympathefo_trunk Homo seplens cDNA clone IMAGE:4080251 3° similar to 203 cold CSS DL7660223 1° similar to 203 cold CSS DL766023 1° similar to 203 cold CSS DL766023 1° similar to 203 cold CSS DL766023 1° similar to 203 cold CSS DL766023 1° similar to 203 cold CSS DL766023 1° similar to 203 cold CSS DL766023 1° similar to 203 cold CSS DL766023 1° similar to 203 cold CSS DL766023 1° similar to 203 cold CSS DL766023 1° similar to 203 cold CSS DL766023 1° similar to 203 cold CSS DL766023 1° similar to 203 cold CSS DL766023 1° similar to 203 cold CSS DL766023 1° similar to 203 cold CSS DL766023 1° similar to 203 cold CSS DL766023 1° similar to 203 cold CSS DL766023 1° similar to 203 cold CSS DL766023 1° similar to 203 cold CSS D
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ORF SEQ ID NO: 27563 27563 28378 309623 309623 309623 32310 31101 25748 26685 27768 20017 30018 30018 30018 30018
Evan NO: NO: 14823 14823 14823 15728 2085 15728 24843 13108 17120 17120 17120 17120 17130 17120 17130 17120 17130
Probe SEQ ID NO: NO: 2088 2088 2088 2088 2284 2284 2284 6439 6543 6543 6543 6543 6543 7056 7056 7056 7056 7056 7056 7056 7056

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Page 10 Che SE2 Egerwein Chep H August Chep H Augus Chep H August				_	_		_		_	- -	_	,	_			_ _	-	 -		_		,	_	_				.,	-1,00		,
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Expn NO: CRF SEQ ID NO: Expression Signal Signal (Top) Hit ID NO: Top Hit Signal ID NO: Top Hit ID NO: Top Hit Signal ID NO: Top Hit ID NO: Top Hit Signal ID NO: Top Hit ID NO: Top Hit ID NO: Top Hit Signal ID NO: Top Hit ID NO: Top H	Top Hit Descriptor	uterine water channel≕28 kda erythrocyte Integral membrane protein homotog [human, uterus, mRNA, 1 nt]	Novel human gene mapping to chomosome 13	Novel human gene mapping to chomosome 13	Novel human gene mapping to chomosome 13	Homo sepiens polymenese (DNA directed), alpha (POLA), mRNA	Homo sepiens NGFI-A binding protein 1 (ERG1 binding protein 1) (NAB1), mRNA	Homo sepiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA	Homo saplens Ce2+-binding protein CABP3 (CABP3) gene, exon 6 and partial cds	Homo expiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA	Homo septens ubiquitin specific protesse 13 (isopeptidase T-3) (USP13) mRNA	Homo saplens glutemete receptor, tonotrophic, AMPA 4 (GRIA4), mRNA	Homo sepiens purinegic receptor P2X-like 1, orphen receptor (P2RXL1), mRNA	Homo septens aconitase 2, mitochardriai (ACO2), mRNA	Homo septens chromosome 21 segment HS21C009	Hamo sapiens nuclear protein Skip mRNA, complete ods	Hamo sepiens nuclear proben Skip mRNA, camplete cds	Homo saplens leupadn (LDPL), mRNA	Human plasminogen gene, econ 7	Human plasminogan gane, exxn 7	Homo sepiens DKFZp434P211 protein (DKFZP434P211), mRNA	Homo sapiens chromosome 21 segment HS21C080	Homo seplens heet shock transcription factor 2 binding protein (HSF2BP), mRNA	Homo sepiens chromosome 21 segment HS210068	Homo sapiens ribosomal protein L27 mRNA, complete cds	Homo sapiens MSTP030 mRNA, complete cds	Homo sepiens DEAD/H (Asp-Glu-Ale-Asp/His) box polypectide 10 (RNA helicase) (DDX10) mRNA	Homo sections DEAD/H (Asn-Cit-Ale-AsnHis) bus protocomide at (PNA business) (PNA business)	262001.r1 Source Instits INHT Homo sapiens cDNA clone IMAGE:726890 5' similar to TR:G1335799 G4335799 GAC-POX POX VPROTEIN .	Homo sapiens diromosome 21 segment HS210084	
SEQ ID NO: ORF SEQ Signal Signal Most Smiler IASTE Most Smiler Signal Value Top Hit Acession PASTE Most Smiler PASTE Top Hit Acession No. 18675 31844 1.41 1.0E-84 S73482.1 19625 32552 1.66 1.0E-84 ALO49784.1 19626 32753 2.32 1.0E-84 ALO49784.1 19626 32753 2.32 1.0E-84 ALO49784.1 2013 33283 1.0E 1.0E-84 ALO49784.1 2014 33130 1.22 1.0E-84 ALO49784.1 2232 3518 3.05 1.0E-84 ALO49784.1 2232 35519 0.53 1.0E-84 ALO49784.1 27313 3.05 1.0E-84 ALO49784.1 2732 35519 0.53 1.0E-84 AF07841.1 17900 30589 3.05 1.0E-84 AF07841.1 17900 30589 3.05 1.0E-84 AF07841.1 17800 30589 3.05 1.0E-84 AF07841.1 13310 28499 3.05 1.0E-84 AF0782421.1 14319 27706	Top Hit Detaberse · Source	Į.	L	LN	LN LN	F	Z	TN	L	TN.	N.	LN	Z	Z	Z	¥	Z	K	Ā	Ę	ŊŢ	TN	NT	Z	Ę	NT	F	5	EST HUMAN		
Expn NO: ORF SEQ ID NO: Expression Signal Mos ID NO: 18875 31844 1.41 19625 32552 1.66 19626 32753 2.32 19626 32753 2.42 20137 33229 2.42 20147 33229 2.42 22142 35519 0.53 17900 30588 3.05 17900 30588 3.05 17900 30588 3.05 17900 30588 3.05 17900 30588 3.05 17712 3.05 14319 27004 1.23 14416 2704 1.23 14319 27004 1.23 14319 27006 1.25 14319 27006 1.45 24239 37301 3.35 24239 37301 3.35 23898 37301 1.49 23898 37792 1.49	Top Hit Acession No.	S73482.1				3994	11430846			4507848	4507848	11437356	11417812	11418185		1	1	4758669	1	1	7657020	0.2	5901979	8.2		0.1	11438573	11438573			
Evan ORF SEQ Express SEQ ID NO: Sign NO: S1875 31844 19626 32753 32563 19626 22413 22322 35519 17000 30588 17700 30588 17712 24638 31730 24638 14319 27004 14108 20591 17566 30177 17566 30177 17565 30208 13871 26530 24239 23598 37301 23898 37301 25958 15056 27792	Most Similar (Top) Hit BLAST E Value	1.0E-84	1.0E-84	1.0E-84	1.0E-84	1.0E-84	1.0E-84	1.0E-84	1.0E-84	1.0E-84	1.0E-84	1.0E-84	1.0E-84	1.05-84	9.0E-85	9.0E-85	9.0E-85	9.0E-85	9.0E-85	9.0E-85	9.0E-85	9.0E-85	9.0E-85	9.0E-85/	7.0E-85	7.0E-85 /	6.0E-85	6.0E-85	6.0E-85	5.0E-85	
Exan SEQ 1D DRI 19875 19825 19825 19825 19825 19825 19826 22438 13712 24319 14415 19898 23	Expression Signal	1.41	1.68	1.66	2.32	1.26	2.42	3.05	0.53	3.05	3.05	1.08	234	3.2	1.06	2.39	2.39	0.95	1.23	1.23	3.6	98.0	98.0	1.12	1.45	4.32	3.35	3.35	62,1	1.49	
-8	ORF SEQ ID NO:		32552	32653	32758	33130	33229		35519	30588	30589	36368		31098		26469	28470	26783	27004	27005	27108	29591	30177	30208	26530		37300	37301	37690	277782	
	SEQ ID	18875	19525	19525	19699	20049	20137	2213	22322	17900	17900	23142	24566	24638	13712	13810	13810	14108	14319	14319	14415	1898	17565	17585	13871	24239	23998	86682	24357	15056	
Probe SEQ ID NO: NO: 7369 77601 7369 7501 9480 10486 12161 1960 1572 1672 1672 1672 1672 1172 1172 1173 11382 11382	8	8	138	3	8	8	돐	435	S	8	8	8	इ	151	8	051	9	影	572	272	670	22	2	ङ्क	<u> </u>	3	392	392	98	332	

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Top Hit Detabase Source Top Hit Detabase Top Hit Descriptor	Homo septens KIAA0783 gene product (KIAA0783), mRNA Homo septens KIAA0783 gene product (KIAA0783), mRNA Homo septens KIAA0783 gene product (KIAA0783), mRNA Homo septens GTPese regulator associated with the focal adhesion kinsse pp125(FAK); KIAA0821 protein (KIAA0821), mRNA Homo septens GEN mRNA, complete cds Homo septens DENN mRNA, complete cds Homo septens mail nuclear ribonucleoprotein polypeptide B" (SNRPB2), mRNA Homo septens anall nuclear ribonucleoprotein polypeptide B" (SNRPB2), mRNA Homo septens anall nuclear ribonucleoprotein polypeptide B" (SNRPB2), mRNA Homo septens anall nuclear ribonucleoprotein polypeptide B" (SNRPB2), mRNA Homo septens anall nuclear ribonucleoprotein polypeptide B" (SNRPB2), mRNA Homo septens anall nuclear ribonucleoprotein polypeptide B" (SNRPB2), mRNA Homo septens RNA for KIAA1107 protein, partial cds Homo septens Ran GTPase activeting protein 1 (RANGAP1), mRNA Homo septens Ran GTPase activeting protein 1 (RANGAP1), mRNA
Top Hit Detabase Source Source NT EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN NT NT NT NT NT NT NT NT NT NT NT NT NT	NAN EST HUMAN
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Most Similar Top Hit BLAST E Value (Top) Hit BLAST E Value 5.0E-85 AF21111 5.0E-85 BF0356 5.0E-85 BF0356 5.0E-85 BF0779 4.0E-85 BF0779 4.0E-85 BF0779 3.0E-85 BE0773 3.0E-85 BE0773 3.0E-85 BE0773 3.0E-85 BE0773 3.0E-85 BE0773 3.0E-85 BE0773 3.0E-85 BE0773 3.0E-85 BE0773 3.0E-85 BE0773 3.0E-85 BE0773 3.0E-85 3.	3.0E-85 3.0E-8
Expression Signal Signal Signal 1.4.5 1.1.	0.91 0.94 0.96 0.096 0.096 0.096 0.096 0.096 1.88
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Table 4
Single Exon Probes Expressed In Brain

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No Expressed in Digili	Top Hit Descriptor	Homo septens intersectin 2 (SH3D1B) mRNA, complete cds	Homo sepiens CGI-201 proben (LOC51340), mRNA	Homo septens apolipoprotein C-II (APOC2) mRNA	Homo sapiene apolipoprotein C-II (APOC2) mRNA	Human DNA polymense beta gene, exons 12 and 13	Homo septens similar to rat Integral membrane glycoprotein POM121 (POM121L1), mRNA	Human Ku (p70/p80) eutounit mRNA, complete cds	Homo sapiens plesminogen (PLG) mRNA	Homo sapiens reelin (RELN) mRNA	Homo sepiens chromosome 21 segment HS21C084	W67h08.X1 NCI_CGAP_Kid12 Homo septens cDNA clone IMAGE:2398431 3' similar to contains element MSR1 madelles alement	WARDING AT CAME NET TODE OF Home contains Alone \$140EF-2284484.2"	WINDACTOR INC. CGAP UP Homo seniors cDNA done IMAGE-244867.3	601501416F1 Niff MGC 7 Home seniors CDNA close IMAGE-3048818 K	801482817F1 NIH MGC 67 Hamo sapiens cDNA clone IMAGE:3888021 5	801482817F1 NIH_MGC_67 Hamo septens oDNA clane IMAGE:3888021 5	801109738F1 NIH_MGC_16 Hano sapiens cDNA clane IMAGE:3350563 5	245f03.s1 Soares_fetal liver_splean_1NFLS_S1 Homo supiens cDNA clone IMAGE:453245.31	246f03.s1 Source_fetal_liver_spleen_1NFLS_S1 Homo supiens cDNA olone IMAGE:453245 31	601897003F1 NIH_MGC_19 Hamo sepiens cDNA clane IMAGE:4128440 5	601897003F1 NIH_MGC_19 Homo sepiens cDNA clone IMAGE:4128440 5	Human mRNA for T-cell cyclophilin	qt58a07.x1 NCI_CGAP_Bm25 Homo saplens cDNA clone IMAGE:1860468 3'	Homo seplens calcineum binding protein 1 (KIAA0330), mRNA	Homo explens celoineurin binding protein 1 (KIAA0330), mRNA	001120778F1 NIH_MGC_20 Hamo septens cDNA clane IMAGE:2987090 5	Homo septens cytochrome P450, subfamily IIF, polypeptide 1 (CYP2F1) mRNA	aj88f08.s1 Source_perathyroid_tumor_NbHPA Homo sapiens aDNA clane IMAGE:1403559 3*	aj88/08.s1 Soares_paraffnyrold_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1403559.31	Homo sapiene tumor endothetal marker 7 precurecr (TEM7), mRNA	Homo saplene tumor endothetel marker 7 precurecr (TEM7), mRNA	Homo septens Text (human T-cell feukernia virus type I) binding protein 1 (TAX1BP1), mRNA	Homo sapiens galactocerebrosidase (GALC) gene, exon 15	
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5	Top Hit Acession No.	AF248540.1	TN82051	5174775 NT	5174775 NT	J10525.1	7657468 NT	VI30938.1	4505880 NT	4826977 NT	NL163284.2	2 OF BA 1780820 4	2 0E-BS AID44450 4	2.0E-85 AIRBA384 1	F 70420A 1	3E618302.1	3E618392.1	3E257917.1	1.0E-85 AA778785.1	\A778786.1	1.0E-85 BF311662.1	3F311552.1	700052.1	1.0E-85 A1198420.1	11417862 NT	11417862 NT		4503224 NT	A860801.1	A860801.1	IN 9889966	TN 988886 NT	11421737 NT	(
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	Expression Signal	2.34	76.0	8.28	8.28	1.53	5.28	1.18	4.51	1.22	76.0	8, 6	2 2	132	286	8.42	8.42	4.38	277	2.77	1.73	1.73	1.28	2.41	4.4	4.74	11.19	1.57	2.34	2.34	1.02	1.02	6.65	3.06	
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	Probe SEO ID NO:	1017	1383	1399	1300	2228	2826	3022	4300	4527	4854	9173	0540	10162	2285	2302	2392	18881	10842	10842	10919	10010	10997	11773	12050	12295	1409	11698	916	916	ൺ	କୀଊ	9880	8843	

Page 391 of 536 Table 4

0667 Homo sapiens similar to ectoruclectide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), yz19e08.r1 Soeres_multiple_scierosis_2NbHMSP Homo sepiens cDNA clone IMAGE:283478 5* Homo sepiens neuredin III (NRXN3) mRNA Homo sepiens lysophosphatidic acid scyltransferese detta (LPAAT-detta) mRNA, complete cds Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete ods Homo sepiens similar to transcription factor CA160 (H. sepiens) (LOC83170), mRNA Homo sepiens similar to transcription factor CA150 (H. sepiens) (LOC63170), mRNA Homo septens cAMP-specific phosphodiesterase 8A (PDESA) mRNA, partial cds x292h12x1 NCI_CGAP_Lu24 Homo sepiens cDNA done IMAGE:2871719 3' 601509696F1 NIH_MGC_71 Homo sepiens cDNA clone IMAGE:3911303 5' 801508696F1 NIH_MGC_71 Homo sepiens cDNA clone IMAGE:3911303 5' bu18b02x1 NCL_CGAP_Pr28 Homo sepiens cDNA clone IMAGE:2251371 3' hd87g08 x1 NCI_CGAP_GC8 Homo sepiens cDNA dane IMAGE:2916542 3' 601176865F1 NIH_MGC_17 Homo sepiens cDNA clone IMAGE:3531953 5* 601072564F1 NIH_MGC_12 Homo sepiens cDNA clone IMAGE:3458830 6* 601072594F1 NIH_MGC_12 Homo septems cDNA clone IMAGE:3458830 5 Homo sapiens DiGeorge syndrome critical region gene 6 (DGCR6), mRNA Homo sepiens accelutarate dehydrogenese (lipoemide) (OGDH) mRNA Homo sepiens 24 kDa Intrinsic membrane protein (PMP24), mRNA Top Hit Descriptor EST378215 MAGE resequences, MAGI Homo sepiens cDNA AV722329 HTB Homo sepiens cDNA clone HTBBSD04 5 EST177232 Jurket T-cells VI Homo sepiens oDNA 5' end Homo sepiens RAN binding protein 7 (RANBP7), mRNA Homo saplens mRNA for KIAA1277 protein, partial cds Homo sapiens enteropeptidase gene, excrs 20 and 21 Homo seplens chromosome 21 segment HS21C003 Homo seplens chromosome 21 segment HS210027 Human endogenous retrovirus, complete genome H.sapiens mRNA encoding phospholipase c H.sapiens mRNA encoding phospholipase c Homo sepiens neuredin III (NRXN3) mRNA Homo sepiens myosin X (MYO10), mRNA Single Exon Probes Expressed in Brain **MRNA** EST_HUMAN EST_HUMAN EST HUMAN EST HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST HUMAN **EST_HUMAN EST HUMAN EST HUMAN** HUMAN 世の世 Database Source EST. 11037056 NT 호 눋 눋 Ę 눋 5453997 NT 4758827 NT Ł 11526307 NT 11417012 NT 11417012|N 9635487 NT 11419429[NT 6005833 4505492 Top Hit Acessian 4758827 2.0E-86|AW906142.1 4.0E-86 BE547173.1 4.0E-86 BE295843.1 4.0E-86 BE547173.1 3.0E-86 AW340946.1 3.0E-86 AV722329.1 3.0E-86 BE886479.1 2.0E-88 AA308284.1 2.0E-86 AL163203.2 2.0E-86 AB033103.1 3.0E-86 BE896479.1 2.0E-86 AF156776.1 2.0E-88 AW 515742. 2.0E-86 AL163227.2 2.0E-86 AF156776.1 2.0E-86 AF056490.1 3.0E-86 AI659240.1 2.0E-86 N58977.1 6.0E-86 Y19139.1 2.0E-86 U84744.1 Z16411.1 2.0E-86 Z16411.1 2.0E-86 7.0E-86 6.0E-86 2.0E-86 2.0E-86 7.0E-86 7.0E-86 2.0E-88 3.0E-86 Most Similar (Top) Hit BLAST E Value 2.88 1.07 2.18 1.72 4.98 121 3.37 3.37 202 259 3.21 5.00 1.83 1.56 3.54 86 0.60 0.47 Signe 28688 25680 31684 25660 31208 35980 36408 25708 33985 37628 28584 26910 22118 30106 31502 32478 ORF SEO 35981 20011 27651 33733 28817 31501 ÖNQ 23562 22768 22768 23180 13068 SEQ ID 14020 17823 13018 18726 13018 14225 14002 16168 28854 24303 13190 13922 14225 16481 16765 17469 18573 25098 20603 18307 14917 21107 16481 ë 5105 9698 9658 10882 10882 5944 11205 5509 8 10120 11413 11708 1168 1478 2188 2266 3410 7908 414 SEQ ID 5107 206 10120 3729 3729 4019 4260 8 405 1478 1271 ÿ

Page 392 of 536 Table 4 Single Exon Probes Expressed in Brain

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(BBOX), mRNA | Homo septens phospholipid scremblese 1 (PLSCR1), mRNA | Homo sepiens chromosome segregation 1 (yeast homolog)-like (CSE1L), mRNA | Homo saplens besic-helix-toop-helbt-PAS protein (NPAS3), mRNA | Homo sepiens besto-helix-toop-helix-PAS protein (NPAS3), mRNA | Homo sapiens mRNA for KIAA1411 protein, pertial cds | Homo sepiens ribosomal protein S8 kinasa, 90kD, polypoptide 5 (RPSBKA5) mRNA | Homo seplens thyroid autoentigen 70kO (Ku antigen) (G22P1), mRNA | Homo saplens gene for AF-6, complete cds | Homo septens NADH defrydrogenase (ubiquinone) Fe-S protein 1 (76kD) (NADH-coenzyme Q reductase
(NDLIES1) mRNA | Homo septems (fib.LNS) mRNA | Human gamma-glubamy transpectidase mRNA, complete cds | Homo septens chromosome 21 segment HS21C009

 | Homo sepiens chromosome 21 segment HS21C009 | Homo saplens hypothetical protein (LOC51318), mRNA | Homo sepiens hypothetical protein (LOC51318), mRNA | Homo sapiens chromosome 21 segment HS21C100 | Homo saplens synaptojenin 1 (SYNJ1), mRNA
 | Homo sepiens chromosome 21 segment HS21 C084 | Homo seplens chromosome 21 segment HS210084 | qb77c09x1 Source, fekal, finert, NbH119W Homo explens cDNA clone IMAGE:1706128 3' similar to SW:K1CJ, MOUSE P02636 KERATIN, TYPE I CYTOSKELETAL 10: | Homo septens a distributin and metalloproteinase domain 22 (ADAM22), mRNA | Homo sepiens a disintagrin and metalloproteinase domain 22 (ADAM22), mRNA | O.cumiculus mRNA for elongetion factor 1 aipha
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Expression	3.85	3.85	0.51	6.65	5.65	8.0	0.00	2.02	4.13	1.42	1.56	1.51	13.58	1.83	1.03	1.03	1.8	2	8			1.5	1.5	225	277	0.83			10.34	10.34	9.81
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Page 395 of 536 Table 4 Single Exon Probes Expressed in Brain

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Single Exolitrictes Expressed in Digili	Top Hit Descriptor	Homo sepiens polycythemia rubra vera 1; cell surface receptor (PRV1), mRNA	Homo sepiens v-ral similar leukerrila viral oncogene homolog A (ras related) (RALA), mRNA	Homo espiens interfeuldin 13 (IL13), mRNA	Homo sepiens activator of S phase kinase (ASK), mRNA	Homo sapiens activator of S phase kinase (ASK), mRNA	Homo sepiens putative anion transporter 1 mRNA, complete cds	Homo seplens retindulastome-binding protein 2 (RBBP2), mRNA	Homo sapiens growth differentiation factor 5 (cartilage-derived morphogenetic protestor) (GDF5), mRNA	Homo sapiens molybdenum cofactor biosynthesis protein A and molybdenum cofactor biosynthesis protein C imRNA, complete cds	Homo saplens wets avian erythroblastosis virus E28 oncogene related (ERG), mRNA	Homo seplens mRNA for RALDH2-T, complete cds	Homo sepiens mRNA for RALDH2-T, complete cds	Homo sepiens acyl-Coenzyme A dehydrogenese family, member 8 (ACAD8), mRNA	Homo sepiens transcobalamin II; macrocytic enemia (TCN2), mRNA	Homo saplens Calsenille, presentin-binding protein, EF hand transcription factor (CSEN), mRNA	Homo sepiens SNARE protein kinese SNAK mRNA, complete cds	Homo septens SNARE protein kinase SNAK mRNA, complete ods	Homo sepiens SNARE protein Idnasa SNAK mRNA, complete ods	Homo saplens dynein, excremel, fight polypeptide 4 (DNAL4), mRNA	UHH-BI1-ass-d-04-0-UI.s1 NCI_CGAP_Sub3 Homo espiens cDNA clone IMAGE:2718750 3'	UHH-BI1-ece-d-04-0-UI.s1 NCI_CGAP_Sub3 Homo septens cDNA clone IMAGE:2718750 3'	Homo septens KIAA0417 mRNA, complete cds	Homo septens KIAA0417 mRNA, complete cds	wq70m12.x1 NC _CGAP_GC8 Homo septens cDNA done IMAGE:2478806 31	se54s11.s1 NCI_CGAP_GCB1 Homo sepiens cDNA clone IMAGE:824732 3' similar to WP:B0272.2 CE00851;	2987c02.rf Stratagene HeLa cell e3 837216 Homo sapiens cDNA clone IMAGE:627170 5' similar to	DVEZ-JAMMAN 1920 ILLINOVINCE ALED FOLFOLFINISM (1977)	LNT-ZP434NU3Z3_T1 434 (Synon)mt. mees) Homo septems cDNA clone DKF-Zp434N03Z3 5	DESTRUCTURED CANTERS FROM SEPTING SEPTING CHARGE: 1612/65 3' SIMILET TO GENITISSAZ HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS C1/C2 (HUMAN);	Homo saplens chromosome 21 segment HS21C046	
	Top Hit Database Source	5	뉟	Z	٦	ž	뉟	님	Ę	_ 5	Ę	Ę	¥	¥	IN	IN	TN	۲	TN.		EST_HUMAN	EST_HUMAN	N	NT	EST HUMAN	EST_HUMAN	MANUEL FOR	ECT LE MAN	ESI HOMAN	EST_HUMAN	NT	
0	Top Hit Acession No.	TN 8888866	11420697 NT	11417370 NT	11419210 NT	11419210 NT	AF279265.1	11436400 NT	11421726 NT	AF034374.1	11528282 NT	AB015228.1	AB015228.1	11439085 NT	11417974 NT	7305198 NT	AF246219.1	VF246219.1		5031696 NT	1.0E-88 AW 139565.1	1.0E-88 AW139565.1	AB007877.1	AB007877.1	N969034.1	1.0E-88 AA488981.1	4 OF 89 A 44000889 4	4 OF 90 Al 042244 2	NLU45314.2	1.0E-88 AA991479.1	1.0E-88 AL163246.2	
	Most Similar (Top) Hit BLAST E Vakie	3.0E-88	3.0E-88	3.0E-88	3.0E-88	3.0E-88	3.0E-88 AF27926	3.0E-88	3.0E-88	3.0E-88 AF03437	3.0E-88	3.05-88	3.0E-88 AB015228	3.05-88	3.05-88	2.0E-88	2.0E-88 AF24621	2.0E-88 AF24621	2.0E-88 AF2462	2.0E-88	1.0E-88	1.0E-88	1.0E-88 AB00787	1.0E-88 AB00787	1.0E-88 A1989034	1.0E-88	, t	7 20 20 7	1.05-501	1.0E-88	1.0E-88/	
	Expression	4.13	3.58	0.61	1.18	1.18	14.59	6.15	9.68	1.35	98.	0.58	0.58	1.28	5.97	3.32	1.38	3.13	1.52	2.13	5.63	5.63	23.61	23.81	1.4	4.42	ď	200)R7	2.89	3	
	ORF SEQ ID NO:		31327	31812	32076		32465	33206	33642	33921	33521	35680	35681	35705		26432	27058	27185	28967	29760	31539	31540	32317	32318	32771	32839	35047	25244	300	36420		
	Exon SEQ ID NO:	18296	18414	18848	25088	25088	19447	20117	20518	20790	20405	22479	22479	22507	24628	13773	14367	14486	1624	17128	18610	18610	18313	19313	19714	19774	24872	22434		23189	24700	
	Probe SEQ ID NO:	5498	5618	6909	6319	6319	9969	7440	7821	9080	9334	9828	9828	9857	12139	1013	1620	1744	3458	4391	5821	5821	88	8548	7022	7084	0141	877A	1	11422	12356	

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	Top Hit Descriptor	601142409F1 NIH_MGC_14 Homo sepiens cDNA done IMAGE:3506186 5"	Homo septens similar to sema domain, Immanoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 34 (H. saptens) (LOC63232), mRNA	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA	Homo seplens hormonally upregulated neu tumor-associated kinase (HUNK) mRNA	Homo sepiens complement component 8, beta polypeptide (C8B) mRNA	DKFZp434E246_r1 434 (synonym: htes3) Homo septens cDNA clone DKFZp434E246 5	H.saplens CLN3 gane, complete CDS	H.sapiens CLN3 gene, complete CDS	Homo septens plessin 3 (T teoform) (PLS3), mRNA	Homo espiens plastin 3 (T lacform) (PLS3), mRNA	Homo sepiens actin related protein 2/3 complex, subunit 1A (41 kD) (ARPC1A), mRNA	Homo sapiens KIAA0433 protein (KIAA0433), mRNA	Homo sepiens KIAA0433 protein (KIAA0433), mRNA	Homo sepiens mRNA for KIAA0561 protein, partial cds	H. sepiens Weet hu gene	H. sepierrs Weet hu gene	Homo septens mRNA for KIAA0823 protein, pertial cds	Homo septens mRNA for KIAA0823 protein, pertial cds	Human aldose reductase (AR) gene, segment 2	Human accritate hydratase (ACO2) gene, excn 2	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA	Homo septens serine/threonine-protein kinase PRP4 homolog (PRP4) mRNA	Homo septens ubiquitin-conjugating enzyme E2L 3 (UBE2L3) mRNA	Homo explene ubiquifin-conjugating enzyme E2L 3 (UBE2L3) mRNA	Homo septens HSPC159 protein (HSPC159), mRNA	Hamo septens mRNA for KIAA0406 protein, pertial cds	Homo sepiens mRNA for KIAA0408 protein, pertial cds	Homo septens low density ipoprotein-related protein 2 (LRP2), mRNA	Homo saplens low density ipoprotein-related protein 2 (LRP2), mRNA	TCBAPZE0383 Pediatrio pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapienza cDNA close TCBAPC883	TCBAPZE0383 Pediatric pre-B cell acute lymphoblastic leukemia Baykor-HGSC project=TCBA Homo sapidas cDNA cone TCBAP0383	
,	Top Hit Detabase Source	EST_HUMAN	Ę	LN.	L	F	EST_HUMAN	FZ.	Z	 	Ę	FZ		F	N	NT	N	Z	Z	LN	LN TA	4T	۲۲	77	١	4T	NT	Ę	41	5 1	EST HIMAN	EST HUMAN	ı
	Top Hit Acession No.	8.0E-89 BE311557.1	11421514 NT	7857213 NT	7657213 NT	4567390 NT	48.1	1	_	7549808 NT	7549808 NT	11420754 NT	11417118 NT	11417118 NT	33.1	1		30.1	7.0E-89 AB020630.1	1	.1	5803114 NT	4506124 NT	4507788 NT	4507788 NT	7861817 NT	38.2	B007868.2	6806918 NT	5805918 N	3.1	23.4	
	Most Similar (Top) Hit BLAST E Value	8.0E-89	8.0E-80	7.0E-89	7.05-89	7.0E-80	7.0E-89 AL0457	7.0E-89 X99832	7.0E-89 X99832	7.0E-89	7.0E-89	7.0E-80	7.0E-89	7.0E-89	7.0E-89 AB0111	7.0E-89 X62048	7.0E-89 X62048.	7.0E-89	7.0E-89	7.0E-89 M59783.	7.0E-89 U87927	6.0E-89	6.0E-89	6.0E-89	6.0E-80	6.0E-89	6.0E-89 AB0078	6.0E-89 AB0078	6.0E-89	6.0E-89	5.0E-89 BF24433	5.0E-89	
	Expression Signal	1.33	1.2	1.72	1.72	2.86	3.35	1.34	1.34	0.57	0.57	2.06	0.67	0.57	9.0	1.11	1.11	2.33	2.33	1.45	1.7	0.73	1.27	1.06	1.06	0.88	3.02	3.02	0.81	0.81	274	274	
	ORF SEQ ID NO:	28184	32519	25856	25857	30181	30228	30827	30828	31997	31998	33156	33598	33286	35421	38296	36297	36320	36321	37154		28423	27676	27888	27889	28925	29954	20055	30436	30437	30345	30346	
	Exon SEQ ID NO:	15445	19495	13210	13210	17559	17805	18148	18148	19024	19024	20076	20474	20474	22237	23075	23075	23091	23001	23867	25028	13762	14938	15155	15155	16271	17328	17328	17819	17819	17737	17737	
	Probe SEQ ID NO:	2739	9833	424	424	4828	4878	5345	5345	6250	9250	7398	7779	<i>111</i> 8	9584	10429	10429	10445	10445	11203	12774	1002	<u>Ş</u>	2534	2434	3515	4593	\$ 8	218	28	5016	5016	
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	ā	9		3,			MAGE:259148 5'							3° similar to gb:J04131 repetitive element;						ď .		E.				ANGE (CALCO 10) C	MDGF Z (SLCZ4AZ), IIINAY			5 	6
Top Hit Descriptor	QV3-NT0022-080600-219-g03 NT0022 Homo sapiens cDNA	wed log 3 X Soares NFL T GBC S1 Hamo sepiens cDNA done IMAGE:2348452 3	ESTREAMON MACE AMENIANCES, MAGN Homo sepiens CDNA	EST SOCKED MACE TO CAR SA Homo senions odNA clone IMAGE:1844915 3'	Chit As Via Account partial cola	THE THE TANK TO LANGE BOTTON FOR THE AND THE TANK THE TAN	yw88e11.r1 Soeres_placerta_8to@wedss_2NbHp8to9W Homo sapiens cDNA clone IMAGE:259148 5' senier to SW:pl4K_HUMAN P42356 PHOSPHATIDYLROSITOL 4-KINASE ALPHA;	Homo sapiens PXR2b protein (PXR2b), mRNA	Homo sablens PXR2b protein (PXR2b), mRNA	Come amine DYROP worth (PXROb) mRNA	TOTIO SELECTION DE PARTIE (L'ACET), TELEMENTE DE PARTIE (D'ACET), TELEMENTE (D'ACET),	FIGURE SECRETARY AND A COMMING TO SECRETARY OF SECRETARY	Homo sapients mercy to the same at the sam	qg80c08.x1 Soares_NR_T_GBC_S1 Homo septens cDNA clone INAGE:1843022 3' striller to gb.J04131 GAMMA-GLUTAMYLTRANSPEPTIDASE 1 PRECURSOR (HUMAN);contains Alu repetitive element;	ah70e03.s1 Soeres, testis, NHT Homo espiens duna dane 13,20e03.s	en/Jedus.81 Sogres useus Inni notice septicities con in the septical con in the septical control in th	That is supposed to turne for turneline (PTK) excess (0-11	It employs HCK come for tyrosine kinese (PTK), excris 10-11	Liver carians chromosome 21 segment HS2I C003	Liven earliest GGT trene extra 5	POTATION OF THE WAR TO HOME SECTIONS CON HOME IMAGE:3452423 6	Homo septens gene for LECT2, complete cds	Human N-erhylmatehnide-eenstitive factor mRNA, partial ods	Homo saciens chromosome 21 segment HS210085	Human GT24 (GT24) mRNA, partial cds		Homo septens solute certer family 24 (sodium/potessium/calcium exchanger), member 2 (SLUZ4442), minuty.	Homo sepiens partial mKNA for PEX5 resear process	Homo saplens mRNA for KIAA1333 protein, per usi cus	Homo sapiens (Rabro) (CADRO) gene, examily	Hamo sapiens cabro (chars) yars, exal s
Top Hit Databese Source	EST HUMAN	DOT LIMAN	NOW LOS	ESI HUMAN	EST HUMAN	Ę	EST HUMAN	1 5	E L	Ž	Z	Ł	Ę	EST_HUMAN	EST_HUMAN	EST HUMAN	<u>L</u>	L L	Z	z !	I LOL	NAMOU ICE		E A	2 2	2	INT	N	LN-	<u>L</u>	L
Top Hit Acession No.	E762749.1	TOOCTO 4	1/300/21	3.0E-89 AW978181.1	1217359.1	B002297.1	157367 1	TM 02820	0,0001	I NOOD/	7706670 N	7706870 NT	NB037763.1	2.0E-89 Al222095.1	2.0E-89 AA759149.1	4A759149.1	AF089897.1	X58742.1		2.0E-89 AL163203.2	2.0E-89 AJ007378.1	2.0E-80 BE541/44.1	Z.UE-69 ABOU/ 340.1	1.000001	2.0E-89 AL163289.2	081004.1	11428801 NT	2.0E-89 AJ245503.1	2.0E-89 AB037754.1	20E-89 AF170814.1	20E-89 AF170814.1
Most Similar (Top) Hit BLAST E Value	4 0F-89 BE762749	100	4.0E-88 AI/860/2	3.0E-89	3.0E-89 AI217359.	3.0E-89 AB002297	2 OF 30 N57357	1000	Z.UE-88	2.05-89	2.0E-89	20E-89	2.0E-89 AB037763	2.05-89/	2.0E-89	2.0E-80 AA759146			Ì								2.0E-89				
Expression Signal	ş	3	1.56	1.51	1.28	0.48	76.0	5	0.87	0.87	1.65	1.55	3.17	25		1.01										5.33	3.07			0.68	0.68
ORF SEQ ID NO:	22264	3250	37034	28289	32790	36374		١		25833	25832	25833				28947	29494			29679						33341	33657				35558
Exen SEQ ID NO:	25.00	8	23758	15646	19731	Ł.	<u> </u>			13184		13184	1_	<u> </u>	١	16296	16867				17199		H	1		7 20237	20530	1.	1.		
Probe SEQ ID NO:	18,5	è	11088	2870	7040	10502		10702	123	123	389	300	517	3000	356	3540	4126	4133	4133	4315	4463	5259	5393	5702	9116	7567	7835	8316	9452	97710	9710

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Single Excitations Lybraced at the second at	Top Hit Descriptor	Homo sapiens integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor) (ITGA3), mRNA	Homo sapiens hect domain and RLD 2 (HERCZ), mruva	Homo sepiens cell adheston indecule with homology to L1CAM (close homologue of L1) (CHL1), mRNA	Human MAGE-7 antigen (MAGE7) pseudogene, compress cus Thurst MAGE-7 antigen (MAGE7) pseudogene, compress cus	hreidobari NCI_CGAP_Kuti i Homo especie Cara cario inscensioni di CGAP_Kuti i Homo especie Cara i NCI_CGAP_Kuti i Homo especie CARA (Ano INA) COAD Kitat Homo especies CDNA clone IMAGE:3134897 3' similar to TR:054778 054778	SOLUTE CARRIER FAMILY OF A SOLUTE CARRIER FAMILY	Homo septens difference 21 septembril 1921 Co. 18	Homo separa dilumbania zi aspirani rozi di	Home septens of a comment HS21C048	Home septems criticalities at sequential content of the MAGE 3284583 3	7636708.XT NCI_COAP_LLIZE FIGURE SEPARA CITIES MAGE:3284583 3'	7 e3df08.XT NOT COAT TURNS ACTION SECT	RC14110369124700422 500111509	og96c08.x1 Soeres_NRT_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GANMA-GLUTAMYLTRANSPEPTIDASE 1 PRECURSOR (HUMAN);contains Atu repetitive element.	qg86c08.x1 Soaree_NFL_T_GBC_S1 Homo saplens cDNA clone IMAGE:1843022 3' similer to gb:J04131 1' GAMMA-QLUTAMM_TRANSPEPTIDASE 1 PRECURSOR (HUMAN);contains Alu repetitive element;	282010.81 Source jobs INC. sprowt INC. St. Homo septems dNA clone IMAGE: 401442.3'	1982010.81 Source parties of the series of t	spilosd	aj63d08.s1 Sogress Bests NHT From seviens Chiva de IMAGE:3855824 3	6016556S/KI NIT MCC_0010010 September CONA Clone IMAGE:3865824 3	similar to			
III EXUIT F IVE	Top Hit Detebase Source					EST HUMAN	T HUMAN	NT	닐	Z	N	EST_HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	TN	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	
	Top Hit Acession No.	11434411 NT	5729867 NT	11433673 NT	U10892.1	1.0E-89 BF198052.1	1.0E-89 BF198052.1	9.0E-80 AL163245.2	9.0E-00 AL163248.2	8.0E-90 AL163246.2	8.0E-90 AL163246.2	8.0E-90 BE670581.1	8.0E-80 BE670561.1	8.0E-90 BE177830.1	8.0E.80 A1222095.1	8.0E-90 Al222095.1	8.0E-90 AA705222.1	AA705222.1	7.0E-90 AF223391.1	7.0E-90 AA782877.1	BE962525.2	7.0E-90 BE962525.2	7.0E-90 H68849.1	7.0E-60 H68849.1	
-	Most Similar (Top) Hit BLAST E Value	2.0E-30	2.0E-89	2.0E-80	2.0E-89 U10892.	1.0E-89	1.05-89	9.0E-80	9.0E-90	8.0E-90	8.0E-90								!	l					
	Expression Signal	, 88	23	20	2.11	5.97	5.97	1.67	1.57	2.23	2.0	3.78	3.78	0.55	1.52	1.52		1.32	4.12	2.08		1.62	1.9		
	ORF SEQ ID NO:	27930		Ì			37484						١.			36532			-	100	34701	1]		
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Page 400 of 536 Table 4 Single Exon Probes Expressed in Brain

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Top Hit Descriptor	602071208F1 NCI_CGAP_Bm64 Hamo sepiens cDNA clone IMAGE:4214257 5	Homo sepiens hypothetical protein FLJ10388 (FLJ10388), mRNA	Homo saplens hypothetical protein FLJ10388 (FLJ10388), mRNA	Homo sepiens HeGCN1 mRNA, pertial cds	Homo saplens HsGCN1 mRNA, pertial ods	Homo sepiens inositiol 1,4,5-triphosphate receptor, type 3 (ITPR3) mRNA	Homo septens incettal 1,4,5-triphosphate receptor, type 3 (ITPR3) mRNA	Homo septens TCL6 gene, exon 1-10b	Hunan gamma-aminobutynic acid transaminase mRNA, partial cds	ogeoco8x1 Soares_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:1843022 3' similiar to gb:J04131 GAMMA-GLUTAMYLTRANSPEPTIDASE 1 PRECURSOR (HUMAN);contains Alu repetitive element	9986-08.x1 Soerce_NFL_T_GBC_S1 Homo sepiens cDNA done IMAGE:1843022 3' similer to gb:J04131 GAMMA-GLUTAMYLTRANSPEPTIDASE 1 PRECURSOR (HUMAN);contains Alu repetitive element	Homo septens intersectin long factorm (ITSN) mRNA, complete ods	Homo septens pregnancy-zone protein (PZP) mRNA	DKFZp762P1616_r1 762 (synonym: hmel2) Homo sepiens cDNA clone DKFZp762P1616 5	H. sapiens mRNA encoding phospholipase c	Homo septens ELKS mRNA, complete cds	H. sapiens mRNA encoding phospholipase c	Homo sepiens Carbonic anhydrase-related protein 10 (LOCobed-4), mrkhy	Homo sapiens Carbonic ennydrase-remina protein to (LCCCCCCC), minoria	Homo sapiens angiopoleen 4 (ANG4) mittha, perusi cus	Homo sapiens angroporedn 4 (ANG4) mitow, par ea cas	Homo espiens adenyrate cycleses e (ALICTS) minuth	Homo saplens ryanodine receptar 3 (RTRS) mixtra	Homo saplens hypothetical protein FLJ13222 (FLJ13222), mrvvv	Homo sepiens cacherin 18 (CDH18) mRNA	Homo sepiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. saptens) (LOCc3214),	11 Table 1	Homo septems cacum-onging usinsporter minum, perus oue	Homo sepiera Kladusts protein (Nizarossa), Illinian	Homo sepiens KIAAUASS proper (NAAUASS), mitain
Top Hit Database Source	EST_HUMAN	5	Þ	Ę	Į.	5	Į.	2	NT	EST_HUMAN	EST_HUMAN	N	Į.	EST HUMAN	NT	NT	NT	NT	보	¥	닏	LX.	Ę	뒫	NT	<u> </u>	Z !	٤	Ę	5
Top Hit Acession No.	-	B922398	B922398			4504704	4504794 NT	-		7.	5.0E-00 A1222005.1	2	4506354	5 0F-90 AI 135549.1		7.1	216411.1	\$910365 NT	9910305/NT		5.0E-90 AF113708.1	4557258 NT	4506758 NT	11345483 NT	4826670 NT		11418420 NI	5.0E-90 AF123303.1	11417118 NT	11417118NT
Most Similar (Top) Hit BLAST E Value	7.0E-90 BF528089	8 OF 80	00-PO	8 0E DO 177700 \$	A OF-201177700 1	200	00-10-0	5 OF 90 AB03534	5.0E-90 U80226.1	5.0E-80 At222095	5.05-90	5.0E-90 AF11448	5.0E-00	5 OF-90	5.0E-90 Z18411.1	5.0E-90 AB01561	5.0E-90 Z16411.1	5.0€- 0 0	5.0E-90	5.0E-00				5.0E-90	5.0E-90	1	İ	Ì		5.0E-90
Expression Signal	1.17	0 12	0 12	16.6	20.2	3.51	77.0	19.61	3.08	1.47	1.47	2.79	205	8	294	131	2.38	0.74	0.74	2.04	2.04	10.6	77 '0	5.08						0.5
ORF SEQ ID NO:	36218	20568	20290	24805	24826	31020	24057	3	28586	78272	27.268	28011							32408	32806	32867	33228	33609	34025						36176
SEQ ID NO:	22899	18042	18045	1001	2001	2/00/2	SUBJECT OF STREET	1306		<u> </u>	14653	1_		1	1	1	1		19393	19802	19802		20485	ட	L	1_		Ц	22959	22959
Probe SEQ ID NO:	10352	100			8	1	2220	15.	12/2	1813	, g	268	3	\$ P	2504	5606	5679	6831	9631	7114	7114	7463	7790	8192	9008		9579	10181	10312	10312

Page 401 of 536 Table 4 Single Exon Probes Expressed in Brain

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Single Exort Process Expressed in Drain	Top Hit Descriptor	Homo sepiens ATPese, eminophoepholipid transporter-like, Cless I, type 8A, member 2 (ATP8A2), mRNA	Homo septens KIAA0317 gene product (KIAA0317), mRNA	Homo sepiens KiAA0317 gene product (KIAA0317), mRNA	Homo sapiens KIAA0305 gene product (KIAA0305), mKNA	Homo septems gene for AF-6, complete cds	er78h05.X1 Barstsad acrts HFLX60 Home squarts CUIVA conditional London	Homo septens chromosome 21 universe minutes	Homo septers chromosome 21 univident minuty	Homo septems mydein prospinatase, target subulitir () (11) till target	H. sapiens gene encoding discodul receptor tyrostre vinase, exur 10	Homo septens prostate specific membrane anagen (FOM) gens, curipmes cus	Hamo saplens low density ilpoprotem-related protein 2 (LINT 2), minum	Hamo septens low density lipoprotein-resided protein a (Livin A) minuth	Homo saplens DNA for smykold precursor protein, complete cas	Hamo sapiens mRNA for KIAA1244 protein, parties cas	Human prohomnone converting enzyme (NECZ) gene, exert o	UI-H-BW1-emyb-04-0-UI-s1 NCI CCAPP Sub/ Indian september CONA Curio INVIGE 20030839 3	UI-H-BW 1-arry-b-04-C-UI-81 NCI_C-G-M_ SUG/ TIMIN SQUARE SURVING SUB-18-20-00-00-00-00-00-00-00-00-00-00-00-00-	601335244F1 NIH MGC 38 Home separas Guity carre investigation of	601050378F1 NIH MGC TO Form Sequence characteristics of THMG17 mRNA	Home supering and the received an entire process of the process of	HOMO supports ingratitionally group (Inclination of Inclination Control of Inclination Cont	ec54c02.x1 Sorres_percent outsets ZNBT oten Train expense Constitution of Similar to SW: Oten Mouse P23275 OLFACTORY RECEPTOR OR3.;	Homo sapiens mRNA for KIAA0289 gene, parties cds	Home septems GKB2-related adaptor protein (JATAP) mistra	be40405.y3 NIH_MGC_10 Hamo septens cDNA clone IMAGE:2899881 o smiller to Inc. 0.3200 of 3200 HYPOTHETICAL 35.5 KD PROTEIN:	Homo saplens similar to laminin receptor 1 (67kD, ribosomal protein SA) (H. sapiens) (LOC83484), mRNA	5A) (H. sepjens) (LOC83484), mRNA	AU118985 HEMBA1 Homo septens dONA done HEMBA1004793 5
שהוש ביים	Top Hit Database Source	N	Ę	NT	NT	NT	EST HUMAN	NT	NT	Z.	L L	Ę	Į.	۲	F	L		EST HUMAN	EST HUMAN	EST_HUMAN	EST HOMAN	<u>L</u>	LN	EST_HUMAN	LN	N.	EST_HUMAN	Ę	· NT	EST_HUMAN
Sing	Top Hit Acession No.	11433721 NT	7662051 NT	7662051 NT	7662047 NT	5.0E-90 AB011399.1	-		4.0E-90 AF231920.1	4505316 NT	(99033.1	4		6806918 NT	4.0E-80 D87675.1	AB033070.1	M95967.1	BF516168.1	BF516168.1	3.0E-00 BE563833.1	2.0E-90 BE537913.1	5031748INT	5031748 NT	AI138213.1	121	6729855 NT	2.0E-90 AW672686.1	11427320 NT	11427320 NT	2.0E-90 AU118985.1
	Most Similar (Top) Hit BLAST E Value	5.0E- 9 0	5.0E-90	5.0E-90	5.0E-90	5.0E-90 /	5.0E-90 AI52339	4.0E-90/	4.0E-90 /	4.0E-90	4.0E-90 X99033.	4.0E-80 AF0075	4.0E-90	4.0E-D0	4.0E-90	4.0E-90 AB0330	4.0E-00 M95967	3.0E-80 BF5161	3.0E-90 BF5161	3.0E-90	2.0E-90	2.0E-90	2.0E-90	2.0E-90 AI1382	2.0E-90 AB0080	2.0E-90	2.0E-00	2.0E-90	<u> </u>	2.0E-90
	Expression Signal	9.16	9.0	0.54	2.41	2.08	4.43	1.83	1.93	3.28	8.09	0.98	1.07	1.07	7.65	2.17	2.33	1.08	1.08	17.81	4.71	2.67	2.67	1.7	1.05	7.31	4.86	4.78		1.37
	ORF SEQ ID NO:	36209	38284					25742	25743	28482									33571	37551		26567	26568	29209			<u> </u>			
	Exan SEQ ID NO:	22001	23048	23048	24324	24948	24938	13101	13101	13822	14428	15758	L	1_	1_		1_	1	20447	L	<u>l_</u>	13906	13905	l _	L	L			1	22510
	Probe SEQ ID NO:	10344	10402	10402	11731	12591	12641	202	282	1064	28	2802	3023	3023	4808	4743	4768	7751	7751	11630	208	1150	1150	3828	4840	4853	Seo.	0690		0986

Page 402 of 536 Table 4 Single Exon Probes Expressed in Brain

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Top Hit Descriptor	AU118985 HEMBA1 Homo septens cDNA clone HEMBA1004795 5	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mrvnA	Homo sepiens amyloid beta (A4) precursor protein (proteese nextn-li, Alzheimer discesse) (APP), mRNA	Homo sapiens dramosane 21 unknown mRNA	Homo sepiens chromosome 21 unknown mRNA	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), perus	Homo sapiens mRNA for T-box transcription rector (LEXZO gene), per use	Homo septiens ALR-like protein mRNA, pertial cds	Homo sepiens ALR-like protein mRNA, pertial cds	Homo sapiens Kruppel-line tactor 7 (ubiquitous) (RLF7), mixinA	Homo sapiens protein phospharase 2A BK garmine suburing gare, exul 3	Homo sapiens protein phosphatase 2A EK gamma suburin gane, wwill a	601158563F2 NIH MGC 53 Home septens clowe transfer 3011110 5	Home saplens similar to SALL1 (see (LYGsophisa)-use (LYGsophisa)-use (LYGsophisa)	Homo sapiens chromosome 8 open resping mame 2 (CoURTA), mank	Homo sapiens soluble interfeuktin 1 receptor accessory protein (IL1KAP) gains, oxon o, arustinauve oxons s and consistence of a stematikary sulfact	Homo sentena mRNA for KIAA0633 protein, pertiel cds	Harms comitmen KIA A (ACC) Access provided (KIA A 0623), TIRNA	Liams emission Authorities (A. Cancelera 14-abha-demethylese) (CYP61), mRNA	India signals cylindrical root of motors of making complete cds	Human regime derived in Countries in the Countries 24 (GRIN2A) mRNA	HOME SECTION S	Homo sapiens soute carrier family 1 (high an intri) aspending contraction us reported by the contraction of	Homo sapiens brefeldin A-inhibited guanine nucleotide exchange protein 2 (BIG2), mRNA	Hamo sapiens SNCA Isofam (SNCA) gene, complete ods, alternatively spiloed	Homo sapiens CGI-15 protein (LOC51006), mRNA	Homo sepiens CGI-15 protein (LOC51008), mRNA	vc44d11.72 Source infant brain 1NIB Homo sepiens cONA clone IMAGE:35477 5'	Human branched chain alpha keto acid dehydrogenase mRNA, 3' end	Homo serviens DNA for Human P2XM, complete cds	Library sessions DNA for Hisman POXM complete cds	India separate DIVA (V. Harriston, Company CONA chora #381.3)	HOMOUSSOI LIVE TIGLOZ COI IIIO. I SAIO COLINO CALIN
Top Hit Detabere Source	EST_HUMAN	NT	NT	17	NT.	NT	MT	M	NT	NT	INT	NT	EST HUMAN	NT	LN	ţ	E L		N.	Z	LV.	NT	L	INT	Z	INT	TNT	EST HIMAN	LY.	Į.		Z	EST HUMAN
Top Hit Accession No.	JU118985.1	11024711 NT	4502168 NT	1.0E-90 AF231920.1	VF231920.1	J237589.1	1.0E-80 AJ237589.1	1.0E-90 AF264750.1	4F264750.1	4507828 NT	1.0E-90 AF098154.1	1.0E-00 AF098154.1	1.0E-00 BE379884.1	11420514 NT	F005720 NT		1.0E-90 AF16/340.1	1.0E-60 AB014333.1	11428910 NI	11419408 NI		6006002 NT	11426758 NT	11422086INT	AF163864.1	1.0F-00 11422109 NT	11422109 NT	4 AE ON DOCASE 4	104474 4	1.05-80 3044/4.1	1.0E-90 ABOUZUSE.1	1.0E-90 AB002059.1	8.0E-01 D12234.1
Most Similar (Top) Hit BLAST E Vatue	2.0E-90 AU118985	2.0E- 9 0	1.06-90	1.0E-90/	1.0E-90 AF231920	1.0E-00 A 1237580	1.0E-90	1.0E-90	1.0E-90 AF284750	1.0€-90	1.0E-90	1.0E-00	1.0E-B0	1.0E-00	1.0E-90		1.05-50			1.0E-90	1.0E-00 U01934.	1.0E- 0 0	1.05-00				1						
Expression Signal	1.37	2.8	4.56	1.36	1.43	232	2.32	13.22	13.22	247	5.58	5.56	1.23	3.33	6.48							0.04	74									1.49	90
ORF SEQ ID NO:	35707	38448				L		L			28703			27342								32965	24345			35082		1			_		29642
Exan SEQ ID NO:	22510	23214	13078	15518	15518	13454	13454	13487	13487	13846	14033	14033	L	1	L		╝	18385		19240	19455	19899		1		Ĺ		\perp	\bot	┙		24904	16912
Probe SEQ ID NO:	0890	11447	6	18	3	8/2	8/8	713	743	1088	1283	1283	1662	1895	2858		4389	5589	5748	6473	6973	720	7874	1/0/	8 8	200	22.10	2128	10667	10967	12580	12680	4172
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Table 4
Single Exon Probes Expressed in Brain

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			Ī	T	T	T	T	T	ė	3	T	T	şċ	T	T	T	P	47	7	7	7	1	1	1	1	7	P	75	67
Top Hit Descriptor	Rettus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cots	Homo saplens melcorin, ring finger protein, 1 (MKRN1), mRNA	CM-BT043-090259-075 BT043 Hamo sepiens cDNA	280b04.s1 Soares, fetal liver splean 1NFLS S1 Homo sapiens cDNA clone IMAGE-448015.31	AU143539 Y79AA1 Homo sepiens cDNA clone Y79AA1002087 5	AU143539 Y79AA1 Homo sepiens oDNA clone Y79AA1002087 5	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA	Homo saplens chromosome 22 open reading frame 5 (C22ORF5), mRNA	BU49709X1 Schneider fetzi brain 00004 Homo sepierse CDNA cione INAGE-2518121 3' similar to SW ASPG FLAME 047888 NA-RETAL-W-ACETY1 CH INCOSAMINY1 VIL ASPARACINA CE DEFICI DECOD	801901624F1 NH MGC 19 Homo sepiens cDNA clone IMAGE-4130633 6	AV649878 GLC Hamp septens aDNA clane GLCBYFOR 3"	AV649878 GLC Homo sepiens cDNA clone GLCBYF08 31	de70f11x1 Soares_fetal_king_NbHL19W Home sapiens cDNA clone IMAGE:1744365 3' similar to contains MIR.b2 MiR MIR recetifive element:	Homo sepiens isophosphatidic acid acvitransferase-delta (I PAAT-delta) mRNA complete ode	Homo sapiens (ysophosphatidic acid acytransferase-delta (LPAAT-delta) mRNA complete ode	Homo septens chromosome 21 segment HS21C084	EST01579 Hippocampus, Strategene (cet. #636205) Homo sapiens cDNA clone HHCMC80 similar to Retrovirus-related gag polyprotein	EST01579 Hippocampus, Stratagene (cat. #938205) Homo sapiens cDNA clone HHCMO90 similar to	Home envises e	Harro satisfies acting carrier family 4, anton archanger, marrhay 2 (3) 7445), mixed	Homo satiens chromosome 21 segment HS21C083	Homo septens mRNA for KIAA1278 protein, pertial cols	Homo saplens mRNA for KIAA1278 protein, partial cds	Homo sepiens cyclin-D binding Myb-like protein mRNA, complete cds	Human Ku (p70/p80) subunit mRNA, complete cds	Homo seplens epididymal secretory protein (19.540) (HE1), mRNA	Homo sepiens cyclin-dependent kinase 8 (CDK6) mRNA	Homo septens genma-eminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA	
Top Hit Database Source	۲	¥	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	1	ĮN.	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	N IN	NT.	N.	EST HUMAN	COT LITTER		Ļ	Į,	K	LN	K	N	Ę	5	ZI.	
Top Hit Acession No.	7.0E-91 AF053769.1	11419234 NT	7.0E-01 AID04151.1	AA702794.1	5.0E-01 AU143539.1	5.0E-01 AU143539.1	7110834 NT	7110634 NT	5.0E-01 AI879695.1	5.0E-91 BF314682.1	5.0E-01 AV649878.1	5.0E-91 AV649878.1	N193566.1	6.1	6.1		AT7894.1	77007.1	44490103 NT	114301gg NT	3.0E-01 AL163283.2					11434964 NT	4502740 NT	11497611 NT	
Most Similer (Top) Hit BLAST E Value	7.0E-91	7.0E-91	7.0E-01	5.0E-81 AA70278	5.0E-91	5.0E-01	5.0E-91	5.0E-01	5.0E- 0 7	5.0E-91	5.0E-01	5.0E-91	5.0E-91 A1193588	4.0E-91 AF15677	4.0E-91 AF15677	4.0E-91	4.0E-91 M77994.	4.05.04 1477004	3.0F.01	3.0E-91	3.05-01	3.0€-91 /	3.0E-91	3.0E-91 AF08453	3.0E-01 M30038.	3.0E-91	3.0E-91	3.0E-91	•
Expression	1.06	1.8	0.68	1.83	11.73	11.73	76.0	0.97	1.25	1.2	1.52	1.52	1.74	1.80	1.00	4.49	1.98	8	3.07	3.07	1.62	3.39	3.39	1.45	3.70	127	2.48	5.82	
ORF SEQ ID NO:	26859	34036	38062		29840			30117	32280	33931	34495	34496		28611	28612	36775	31082	34127	27049	27050	28746	28863	28864	29159	20015	31305		32256	
Exen SEQ ID NO:	14174	20899	22846	16223	17215	17215	17480	17489	19285	20799	21350	21350	24919	15960	15960	23530	24596	24508	14360	14360	16094	16211	16211	16520	17286	18395	18987	19265	
Probe SEQ ID NO:	1427	8205	10198	3467	4480	4480	4757	4757	6219	8105	8658	8858	12612	3197	3197	10848	12094	12004	1613	1613	3334	3456	3465	3768	4551	2600	0212	6488	

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			T				Ī	Τ				T		T	T	Τ	T		T	1	Ŧ	T.	7	h	5	1	E	3 2		7	Щ		567
Single Exon Probes Expressed in Brain	Top Hit Descriptor	Homo sepiens gentine-envirobutivity acid (GABA) B recentor, 1 (GABBR1) transcript varient 2 mRNA	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, excus 10 and 11	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, excus 10 and 11	Human mRNA for vary low density lipoprotein receptor, complete cds	Homo septens mRNA for KIAA0694 protein, partial cds	Homo sepiens EHM2 mRNA, complete cds	Homo sapiens mRNA for KIAA1080 protein, partial cds	Homo septens mRNA for KIAA1080 protein, perties ods	Homo septens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) oenes, complete cds	Homo sapiens beta-ureldoproplonase (BUP1) dene, expn 6	Homo seplens befa-ureldoproplonase (BUP1) cene, econ 6	Homo sapiens chromosome 21 segment HS21C084	UI-H-Bi3-eks-d-01-0-UI:s1 NCI CGAP Sub5 Hamo sablens cDNA clane IMAGE: 2735/280 31	Homo sapiens hypothetical protein PRO1855 (PRO1855), mRNA	602022088F1 NCI CGAP Bm67 Homo septens cDNA clone IMAGE:4157804 5'	602022068F1 NCI_CGAP_Bm67 Homo sapiens cDNA clore IMAGE:4157804 5	ym30e03.r1 Soures infant brain 1NiB Homo sepiens cDNA clone IMAGE:49587 51	Homo sapiens NKGZD gene, exon 10	Homo sepiens NKG2D gene, exon 10	Homo saplens mRNA for KIAA0833 protein, partial cds	Human Ne+,K+ ATPase alpha-eubunit mRNA, partial cds	Homo sapiens hypothetical protein FL/20260 (FL/20260), mRNA	Homo sepiens NALP1 mRNA, complete cds	Homo saplens partial TMASF2 gene for tetraspenin protein, econ 5	Homo suplens partial TM4SF2 gene for tetraspanin protein, exon 5	Homo septens mRNA for KIAA1512 protein, perties cds	Homo saplens mRNA for KIAA1512 protein, partial cds	Homo sepiens brefeldin A-Inhibited guenine nucleotide exchenge protein 2 (BIG2), mRNA	Homo septems RNB6 (RNB6), mRNA	2013 Human retina cDNA randomly primed sublibrary Hono eaplens cDNA	801273513F1 NIH_MGC_20 Homo septens cDNA clone IMAGE:3614687 5	
gie Exon Prot	Top Hit Database Source	N	IN	N	IN	K	N F	N-	Z	IN	Z	LN L	NT TA	EST HUMAN	1	EST HUMAN	EST HUMAN	EST_HUMAN	TN	TN.	TN	INT	TN				L				П	Г	1
	Top Hit Acession No.	11497 0 11 NT	U86959.1	U86069.1	1		3.0E-01 AB032179.2		3.0E-91 AB029003.1	_		3.0E-01 AF169656.1			4402	1.0E-01 BF348182.1		_		9.0E-02 AJ001689.1	0.1		27149	5.1				9.0E-62 AB040945.1	11422086 NT	7706886 NT		2	:
	Most Similar (Top) Hit BLAST E Value	3.05-€1	3.0E-91 U86959	3.0E-01 U80069.	3.0E-81 D16494.	3.0E-01	3.0E-01	3.0E-01	3.0E-81	3.05-01	3.0E-01	3.0E-01	1.0E-91	1.0E-91	1.0E-91	1.0E-01	1.0E-91	1.0E-91 H15212	9.0E-02	9.0E-92	9.0E-92	9.0E-02 J03007.1	9.0E-92	9.0E-92/	9.0E-92 A.1250586	9.0E-02 /	9.0E-02/	9.0E-92 /	9.0E-02	9.0E-92	8.0E-92 W 26367.1	8.0E-02 BE38636	
	Expression Signal	6.82	4.97	4.97	2.58	2.83	1.41	1.66	1.06	2	4.35	4.35	5.08	6.34	76.0	2.28	2.26	1.35	9.06	90.6	0.9	4.86	283	4.03	7.17	7.17	0.92	0.92	1.95	1.95	2.25	3.20	
	ORF SEQ ID NO:	32257	33308	33307	34508	35023	36723	37105	37108	31067	30489	30490	25501	26845	30790	32810	32611		20639	28840	30454	30867	31217	32127	33576	33577	34107	34108	35010		25554	25728	
	Esca SEQ ID NO:	19255	20208	20208	21361	21858	23486	23827	23827	24749	17898	17898	12876	13973	18131	19577	19677	25340	13970	13970	1788	18176	18316	19132	2452 52	8452	20806	8 8	21844	23828	12017	13086	l
	Probe SEQ ID NO:	6488	7538	7538	6998	9188	10803	11160	11180	12335	12867	12067	47	1223	5328	6743	6743	12245	1219	1219	2750	5378	2218	6362	77.50	1,58	8272	8272	27	119	ढ	278	

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667 N-CAM≐145 kda neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2966. N-CAM-145 Idea neural ceil edhesion molecule (human, small ceil lung cancer ceil line OS2-R, mRNA, 2890). Homo saplens FYVE domain-containing dual specificity protein phosphetase FYVE-DSP2 mRNM, complete Hamo sepiens ditrydrolipoemide S-succinytransferase (E2 companent of 2-axo-glutarate complex) (DLST) Hamo sapiens nuclear mitogen- and stress-activated protein kinaso-1 (MSK1) mRNA, complete cds Bu83h08.x1 Schneider fetal brain 00004 Home septens cDNA clone IMAGE:2782911 3' stmiler to Homo septens DNA polymenase zeta catalytic subunit varient 1 (REV3L) mRNA, complete ods Homo septens cysteine-rich repeat-containing protein SS2 precursor, mRNA, complete cds TR:060302 060302 KIAA0555 PROTEIN; contains element MER22 repetitive element; Homo septens transcription termination factor, RNA polymerase II (TTF2), mRNA Human von Willebrand factor pseudogene corresponding to exons 23 through 34 Homo sepiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA Homo sepiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA Homo saplens cyloplesmic Seprase truncated isoform mRNA, complete cds Homo sepiens T-cell lymphome invesion and metastasis 1 (TIAM1) mRNA Homo sepiens T-cell lymphoma invesion and metastasis 1 (TIAM1) mRNA Homo sepiens DNA, MHC class I region, 7.1 ancestral hapictype Homo sapiens DNA, MHC class I region, 7.1 ancestral haplotype Top Hit Descriptor Homo saplens B-cell CL Llymphoma 7b (BCL 7B) mRNA Homo septens mRNA for KIAA0758 protein, partial cds Homo sapiens mRNA for KIAA0758 protein, pertial ods Homo septens NRAS-related gene (D1S155E), mRNA Homo sepiens mRNA for KIAAD611 protein, partial cds Homo sapiens mRNA for KIAA1600 protein, partial cds Human lens membrane protein (mp19) gene, exon 11 Human lens membrane protein (mp19) gene, exon 11 Homo sepiens AIM-1 protein (LOC51151), mRNA Homo sepiens mRNA for MBNL protein Homo sepiens MCP-4 gene **ANNE** Έ 쁑 EST_HUMAN Top Hit Database Source Ż 눋 뉟 z FN|85738|NT 4607500 NT 눋 4502384 NT 5031570 NT 4507500 NT 눋 Ę 11416961 NT 눋 Ż 4503340 NT Z 눋 11428589 NT 5031570 Top Hit Acession 7.0E-92[AB031007.1 8.0E-02|AF074393.1 7.0E-92 AB018301.1 7.0E-92 AF167708.1 8.0E-92 AW 157571.1 AB018301.1 7.0E-92 AF007822.1 8.0E-92 AB014511.1 AB031007.1 8.0E-92|AF264717.1 AB046820.1 8.0E-02|AJ000979.1 8.0E-92|AF179428.1 7.0E-02|S71824.1 7.0E-92 M80678.1 7.0E-92|S71824.1 104193.1 8.0E-92 Y13829.1 L04193.1 7.0E-02 7.0E-02/ 7.0E-92 7.0E-02 7.0E-92 7.0E-92 8.0E-02 8.0E-02 8.0E-92 8.0E-92 8.0E-92 Most Similar BLASTE 五(4) 2.59 227 2.50 0.87 90. 0.58 3.2 8 1.34 88 227 1.61 0.87 90.0 0.92 0.55 3.91 2 0.0 1.31 3.91 0.65 Expression Signal 29913 29912 25525 25680 26675 27645 27646 28205 28750 38636 37320 25468 25681 28171 34152 34263 34801 30918 34153 30374 32217 32222 3577 ORF SEQ 3077 ÖNQ 17282 17282 15538 14006 14913 15282 15435 24024 12892 15538 14913 17871 18210 19219 23397 17760 22017 22573 13357 17871 18113 21651 19223 20685 21017 SEQ ID <u>ق</u> ÿ 4547 1257 2184 2588 2588 2728 2757 3340 4547 57.230 7990 8980 10707 1333 2 230 266 8324 8324 5041 6451 5308 4 SEQ ID ö

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III EXOII FIUD	Top Hit Datebase Source	F	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	LN	Z	7	Į.	ĮŅ.	EST HUMAN	EST HUMAN	NT	FST HIMAN		EST_HUMAN	NT	NT	NT	Į.	<u> </u>	Į.	EST_HUMAN	NT	5	<u> </u>	Z	Į.	NT	EST_HUMAN	Z
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	Expression Signal	88.0	8.05	1.28	1.6	2.6	2.72	272	1.06	3.57	3.57	1.33	1.33	2.22	90.0	8,7	2.36	5.58	19.2	261	2.61	5.57	123	2.51	18.0		O'O	3.03	0.61	0.78	1.60	4.83
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Homo sepiens zinc finger protein 198 (ZNF198), mRNA	Home service male green's letter (Dracobile) like 1 (MSL2L1), mRNA	TOURS deposit in the requirement of the control of	Homo septens mixing to NAX 1035 process, par on NAS	Homo sapiens calcineum binging process I (numenced), minum	y80e08.rt Soares placenta Nb2HP Homo sapiens dunk dione invivoe: 1430/4 5	y80e08.r1 Source placents Nb2HP Homo sapiens cDNA come IMAGE:1450/4 0	Homo septens ribosomal protein, large, P1 (RPLP1) mRNA	HTM1-288F HTM1 Homo septens cDNA	tg01b02.x1 NCI_CGAP_CLT1 Homo septiens cDNA clone IMAGE:2107467.3 similar to bw :r I Nrntow Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ;contains Alu repetitive element.contains element NED17 recentifius element :	MENT (reported element,	1go1b02x1 NCI_CGAP_CGL1 Home seperts curve finds in the contains Alu repetitive element contains element	MER17 repositive element;	AU12/1681 MANIMAT Homo sapiens culta cone manima i vocase o	EST188414 HCC cell line (matastasis to liver in mouse) II Homo separts cultur o structural an interest cultural	protein L29	Forms suppens calcular chairms explicit subuling control of the co	B01281867F1 NIH_MGC_44 Hamo sepiens cDNA clane IMAGE:3603832 5	Homo aspiens ribosomal protein L10a (RPL10A), mRNA	UI-H-BIO-earth-06-0-UI s1 NCI_CGAP_Sub1 Homo septems cDNA clone IMAGE:2709371 3	UI-H-BIO-eart-h-06-0-UI.s1 NCI_CGAP_Sub1 Homo expiens cDNA clone liMAGE:2706371.3	801400521F1 NIH MGC_88 Home explens cDNA clone IMAGE:3863808 5	Homo sapiens chromosome 21 unknown mitthy	Homo sepiens T cell lymphome investor and measurasis () () () () () () ()	Homo sepiens mRNA for NAA1257 protein, per usi cas	Homo sapiens P I H-responsive desectants or protein (01) innoch, contract of	Homo expiens mRNA for KIAA0611 protein, pertrei cos	wc0ec08.x1 NCI_CGAP_Pr28 Homo septens CUNA cione invade: 2314070 3	wc0gc06.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE.23146/U.3	Human skaletal muscle 1.3 kb mktNA tor topomyosin	Human sometic cycorrome c (HUT) processed pseudogales, curiphece was
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Page 408 of 536 Table 4 Single Exon Probes Expressed in Brain

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	Top Hit Descriptor	Homo septens wheart (WBSCR1) and whear5 (WBSCR5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds	Homo septens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, excn 11, complete cds and attenuatively solded product	Homo sepiens discs, large (Drosochila) homolog 2 (chapsyn-110) (DLG2) mRNA	Homo saplens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA	Homo sepiens secretary pathway component Sec319-1 mRNA, alternativaly spirad, complete cds	Homo septens TAR (HIV) RNA-binding protein 1 (TARBP1) mRNA	Homo sepiens WSB1 protein (WSB1) mRNA, complete cds	Homo seplens nucleobindin 2 (NUCB2), mRNA	Homo sapiens gamma-glutamytransferase 1 (GGT1), mRNA	Homo explens gamma-glutamytransferase 1 (GGT1), mRNA	250e08.s1 Source_bests_NHT Homo sapiens cDNA clone IMAGE:795688 3' similar to SW:CLPA_RAT P37397 CALPONIN ACIDIC ISOFORM	Homo sapiens interferon gamma receptor 1 (/FNGR1) mRNA	Homo saplens interferon gamma receptor 1 (IFNGR1) mRNA	Homo septens pescedillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA	Homo septens hypothetical protein FLJ20731 (FLJ20731), mRNA	Homo sapiens dystrophin (DMD) gene, deletion breatpoints 1-3 in Intron 5	Homo septions DNA polymerase zota catalytic subunit (REV3) mRNA, complete cds	Homo sepiens chromosome 21 segment HS21C101	Homo supiens fumor emigen SLP-8p (HCC8), mRNA	Homo sapiens interfeukin 18 receptor 1 (IL18R1) mRNA	9694c12.r1 Stratagene liver (#837224) Homo sepiens cDNA clone IMAGE:78636 5' straiter to similier to SP-A44391 A44391 SERUM RESPONSE EI EMENT-BINDING PROTEIN SRE-7799 - HI IMAN	AV692051 GKC Homo sepiens cDNA clone GKCDRF07 5	802248554F1 NIH MGC 62 Hamo sepiens oDNA done IMAGE:4332038 5	602246554F1 NIH MGC_62 Hano septens cDNA clone IMAGE:4332036 5	Homo sepiens tensin mRNA, complete cds	th/29g03.xf NCI_CGAP_Bm/25 Hamo septens cDNA cione IMAGE:2169076.3	tr29g03.x1 NCI_CGAP_Brr25 Hamo saplens cDNA clone IMAGE:2159078 3'	
	Top Hit Detabase Source	N F	Ļ	¥	N FN	Į.	F	LN	F	F	F	EST HUMAN	L	Į.	F	H	١	TN	NT	LN	K	ΤN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	NT	EST HUMAN	EST_HUMAN	
	Top Hit Acession No.	5.0E-83 AF045555.1	60	4557528	4557526 NT	18.	5032156		11439589 NT	11417877 NT	11417877 NT	4.0E-83 AA459833.1	4567879 NT	TN 628799	7857454 NT	7857454 NT	TN 838538NT			4.0E-03 AL163301.2	7705396 NT	4504654 NT		7.7						
	Most Similar (Top) Hit BLAST E Value	5.0E-83	5.0E-63 AF06713	50E-83	5.0E-83	5.0E-63 AF27486	5.0E-83	5.0E-03 AF0893	5.0E-03	5.0E-83	5.0E-03	4.0E-83	4.0E-B3	4.0E-83	4.0E-83	4.0E-83	4.0E-03	4.0E-83 AF04767	4.0E-83 AF15747	4.0E-03	4.0E-83	4.0E-93	4.0E-83 T46864.1	4.0E-03	3.0E-03 B	3.0E-03 B	3.0E-03 A	3.0E-03 A	3.0E-63 A	!
	Expression Signel	1.02	3.8	-	7	2.16	1.25	4.0	2.25	2.15	1.44	9.52	1.39	1.30	1.67	1.67	1.53	4.3	0.98	1.65	0.73	1.07	6,4	6.17	7.36	7.35	1.31	6. 0	0.79	
	ORF SEQ ID NO:		33388	34338	34339	36360	35554	35821	39966	30859	30829		25963	25864	26186	26187	28577	27424	27707	27865	28068	29403	31284	37023	29035	28036		31412	31413	
	Exen SEQ ID NO:	18799	20280		21195	92128	22358	22818	23415	25052	25052	12912	13218	13218	13527	13527	13014	14708	14909	15118	16308	16771	18354	23748	16396	16396	16851	18401	18491	
	Probe SEQ ID NO:	8018	7814	8503	8503	8523	9707	0266	10727	12343	12805	98	432	432	735	735	1160	1970	224	2397	3553	4026	6557	11078	3843	3843	4210	2669	5697	
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Single Exon Probes Expressed in Brain

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Cingle Lyon Flobes Lypressed III Dialli	Top Hit Descriptor	Homo septens GCN5 (general control of amtho-add synthesis, yeast, homotop)-like 2 (GCN5;2), mRNA	wb02d05x1 NCI_CGAP_GC6 Harro septens cDNA clane IMAGE;2304489 3'	Chlorocebus aethiops mRNA for ribosomal protein S4X, complete cds	Chlorocebus sectiops mRNA for ribosomal protein S4X, complete cds	Homo septens chromosome 21 segment HS21C085	Homo sapiens chromosome 21 segment HS21C085	Homo septiens tensin mRNA, complete cds	Human Cik-essociated RS cyclophilin CARS-Cyp mRNA, complete cds	601117586F1 NIH_MGC_16 Hamo suplens cDNA done IMAGE:3358220 5'	EST378458 MAGE resequences, MAGH Homo sepiens cDNA	Homo sapiens deafness, autosomal dominant 5 (DFNA5), mRNA	QV3-HT0513-290300-128-h04 HT0513 Homo sepiens cDNA	Homo saplens hypothetical protein (LOC5/318), mRNA	HSU74313 Human chromosome 14 Homo septens cDNA clone 1-86	UI-HF-BNO-aks-g-08-0-UI1 NIH_MGC_60 Homo sepiens oDNA clone IMAGE:3078329 5	AV721646 HTB Homo sapiens cDNA clane HTBAUB04 5"	AV721846 HTB Homo sepiens aDNA done HTBAUB04 5	229c10.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503348 3*	Homo sepiens CYP17 gene, 5' end	601458531F1 NIH_MGC_66 Homa sapiens cDNA clone IMAGE:3862088 5	Homo sapiens CTR1 pseudogene	Homo saplens CTR1 pseudogene	Homo sapiens hypothetical probeh (DJ328E19.C1.1), mRNA	0y84508.x1 NCL_CGAP_CLL1 Homo sapiens cDNA done IMAGE:1672503 3' similar to TR;Q62384 Q62384, ZINC FINGER PROTEIN:	Homo saplens DNA for emyloid precursor protein, complete cds	Homo septems glutamete decerboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD67, mRNA	Homo sepiens hypothetical protein FLI20291 (FLJ20291), mRNA	Homo septems hypothetical protein FLJ20291 (FLJ20291), mRNA	Homo sapiens mRNA for KIAA1563 protein, partiel cds	52 precursor, mRNA, complete cds	Homo sapiens long chain polyunsaturated fatty acid elongation erzyme (HELO1) mRNA, complete cds
	Top Hit Detabase Source	Į.	EST_HUMAN		NT	Z	LY	NT	LN N	EST HUMAN	EST_HUMAN	Į.	EST HUMAN	LN LN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	Ę	EST_HUMAN	NT	NT	M	EST HUMAN	¥	¥	Ę	Ę	F	Ą	NT
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	Most Similer (Top) Hit BLAST E Value	3.0E-83	3.0E-93 AI8248;	2.0E-93	2.0E-03	2.0E-03	20E-03	2.0E-93	2.0E-93	2.0E-03	2.0E-93	2.0E-83	2.0E-03	2.05-83	2.0E-83	2.0E-03	2.0E-83	2.0E-83	2.0E-83 AA1267	2.0E-93 L41825.	2.0E-83 BF0353	1.0E-93 AF2389	1.0E-93 AF23890	1.0E-83	1.0E-03	1.0E-93 D87675.	1.0E-93	1.0E-03	1.0E-93	1.0E-83 AB0467	1.0E-93 AF1677(1.0E-93 /
	Expression Signal	121	4.27	7.51	7.51	9.36	87.8	1.33	1,33	1.68	5.42	0.66	1.04	1.13	0.65	1.1	127	1.27	2.64	217	10.79	2.29	229	4.25	4.57	8.8 1	2.9	7.65	7.65	1.5	06'0	1.33
	ORF SEQ ID NO:	32236	38631		25638			27046	27587	070/2		30824			31270		36946	36947				25564	25585	25923	25994	26292	26560	26632	28633	26744	26748	27798
	Exen SEQ ID NO:	19235	23394				1	14357	14857	15207	18135	18145	18254	18347	18362	19347	23686	23686	24686	24736	24899	12927	12027	13289	13368	13622	13899	13965	13965	14071	14073	15061
	Probe SEQ ID NO:	6488	10703	185	185	315	316	1610	2126	2490	5332	5342	5455	2550	5565	888	11014	11014	12233	12314	12571	Ē	ξ	2 05	586	852	1144	1215	1215	1322	1324	2337

Page 410 of 536 Table 4 Single Exon Probes Expressed in Brain

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and and and	Top Hit Database Source	F	LN LN	FOT HIMAN	TOT WALAN		Z	둗	Z	Z	NT	ΙZ		Ł	5	L	N	Ę	Į.	E L	5 5	2 1	- L	2 1	2 12	114	1	2	INC.	둫	5			Z	IN.	EST HUMAN
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	Most Similar (Top) Hit BLAST E	1 0E-03/	1 05 03 /	10.1	1.05	1.05-63	1.0E-93 D87875.	1.05-93	1.05-93	1.0E-83 U78509.	1.0E-83	1 OF 93		1.0E-83	1.0E-83	1.0E-03	1.0E-83	10F-03	4 OF CO X40483		-								1.0E-83	70500						_]
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Page 411 of 536 Table 4 Single Exon Probes Expressed in Brain

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Top Hit Descriptor	og3d05.s1 Soares, total fetus, Nb2t/F8_9w Homo sepiens cDNA clone IMAGE:1023308 3	BUZNEZIONE INC. CONT. DILINI TIGINO SENIO CONT. CONT. CONT. (MAGE: 116239 3)	ydddodd 81 Coares roug mai gueel i i'w i'r eapinis Con y coares rough and a coares	Home saprens mixture for Nativos/ process, present control (CPSF1), mRNA	HOMO SECRETE CREATER and purposes yourseless of s	Home septens ribosome protein LZ/ intruck, companie dus	Hamb separate property involved the separate control of MAGE:27016793'	MOSTICAL SOURCE INT. T. CRC ST Homo septems CDNA clone (MAGE:2701679.3)	Allosi I Z.K.I. COAP Brn52 Homo septens cDNA clone IMAGE:2259403 3' similar to TR:Q15265 Q15265	PROTEIN TYROSINE PHOSPHATASE;	Hamo seplens solute cerrier family 22 (organic cetton transporter), member 1-like (SLC22A1L), mRNA	Homo explens solute certier family 22 (organic cation transporter), member 1-life (SLC22A1L), mRNA	Homo sepiens huntingth (HD) gene, exan 37	Homo saplens hypothetical protein FLJ12455 (FLJ12455), mRNA	Homo sapiens ASHZL gene, complete cds, similar to Drosophila ashz gene	Hamo sapiens complement component 5 (C3) mrdNA	Home sepiens dysteine-rich repeat-containing protein 332 proteins on, united contains of	HONO SECURITY STATE THAT INSTITUTE PROSESS OF THE STAT	Home septens ETA bridge process poor (ET 500) militaria	Turno espane beneath betterming factor (HLF), mRNA	TANGORNA TO Some total fetus Nb2HF8 9w Homo sapiens cDNA clone IMAGE:774782 6	Homo septems sinc finder protein 277 (ZNF277), mRNA	Homo septementally for MEGF2, partial ods	Homo serviens chromosome 21 open reading frame 18 (C210RF18), mRNA	Homo services personal cell adhesion molecule (NRCAM) mRNA	Lump serviers materialhein albha 13 (PCDH-albha13) mRNA, complete cds	Trans environ mona for KTA And TO protein Derife cls	Total September 12 Tables of September 12	Home enters arms transcot of sweetige (ATSV) mRNA	Limmorkity framed form 1 tecking leucine zioner mRNA, complete de	LIMINAL OLD COLORS
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Most Similar (Top) Hit BLAST E Value	5.0E-84 Al015900.1	5.0E-94 BF529115.	5.0E-04 T89398.1	5.0E-04 D25217.2	5.0E-94	4.0E-84 L05094.1	4.0E-94	4.0E-94	4.0E-94 AW197851	4.0E-94 AI591312	4.0E- 0 4	4.05.04	4 OF DAII 27398 1	4 OF 94	3.0E-04/	3.0E-04	3.0E-94 AF167706	3.0E-04 AF16770	3.0E-04	3.0E-04	3.0E-94	3.0E-04 AA46480	3.0E-04	3.0E-84 ABUT 103	3.0E-64						
Expression Signal	128	1.11	8.89	1.5	1.86	2.64	0.82	1.38	1.38	2.87	1.82	5	4	2 7	44.	0.88	1.19	1.10	2.61					1.3							1.94
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| Top Hit Descriptor | | W30h11x1 NC_CGAP_Co16 Homo sepiens dDNA done IMAGE:2391813 3' | WI30h11 X1 NCI_CGAP_Co18 Home septems d.N.N.A. drone INAIGE.2391613 3 | 601175762F1 NIH MGC 17 Hamp septens CDNA clane IMAGE:3531038 5 | ANTITIONET NIH MAC 18 Homo sections CDNA clone IMAGE:3352559 5 | PANANABOREN NIH MIGG. 16 Homo septems cDNA clone IMAGE:3352559 5

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saplens cDNA clone IMAGE:2340606 3' similar to gb:K00558 | TUBULIN ALPHA-1 CHAIN (HUMAN); | wedge04.x1 NCI_CGAP_Luz4 Homo sepiens cDNA clone IMAGE:2340606 3' similar to go://uu3od | 1 UBULIN ALTHA-1 Chain (Homely), | Hamp septemb Arroya 1 and grace processes and the september of the
september of the septemb | Home separate processome (process), menopelin) 26S subunit, non-ATP ase, 11 (PSMD11), mRNA | Homo septens processure (programs, mean spens) |
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										5			T			Γ		Γ				1						IMP3¥			34	57
	Top Hit Descriptor	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds	Homo sepiens KIAA0255 gene product (KIAA0255), mRNA	Homo seplens KIAA0255 gene product (KIAA0255), mRNA	Homo sepiens proline dehydrogenese (proline oxidase) (PRODH) mRNA	Homo septions mRNA for KIAA1395 protein, pertiel cds	Homo sepiens early growth response 2 (Krac-20 (Drosophile) homolog) (EGR2), mRNA	Homo seplens developmental arteries and neural crest EGF-like protein mRNA, complete cds	Homo sepiens HOF-binding transcription factor Zhangfei (ZF), mRNA	zu84b01.s1 Soeres_testis_NHT Home sapiens cDNA clone IMAGE:7446493' similar to contains L1.t1 L1 repetitive element;	Homo septens DNA for amyloid precursor protein, complete cds	Homo saciens DNA for amyloid precursor protein, complete cds	Homo sepiens Ly-6-like protein (CD59) mRNA, complete cds	Homo sepiens chromosome 21 segment HS210046	HTM1-288F HTM1 Homo sepiens cONA	602071146F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4214147 5	Homo sapiens dedicator of cyto-kinesis 1 (DOCK1) mRNA	EST370191 MAGE resequences, MAGE Homo sapiens cONA	EST370191 MAGE resequences, MAGE Homo sepiens cDNA	aus3b08.x1 Sohneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783799 3' similar to TR-080463 060463 TYPE-2 PHOSPHATIDIC ACID PHOSPHOHYDROLASE. [1]:	aus3b08.x1 Schneider felal brain 00004 Homo sapiens cDNA clone IMAGE:2783799 3' similar to TR-Oenues Oenues TVDE-2 PHOSDUATION ACID PUNCEDIOLYMBOLI ACID 1	Homo saplens KIAA0763 pene broduct (KIAA0763), mRNA	Homo septens KIAA0783 gene product (KIAA0763), mRNA	801845212F1 NIH_MGC_55 Hamo explens cDNA done IMAGE:4070451 6	yp87g11.r1 Scares fetal liver spleen 1NFLS Homo septens cDNA clone IMAGE:194488 5	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA	Homo septens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflemmatory) (TIMPS), mRNA	601312161F1 NIH_MGC_44 Homo saplens cDNA clone IMAGE:3858862 5	Homo sepiens G protein-coupled receptor 19 (GPR19) mRNA	Homo sepiens G protein-coupled receptor 19 (GPR19) mRNA	
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Page 414 of 536 Table 4 Single Exon Probes Expressed in Brain

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	Top Hit Descriptor	Homo sapiens glutathione S-transferese theta 2 (GSTT2) and glutathione S-transferese under 1 (GSTT1)	Home sentens alvaba cleavade system protein H (aminometry carrier) (GCSH) mRNA	Trong segments grown mRNA combine ods	Home septicals compared myresin-15 (LOC\$1168), mRNA	Homo septens of contracting the septens of the sept	Homo sapiens unconversionis inyosis-10 (LOCO 1100), militaria	Homo sepiens mRNA for KIAA1300 protein, per use cons. MAGE-1880646 3' striller to WP:T23G7.4	qm01c02.x1 Soares_NhttMru_S1 north septents county down the CE03705;	Homo sepiens hypothetical protein (Hoszczany), mnunh	Homo seplens KlaAutis/ gete product (numbers)	Hamp seplens CGL48 protein (LOCSTURO), minutes	Homo saplens CGI-48 protein (LOCOTUBO), Illinus (Locatidass A) 2 (ACE2), mRNA	Home septens angiocensm I converting or Lynne (hopers) representations A) 2 (ACE2), mRNA	Home sapiens angiotensm I converting enzyma (popular proposer)	Homo saplens membrane protein, paintitoylated 3 (MAGUK p55 subfamily member 3) (MPP3), mRNA	Human musclo-type phosphofructokinase (PFK-M) gene, exon / Human musclo-type phosphofructokinase (PFK-M) gene, exon /	Homo seplens transcription record 4, memory, in 150, memory handle number factor (TCE2), mRNA	Home septens transcription rector 4, respectively, LT-boy, respectively.	Home septens called option from y charter of contract of the called the calle	TOTIC SECTION (NON) IN THE CONTRACT (NON) THE CONTRACT (NON)	Home september KIAA 1045 partein (KIAA 1065), mRNA	Lower services have morphosenetic protein receptor, type IA (BMPR1A) mRNA	THOUS BEHALL WIND HIS PLANTED THE KIND OF THE WAY	House sections Kid Andres Gene broduct (KIAA0783), mRNA	Lives contact ministries Strensferase their 2 (GSTT2) and guitathione S-transferase their 1 (GSTT1)	genes, complete cds	Homo sapiers adenylosuccinate lyase (ADSL), mRNA	223h04.rd Sogres overy furnar NbHOT Hamp septens cDNA clane IMAGE:714007 o samilier to	TR:G1067084 G1067084 F55H2.6; -723h04.rd Sceres overy tumor NbHOT Homo septens cDNA plane IMAGE:714007.5 similar to	TR:G1087084 G1067084 F55H2.6;
Carl July Bull I	Top Hit Deterbese Source		Z	ī	IN	-N	7	NT	EST_HUMAN	NT	뇐	NT.	N	Z	INT	<u> </u>	Z	LN.	NT	Ę	L _N	Į.	Į.	Z	LV.	Ž	뒫	¥		EST_HUMAN	EST_HUMAN
5	Top Hit Acession No.		8.1	4768423	F015452.1	7705000 NT	7705900 NT	2.0E-95 AB037807.1	(290284.1	7857185 NT	T881979 NT	7705784 NT	7705764 NT	11225608 NT	11225808 NT	TN 525883 NT	M50724.1	11427182 NT	11427182 NT		11435773 NT	11421796 NT	11434330 NT	4757853 NT	7662289 NT	7862289 NT	AF240786.1			1.0E-95 AA284651.1	AA284651.1
	Most Similar (Top) Hit T BLAST E Value		2.0E-96 AF24078	2.0E-95	2.0E-95 AF01545	2.0E-95	2.0E-95	2.0E-95	2.0E-95 AI29026	2.0E-95	20E-05	2.0E-05	20E-95	2.0E-05	2.0E-95	2.05.05	2.0E-05 M50724		_							2.0€-95	2 OF OS AF2407				1.0E-95 AA2846
	Expression Signal		3.28	1.85	1.96	3.07	3.07	18	8	1.32	272	424	421	127	1.27	0.4				245		1.06			3.02					8.41	8.41
	ORF SEQ ID NO:		27925	27973			1										3170				32817		3 36142	7 36557	37620	5 37621			30894	31226	5 31227
	SEO ID		15186	15233	15918	16307	16307	46358	46405	47067	1777	48402			L		18446	┸	L		1_	1_	L	23317	l_	L	Ì _	_ [24980	18325	18325
	Probe SEQ ID NO:		2468	2517	3155	3552	35.62	2002		3/32	2707	0100	1002	5844 F844	152		100 P		800	6476	9999	24	10280	10624	11700	11700		12289	1269	5527	6527

Page 415 of 536 Table 4 Single Exon Probes Expressed in Brain

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	Top Hit Descriptor	P. P. ENIANG. 2008/0014-011 FN0019 Hamp septems CDNA	President And And FM0019 Home serions cDNA	ANGELESTING INC. 72 Home services about date IMAGE 3922423 5	60145/25271 NIT MOO, 12 July Plant Socials CDNA	PMU-LIUUTB-USCOOLEGUE II US II II II II II II II II II II II II II	HOTIO SEPRETE CIT ULICALITIE EL LES PARTIENTES PROPINIONES S'ENC	הוות של על של של היא לי היא היא היא היא היא היא היא היא היא הי	Homo sapiens sistytransferase 6 (N-scetyfacosaminide apha 2,3 cialytransferase) (SIAT6), mRNA	Homo septens KilAAU/65 gare product (Nirvay) (V.), IIII de la la la la la la la la la la la la la	Homo septems Kladuros gene product (Nurse), intrody	Homo septens myosin, nestry polytopiece 4, snesom money, many	Home septens NIAAU/03 gens product (Nixayo), in dex	Homo sapiens KIAAU/63 gamp product (Nahata 20), in a con-	HOMO SEPRETS TREATY TO ALPHANE TO PROME OR	HOME SEPTEMBER INVIVATION NATIONAL PROCESSION SEPTEMBER 1998	Hamo septens in the Array of Conference of Conference (A) mena (PDE6A), mRNA	TOTIO SELECTION INTO PARTICIONAL PRIME & (7) (PARTIE)	H. septents Liver for increasing wasses type : (/ / / / / / / / / / / / / / / / / /	Train segments (VOS) process (VOS) and the control of (AKAP1), mRNA	Home segments A Masse (PRKA) anchor protein 1 (AKAP1), mRNA	Liven content mENA for KIAA0900 profes ds	Lamb emine mRNA for 14.3-3cmme, complete cds	Himman fune IV collapsenase (Q.G4B) gene, evon 5	Tulimen tyre IV collapenese (CLG4B) dene, exon 5	Limitary (14 Ant 75 care product (KIAA0175), mRNA	A87112 rt Sonne fabilities adden 1NRS Homo explore cDNA done INAGE:212327 5	The service stronger suitable profescious 4 (meterome essociated) (CSPG4), mRNA	Lives seviere chromosome 21 segment HS21C048	Thoracter Control of the Control of				JAGE:2819351 5	
South South I I I I I I I I I I I I I I I I I I I	Top Hit Deterbese Source	Т	1	Т	Т	HOMAN	Ę	Z	Ę	NT	NT	Z	Z	Ž	L	Z			<u>ال</u> ا	Z	Z	Į.	Į.	Į.	Z !	Ž!	I١	EST HUMAN	Z	IN TOL	NAME OF THE PARTY	ESI HUMAN	HOLL HOMAN	EST HOMAN	LONGIA COMPANY
2	Top Hit Acession No.		F370000.1	1.0E-05 BF370000.1	E807259.1	8.0E-96 AW836047.1	7.0E-96 AF231920.1	126873.1	11422642 NT	7862289 NT	7862289 NT	8923939 NT	7862289 NT	7662289 NT	AB032998.1	5.0E-08 AB032998.1		11416767	X60812.1		11424300 NT	11424399INI	AB023177.1	5.0E-96 AB024334.1	M68347.1	M68347.1	N8/6199/	9988E		AL 163248.2	BE148074.1	BF369731.1	BF369731.1	2.0E-06 AV689461.1	2.0E-96 AW 249440.1
	Most Similar (Top) Hit BLAST E		1.0E-95 BF370000	1.0E-05 B	9.0E-96 BE80725	8.0E-96	7.0E-96	6.0E-96 M26873.1	6.0E-86	8.0E-98	8.0E-98	8.0E-96	8.0E-08	6.0E-96	5.0E-06 AB03299	5.0E-08	6.0E-96 AB03299	5.0E-96	5.0E-96 X60812.	6.0E-08 AF1497	5.0E-96	5.0E-90	6.0E-06 AB0231	5.0E-98	5.0E-96 Md8347	5.0E-98 M68347	5.0E-96	3.0E-06 H08056	2.0E-96		}				20E-80
	Expression Signed	-	4.3	4.3	1.49	277	0.74	20.13	0.74	3.36	3.36	205	1.83	1.83	2.74	4.08	4.08	1.43	1.30	1.15	5.18	5.18	0.71	1.98	1.35	1.35		12.32	4.24					5.63	281
-	ORF SEQ ID NO:		33175	33176	33920		29278	28886	31258						25754	26290				32324	32639	32640					37715						2 33121		
	Econ SEQ ID NO:		20091	20091	20788	18223	10639	16232	18349	24134	24134	24183	1	_	L	<u></u>	ì	15336	1 _	19318	<u>L</u>	19601			20700	20700	24383	16908	13191	13504	17440	20042	20042		24543
	Probe SEQ ID NO:		7414	7414	8	5424	3880	3478	5557	11534	11534	11584	11789	11780	312	822	8	2624	4846	6553	9884	6684	6923	7415	8005	8005	11703	4168	406	730	4708	7361	7361	8879	12009

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<i>y</i> 0	113/2/3	_	7	т-	т-	т-	•	т	Ţ		_	т—	_	1	_	_		_	1	ı JE		-	. 1	-	<u> </u>	-	170	50	1/\	7/1	0 (7. 5	
Single Exon Probes Expressed in Brain	Top Hit Descriptor	Homo sepiens neuronal call adheaton molecule (NRCAM) mRNA	Homo sepiens neuronal cell adhesion motecule (NRCAM) mRNA	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes	EST367124 MAGE resequences, MAGC Homo sepiens oDNA	EST367124 MAGE resequences, MAGC Homo sepiens cDNA	Fells catus superfast myosin heavy chain (sklyHC) mRNA, complete cds	Homo sepiens transient receptor potential channel 5 (TRPC5), mRNA	Homo sepiens guenine nucleotide exchange factor for Rap1 (KIAA0277), mRNA	Homo sepiens HSPC144 protein (HSPC144), mRNA	Homo espiens HSPC144 protein (HSPC144), mRNA	Homo septens similar to ectonuclectide pyrophosphatase/phosphodiesterase 3 (H. septens) (LOC63214), mRNA	Homo explens secretory pathway component Sec31B-1 mRNA, attenuatively spliced, complete cds	Homo sepiens mRNA for KIAA1280 protein, partitel cds	Homo saplens mRNA for KIAA1290 protein, pertial cds	Homo sepiens neuronal cell adhesion molecule (NRCAM) mRNA	Homo sepiens neuronal cell adheeion molecule (NRCAM) mRNA	IL5-HT0117-011089-004-D07 HT0117 Homo sepiens cDNA	601440317F1 NIH_MGC_72 Homo septens oDNA done IMAGE:3925133 5	801440317F1 NIH_MGC_72 Homo septems cDNA clone IMAGE:3825133 5	EST22672 Adipose tissue, white II Homo sepiens cDNA 51 end	EST22872 Adipose tissue, white II Hamo saplens cDNA 5' and	Human mRNA for alpha-actinin	DKFZp434N0323_r1 434 (synonym: https://domo sepiens.cDNA.clone.DKFZp434N0323 5	zv67e12.s1 Sogres_NiNHMPu_S1 Homo sapiens cDNA clone IMAGE:767758 3' skriler to TR:G1304125	RC0-BT0812-250900-032-609 BT0812 Homo sepiens cDNA	MR0-HT0241-150500-010-b02 HT0241 Homo egolens cDNA	MR0-HT0241-150500-010-b02 HT0241 Homo septiens cDNA				Homo saplens brefeldin A-inhibited guenine nucleotide-exchange protein 2 (BIG2), mRNA	
gle Exon Prob	Top Hit Darbbase Source	N	NT	N.	EST_HUMAN	EST_HUMAN	Į.	Ę	LN L	LN	N			¥	Ę	Ę	Ŀ	EST_HUMAN	HUMAN			EST HUMAN		EST_HUMAN		EST HUMAN	1	Г	EST_HUMAN				
ain a	Top Hit Acession No.	4826863 NT	4826863 NT	/18800.1	1.0E-96 AW955054.1	1.0E-86 AW855054.1	J51472.2	6912735 NT	6912455 NT	7861803 NT	7661803 NT	11419429 NT	1.0E-06 AF274863.1		6.1	4826863 NT	4826863 NT	5.0	2.1	2.1	1	2.1		4.2	5 0F.07 AA418028 1	2.1	7.1		4.0E-97 BE004436.1		4.0E-97 AB030176.1	5453572 NT	
	Most Similar (Top) Hit BLAST E Value	1.0E-98	1.0E-96	1.0E-06 Y18900.	1.0E-96/	1.0E-96/	1.0E-98 U51472	1.0E-98	1.0E-96	1.0E-96	1.0E-96	1.05-96	1.0E-06/	1.0E-86 A	1.0E-98 AB03311	1.05-96	1.0E-96	6.0E-07 BE14184	6.0E-97 BE89901	6.0E-97 BE89801	6.0E-97	6.0E-07	6.0E-97 X15804.1	5.0E-97 AL04331	A 05.07	5.0E-07 BF15401	5.0E-07 BE14850	5.0E-97	4.0E-97 B	4.0E-07 AB03017	4.0E-97	4.0E-97	
	Expression Signal	2.6	2.0	3.38	2.58	2.56	1.08	1.3	0.67	1.24	1.24	20.86	200	1.24	1.24	1.97	1.97	2.6	0.69	0.00	0.57	0.67	1.46	1.91	11 73	2.66	1.98	1.98	1.59	1.04	1.04	1.07	
	ORF SEQ ID NO:	26016	28017	28074	27216		2772		32447		33830	34450		35924	35925		28017							33739	33.940	35412	37441	37442	26349	26359	26360	27349	
	Exon SEQ ID NO:	Ш	13386	13433	14516		15527	17946	19431	20805	20805	21308	<u> </u>		70/22	13386	13386	20131			23143	23143	23969	20608	20736	TZZZZ	24135	24135	13685	13695	13695	14840	
	Probe SEG ID NO:	809	809	929	1774	1774	2262	6989	6946	8111	8111	8616	8749	10059	10059	11999	11999	7457	8832	8832	10497	10407	11382	7913	8042	9574	11535	11535	918	878	88	1903	

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Single Exon Probes Expressed in Diam	Top HR Descriptor	Homo sacians apolipoprotein H (beta-2-ghooprotein I) (APOH) mRNA	Limited in the complete modulatory subunit 2A (INR2A) mRNA; complete ods	Turner in the light of the secondary modulatory expunit 2A (INNR2A) mRNA, complete cds	numentations of the Control of the C	Homo eaplette minny for Carly as white 2. Carly market both form	Homo sapiens mixture for detacks against 1, 100 and 1,	Homo saprens ingese III, DAY, ALT - Legical Control (2007)	Homo segled a Cystic tortices we retreated the contraction of the cont	Homo septems terminin, etiphe 2 (mercent, congenius miscone appropriate property) (mRNA	Homo sapients Veto aven eacours (Journal of National Veto 17 17 18 18 18 18 18 18 18 18 18 18 18 18 18	Homo esplens cybodrome retor, subsetting the cybodrome retoring the	Homo septens mitda for furduous protections	Homo sapiens mRNA for KIAA0594 procesn, per use cue	Homo septens AAL receptor (yourse tenesed (your,) server an install MRNA	Homo eaplens AXL receptor (yrosine tunese (yvv.), salekvity raman, yrosine salekvity taken i namana i	Home saplens mitthy, similar to rat injuring and control of	Home seplens mRNA for KIAA1290 protein, parties cus	Homo sapiens mRNA for KIAA1230 protein, perus cus	Tomo saptens (1. set) University and set of the set of	Home saplens mrknA for KlAA11/2 promit, parus was	Homo sepiens amyold beta (A4) precursor protein (protesse nedn-II, Alzhetmer disease) (APP), mRNA	Homo sapiens amykold beta (A4) precursor protein (protesse nexin-II, Abrielmer disease) (APP), mRNA	Homo sablens N-myo (and STAT) Interactor (NMI), mRNA	Human beta-ortme edaptin (BAMZ2) gene, exon 7	Homo explens percentrin (PCNT) mRNA	Homo sendens automotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA	ANY 2005 NET NIH MGC 63 Homo septens CDNA clone IMAGE: 3681621 5	DOO LITERS 24 100 011 - 110 258 Home septens QNA	TOWN LIFTONS 24 4 4 CO. A 1 LOSS Homo septens CDNA	Assess at Some datal Name and American ANET S Homo sections CDNA clone IMAGE: 129134 3'	MOSCOCISI COMBON SPECIAL PROPERTY (KIAAOGAD) mRNA	Trouto sections KitAn648 cene product (KIAA0649), mRNA	
e Exon Floor	Top Hit Database Source					Ę	Ę	5	Ę	N	Į	NT	Z	Ľ.	Į,	Į.	N	IN	NT	NT	Į,	NT	Į.	150	5	15	1	TOUR LOUIS	TS LOWER	LOWER LOWER	EST HUMAN	EST HUMAN	IN I	<u> </u>
Suis	Top Hit Acession No.	Tiviacorasi	201.00				11330.2	7710125 NT	11422155 NT	4557708 NT	11421793 NT	11423233 NT	4B011168.1	4B011166.1	11863122 NT	11863122 NT	4.0E-97 AB042557.1	4.0E-07 AB033116.1		11418318 NT	AB032998.1	4502186 NT	TN 30015084	TARRES NT	٠,	TA 94.479 NT	2746	450347UN	1.0E-97 BE568486.1	1.0E-97 AW378976.1	1.0E-07 AW379976.1	R10887		NI 167124LL
	Most Similar (Top) Hit BLAST E Value		4.05-07	4.0E-07	4.0E-97 U09002.1	4.0E-97 Y11339.2	4.0E-07 Y11339.2	4.0E-97	4.0E-97	4.0E-97	4.0E-97	4.0E-07	4.0E-07 AB01116	4.0E-97 AB01116	4.0E-97	4.0E-97	4.0E-97	4.0E-97	4.0E-07 AB0331	4.0E-97	3.0E-97 AB0329	3.0E- 0 7	20 E 07	3.05	3.0E-87	3.05-07	3.05-07	1.0E-97	1.0E-67	1.0E-07	1.0E-07	1.0E-97 R10887		1.0E-07
	Expression Signal		0.61	0.95	0.95	6.47	6.47	=	1.05	0.57	2.63	0.75	123	1.23	1.88	1.88	3.61	183	1.62	7.78	1.14	29.83	8	3 3	2	80			2.48	1.18	1.16	1.6		3.44
	ORF SEQ ID NO:		31172	31482	31483	32590	32591	32703	32408	33863	34087							l		١	25685								19028	33534	33535			30239
	Esch SEQ ID		18277	18556	18556	19559	19559	19857	19450	1_		L	L	L	1	L	L	1.	1_	L	1_	L					16016	17461	19103	20415	1	Ι.	I_	L. 1
	Probe SEQ ID NO:		5478	5765	5765	67725	6725	692	800	8038	8256	RA18	24.7	9147	1118	11118	44445	7777	14415	42,485	238	7,8	[200	1423	2440	3254	4720	8333	9344	48	998	1000	10804

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מושכ ביינון וכחס ביינון המווו	Top Hit Descriptor	nk29g02.s1 NCI_CGAP_Co11 Homo septens cDNA clane IMAGE:1014862.31	Homo septens ribosomel protein S15 (RPS15), mRNA	Homo saciene ribosomal protein S15 (RPS15), mRNA	PM4-BT0724-010400-008-a12 BT0724 Homo seciens cDNA	Homo septens cat eye syndrone critical region dene 1 (CECR1), mRNA	Homo seplens CLDN12 gene for claudin-12	Homo septens feucyf-fRNA synthetase, mitochondrial (KIAA0028), mRNA	Homo septens A kinase (PRKA) enchor protein (votiso) 9 (AKAP9), mRNA	Homo sepiens death-especiated protein (DAP), mRNA	Homo sepiens death-associated protein (DAP), mRNA	Human mRNA for amyloid A4(751) protein	Homo sapiens succinate-CoA Ilgase, GDP-forming, alpha subunit (SLIC) (31) mRNA	Homo sepiene mRNA for KIAA1365 protein, partial cds	Homo septems 17-bette-hydroxysteroid dehydrocenses IV (HSD1784) neme sexus 8	Homo saciens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a	member 3 (SMARCA3) mRNA	Homo septens SWUSNF releated, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA	Homo seplens inceitor bolivobranhaira 1 - Acceptatissa (INDPA) seesa accessivata acta	Homo sapiens mRNA for KIAA1005 protein, pertial cds	Homo sepiens mRNA for KIAA1005 protein, pertital cds	Homo expiens mitogen-ectivated protein kinase kinase kinase 7 (MAP3K7), mRNA	Homo septens mRNA for MEGF8, pertial cds	Homo septems mRNA for MEGF8, partial cds	Homo septens HPAD-colony10 mRNA for peptidylarginine deiminase type I, complete cds	Homo eeplens PMSZL16 mRNA, perdel ods	Homo sapiens PMS2L18 mRNA, pertiel cds	Human mitochondrial creetine kinasia (CKOAT) gene, complete ods	601507503F1 NIH_MGC_71 Homo eaplene cDNA dane IMAGE:3909097 6	AJ403124 3.4 (downreguleted in larynx carchnoma) Homo sapiens cDNA clone is	Homo saplens mRNA for KIAA0707 protein, partial cds	7B18H01 Chromosome 7 Fetal Brain cDNA Library Homo espiens cDNA clone 7B18H01	Homo sepiens activator of S phase kinase (ASK), mRNA	Homo saplens activator of S phase kinase (ASK), mRNA
מון וווסאיין סול	Top Hit Detabase Source	EST HUMAN	N.	N-	EST HUMAN	NT.	NT	NT	Z	L	Ę	N	Ļ	NT	FZ		TA.	Ę	N.	¥	Ę			Ā			LΝ			EST HUMAN	Г	EST_HUMAN		
	Top Hit Acession No.	AA553761.1	11428272 NT	11426272 NT	BE090973.1	8393092 NT		7861871	11419408 NT	4758119 NT	4758119 NT	-	11321580 NT	AB037786.1	1,00		4507070 NT	4507070		21	21	11418982 NT	11.1	11.1		7.1	7.1				3.0E-96 AB014607.1	3.0E-98 AA077498.1	11419210 NT	11419210 NT
	Most Similar (Top) Hit BLAST E Value	1.0E-97 AA5537	1.0E-97	1.0E-97	9.0E-88 BE0909	9.0E-98	9.0E-98 AJ2507	9.0E-98	9.0E-98	9.0E-98	90-30.G	9.0E-98 X06989	9.0E-98	9.0E-98 AB0377	9.0E-98 AF0577		9.0E-98	9.0E-88	9.0E-08 AF1413;	9.0E-98 AB0232	9.0E-98 AB023Z	9.0E-08	9.0E-08	9.0E-98 AB0115	8.0E-08 AB0337	8.0E-08	8.0E-98 AB01700	8.0E-98 J04409.	5.0E-08 BE88587	3.0E-08	3.0E-98	3.0E-98	3.0E-88	3.0E-98
	Expression Signal	2.03	14.01	14:01	3.52	1.12	0.71	0.67	90	4.70	4.70	6.28	1.5	1.50	96.0		1.14	1.14	0.45	263	263	1.30	1.30	1.30	0.92	2.7	2.7	6.80	0.89	1.14	0.99	2.9	1.0	1.9
	ORF SEQ ID NO:	37235										34854	34977	35027		_	35190	35191	36026	36856			37776	37777	28774	27161	27162	29166	31735	27638	28067		32576	32577
	Exen SEQ ID NO:	23941		23212							20520	21704	21812	21962	21812		22021	22021	22808	23606	23906	23676	24434	24434	4099	14462	14482	16527	18772	14905	15324	15458	19547	19547
	Prabe SEQ ID NO:	11280	11445	11445	881	1253	02210	7190	7286	7825	7825	9014	9124	9192	9238		8287	8267	10180	10926	10926	1004	11850	185	1351		1718	3775	5994	2178	2613	2753	6847	6847

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Table 4
Single Exon Probes Expressed

		Т	T	Ť	Т	7	Т	Т	7	_	Т	_	7	_	Τ-	_	-	—	7	F	ካቻ	7.	1	7	H	#	_	-6"		711	- 18"1 1
Single Exon Probes Expressed in Brain	Top Hit Descriptor	Vol7g09,r1 Soeres adult brain N255HB557 Homo seniens cDNA cirra IMAGE 472220 F	Homo sepiens uncharacterized bone marrow protein RIAPRO (BLATRO) - MONA	AJ403124 3.4 (downregulated in langua cardinana) Homo sentense ciDNA chana is	AJ403124 3.4 (downrequiated in larvix cardinana) Homo seniens cDNA clove is	601673686F1 NIH MGC 21 Home sapiens CDNA clone IMAGE:3956517 51	Hunen funerase precuracy (FH) mRNA nuclear pens expeditor mito-bondries protein	Homo seplens (huc) mRNA, complete cds	801297955F1 NIH MGC 19 Hamo septems cDNA clone IMAGE:3828213 5	Homo seplens Ran GTPase activating protein 1 (RANGAP1) mRNA	601172658F1 NIH MGC 17 Hamo sepiens cDNA clane IMAGE:3528134 5	Homo septens chromosome 21 segment HS21C002	Homo septens potaseitum channel subunit (HERG-3) mRNA, complete cds	Homo sepiens fatty-ecid-Coenzyme A ligase, long-chain 4 (FACL4) mRNA	Homo saplens attractin precursor (ATRN) gene, expn 16	Homo sapiens attractin precursor (ATRN) gene, exon 16	Homo saplens protein tyrosine kinase 2 beta (PTK2B) mRNA	Homo septens PDZ dometh-containing guentine nucleotide exchange factor ((LOC51735), mRNA	Homo sepiene phosphatidylinostici 3-kinase, olase 2, alpha polypopiide (Pilk3C2A) mRNA	Homo septens hypothetical protein FL/10488 (FL/10488), mRNA	Homo saplens hypothetical protein FL/10488 (FL/10488), mRNA	Homo seplens SH3-domain GRB2-Ilike 2 (SH3GL2), mRNA	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA	Homo septens NKAT4b mRNA, complete cds	Homo septens NKAT4b mRNA, complete cds	H.esplene arginase gene excr 3 (EC 3.5.3.1)	Homo suplems AlM-1 protein (LOC51151), mRNA	Human cytochrome P450 (CYP2A13) gene, complete cds	w36b04.x1 NCI_CGAP_Uti Homo septens cDNA done IMAGE:2281743 3' similar to SW:RL2B_HUMAN P20316 60S RIBOSOMAL PROTEIN 1.23A.	PMD-BN0065-100300-001-c06 BN0065 Homo sepierts cDNA	y/23/05.r1 Sogres fetal liver spleen 1NFLS Homo sepiens cDNA clone IMAGE:243585 5's similar to PR:S54204 S54204 fibosomal profein L29 - human;
gle Exon Pro	Top Hit Detabase Source	EST HUMAN	Į Į	EST HUMAN	EST HUMAN	EST HUMAN	NT	LX.	EST HUMAN		EST HUMAN	L	Z	N	IN.	١	Ę	N	NT	TN	NT	거	MT	NT	M	M	לין	Z	EST HUMAN	EST_HUMAN	EST_HUMAN
S S	Top Hit Acesson No.	3.0E-98 H46898.1	N 9602268	AJ40312	3.0E-98 AJ403124.1	3.0E-88 BE900454.1	3.0E-98 U69309.1	_	197	11418177	_	22	7.1	4758331 NT	12.1	12.1	4758975 NT	7706512 NT	4505798 NT	11431271 NT	11431271 NT	11428813 NT	1428813				7705868 NT	1	14	==	1
	Most Similar (Top) Hit BLAST E Veitue	3.05-88	3.0E-88	3.0E-08	3.0E-08	3.0E-98	3.0E-08	3.0E-88 L28405.	3.0E-98	3.0E-98	2.05-98	2.0E-98 AL1632	2.0E-08 AF03290	2.0E-88	2.0E-98 AF21890	2.0E-08 AF21800	2.0E-98	2.0E-88	2.0E-08	2.0E-08	2.0E-98	2.0E-08	2.0E-08	2.0E-98 L79996.1	2.0E-08 L78666.	2.0E-08 X12664.1	2.0E-08	2.0E-98 U22028.	1.0E-98 A1862007	1.0E-86	1.0E-08 N40818.
	Expression Signal	2.73	0.48	1.42	1.42	0.96	4.11	1.56	1.47	3.56	2.66	1.53	0.8	3.21	1.34	1.34	1.39	4.03	1.15	1.07	1.07	2	4.94	0.58	98.0	1.48	1.37	1.42	16.4	2.12	11.24
	ORF SEQ ID NO:	34486			35840	36233	36790	37788			27531			ļ	30129	30130	30466	30757	32329	33286	33287	34342	34343	34421	34422	35290		37103	25820	25871	7227
	SEQ ID NO:	21341	21888	22434		23017	23552			25013	14803	14959				17508	17849		1		20194	21198	2. 88	21283	21283	22115	22080	23822	13181	13228	14520
	Probe SEQ ID NO:	8640	9197	9783	9783	10371	10872	11863	12668	12751	2071	2231	4284	4306	4776	4778	5131	5292	6557	7523	7523	800	8208	200	800	25	10313	11155	396	442	1789

PCT/US01/00667

Page 420 of 536 Table 4 Single Exon Probes Expressed in Brain

			_	_	_	Ψ-		_	_	_			_		~	1	_	-1	74		Ŧ	7	₩	戶	Т	E		47	11		q ₁	1	5 7
	Top Hit Descriptor	299809.11 Strategene muscle 837209 Homo sepiens cDNA clone IMAGE:628240 5' stimilar to TR:C3806362.	COCONCE AND AND ALL HOMO Replace CONA close IMAGE:3800692 5	0012048001 INIT MACCHINIC STATE CONTRACTOR IN CENTRAL CONTRACTOR IN CENTRAL CONTRACTOR IN CENTRAL CONTRACTOR IN CENTRAL CONTRACTOR IN CONTRACT	601284986F1 NIH JAGC 44 Franco saparas curas intra-	Homo septens beta-tubulin mkna, complete cus	Homo sepiens beta-tubulin mRNA, complete cds	QV-8T073-191298-012 BT073 Homo septems cDNA	QV-BT073-191208-012 BT073 Homo sepiens CDNA	EST380711 MAGE resequences, MAGJ Homo separats curity	Imigino7 x1 NCI_CGAP_Bm25 Homo septens cDNA clone IMAGE:2165421 3 Binier to 5 W. DID_1 TOWN V. P55657 BH3 NTERACTING DOMAIN DEATH AGONIST;	Imb8h07.xf NCI_CGAP_Bm26 Hamo sapiens CDNA clone IMAGE:2103421 3 SIMBBT to SW. DID_TOWNYN P35967 BH3 INTERACTING DOMAIN DEATH AGONIST ;	mondo ri Straterere lung cardinorna 837218 Homo septens cDNA clone IMAGE:565443 5' similar to	TR:G6622004 G662004 GPI-ANCHORED PROTEIN P137.;	Human endogenous retroklus, complete genome	Homo sapiens oscillin (hLn) gene, exon 5	Homo espiens NK-receptor (KIR-G2) gene, linker region exon	Human G2 protein mRNA, partial cds	EST388473 MAGE resequences, MAGN Homo sapiens cDNA	Homo sepiens CD34 entigen (CD34) mRNA	Homo saplens GAP-Ille protein (LOC51308), mRNA	Homo eaplens polycystic kidney disease (PKL)1) gene, expris 27-30	Homo sepiens polycysec (diney disease (PADT) gens, cours 21-30	H. septens mrtha for estagen receptor	Homo sapiens ankylin-tke was transferenciare dollierie i (Alaka i Alaka), illi data	Homo septemb NDS 14 mXVA rd N-debody about an atom and 1, vol. procedures	Home sepiens lodestar protein mitthe, complete das	Homo sepiens todestar protein miktuk, complete cas	Homo sepiens inosital 1,4,3-diphosphere receptor, type 1 (1117.1), intran-	CART		Home saciens UDP-glucose;glycoprotein glucosyvianisticasse 1 (HOGT), mixed	
## ## ## ## ## ## ## ## ## ## ## ## ##	Database		ES HOMAN	EST HUMAN	EST HUMAN	IN	NT	EST HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	FST HUMAN		EST_HUMAN	Z	NT	Ę	N.	EST HUMAN	NT	NT	ĮŅ	ᅜ	Ę	Ę	Z	LN-	N _T	NT	NT	LN.	Z.	
	Top Hit Acession No.		-		1.0E-98 BE390627.1			1.7			9.0E-89 AH79829.1	1470820 1	11.0000.1	9.0E-00 AA134604.1	9635487 NT	1.80	7.0E-09 AP001886.1	110001.1	W976364.1	4502660 NT	7706136 NT	43610.1	43610.1	X00101.1	9801589 NT	\B036429.1	AF080255.1		1 1	11431994 NT	11628290 NT	9910279 NT	9910279IN
Most Similar	(Top) Hit BLAST E Value	-	1.0E-98 AA1958	1.0E-98 BE3906	1.0E-98 B	1.0E-08 A	1.0E-08 AF1413	9.0E-99.A	9.0E-89	9.0E-90	9.0E-99	0 00 00 00 00	8.0C 60	0.05-00	8.0E-99	7.0E-89 AF0358	7.0E-09/4	8 0F-09 U10901	6.0E-99!AW976	6.0E-99	8.0E-90	6.0E-69 LA3610	6.0E-89 L43610	6.0E-90	6.0E-89	6.0E-99 AB0364	6.0E-00 AF0802	6.0E-99 AF080	6.0E-99	6.0E-99	6.0E-99	6.0E-99	8.0E.90
	Expression Signal		3.4	1.1	1.1	2.7	27	0 88	0.88	4.21	2.75	c c	6//3	2.13	1.08	10.00	2.90	80	115	121	0.72	1.01	1.01	1.18	0.63	2.28	3.33	3.33	0.0	0.6	3.89		2.01
	ORF SEQ ID NO:		30668	31178	31179	34728	34727	31441	31442	31691	<u> </u>		OLO/S	37288									Ĺ				l	L					36432
	SEQ 1D NO:		18040	18281	1	1_	L	L	Ĺ	Ł	1		23/30	2300		1_	1_	L	1	\perp			1	l _	L	1_	L	L		1_		<u> </u>	L
	Probe SEQ ID NO:		5234	5482	5482	8088	8	200	27.72	2000	80,	3	11068	11300	700	57.43	7,64,4		8000	9000	4502 6602	8678	8578	8003	8022	88	R762	8782	882	83	10620	11433	11433

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Single Exon Probes Expressed in Brain Page 421 of 536 Table 4

A08606x1 NCL_CGAP_HN9 Homo septens cDNA done IMAGE:27398743' stmiter to gb:M31212 MYCSIN x02h02x1 Sourse_NFL_T_GBC_S1 Homo septems cDNA clams IMAGE-2908371 3' etmiler to TR:00271 Homo seplens short chain L-3-hydraxyscyl-CoA dehydragenase precursor (HADHSC) gene, nuclear gene zb46d06.r1 Soares_fetal_lung_NbHL19W Homo septems cDNA clone IMAGE:308635 5' similar to Homo sapiens GA-binding protein transcription factor, alpha subunit (604D) (GABPA), mRNA Homo sepiens FK508-binding protein 6 (36kD) (FKBP6) mRNA, and translated products Homo sepiens FK506-binding protein 6 (36kD) (FKBP6) mRNA, and translated products y81509.r1 Source placenta Nb2HP Homo sepiens dDNA clone IMAGE:145625 5' Homo seplens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds Homo sepiens fruncated Niemenn-Pick C3 protein (NPC3) mRNA, complete cds Homo suplems T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region Homo sepiens potessium channel, subfamily K, member 10 (KCNK10), mRNA 801513157F1 NIH_MGC_71 Homo saplens cDNA clone IMAGE:3914391 5' Homo sapiene ciliary dynein heavy ohain 9 (DNAH9) mRNA, complete cds Human interferon-eipha receptor (Hulf N-eipha-Rec) mRNA, complete cds Homo sapiens cell recognition molecule Caspr2 (KIAA0868), mRNA Homo sepiens intersectin long tectorm (ITSN) mRNA, complete cds gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN); Human E2A/HLA fusion protein (E2A/HLF) mRNA, complete cds Homo saplens fatty acid emide hydrolese (FAAH) gene, econ 14 Homo sepiens fatty acid emide hydrolase (FAAH) gene, expn 14 **Top Hit Descriptor** LIGHT CHAIN ALKALI, NON-MUSCILE ISOFORM (HUMAN); Homo sepiens hundingtin interacting protein 1 (HIP1), mRNA Homo sepiens huntingfin interacting protein 1 (HiP1), mRNA Homo septens myoein X (MYO10) mRNA, complete cds Homo septens glycine receptor, alpha 2 (GLRA2), mRNA Homo seplens glychne receptor, alpha 2 (GLRA2), mRNA Human Ku (p70/p80) subunit mRNA, complete cds Human Ku (p70/p80) subunit mRNA, complete cds Homo sepiens ALEX1 protein (LOC51309), mRNA 002711 PRO-POL-DUTPASE POLYPROTEIN; encoding mitochandrial protein, complete ads H. sepiens E6-AP gene excn 2 H.sapiens IMPA gene, excn 8 HUMAN EST_HUMAN EST_HUMAN **EST HUMAN** EST_HUMAN Defabese きなり Source 먑 눋 눛 눋 눋 10863980 NT 11526150 NT Z ¥ 7427514 NT 4503730 NT Ę 눋 ŁN 7427514 NT 4503730NT 7862349 NT 11421007|NT 11419721 NT Top Hit Acession 11421007 20E-00 AW274792.1 1.0E-89 AW340174.1 1.0E-99 AF098018.1 BE800177.1 2.0E-99 AF095703.1 2.0E-99 AF257737.1 2.0E-89 AF247457.2 I.0E-99 AF114487.1 1.0E-99 AF192523.1 .0E-89 AF192523.1 1.0E-90 AF098018.1 5.0E-99 AF009680.1 ź 2.0E-99 W23507.1 2.0E-99 M30938.1 2.0E-99|R78264.1 1.0E-99 M30938.1 3.0E-89 M95586. 1.0E-99 J03171.1 5.0E-89 Y11365. \$8027.1 5.0E-90 1.0E-89 1.0E-00 .0E-89 1.0E-99 1.0E-90 2.0E-00 1.0E-48 9 HO. - CH-480 1.0F-48 Most Simila BLASTE 至(8) Value 1.56 2.81 9.55 1.46 4.88 88. 8 0.58 0.78 3.39 1.63 1.02 2.09 2.64 204 1.36 20. 0.68 1.41 1.41 2.82 1.71 0.76 2.01 201 Expression Signal 27406 29895 28666 20874 33348 30000 25809 20828 20002 27368 28489 29715 37029 ORF SEQ 28981 27367 20716 35270 31367 32205 37030 26751 32789 D NO: 14693 13068 SEQ ID 17261 20914 19015 21300 24674 17241 20243 23719 24378 13106 14295 22088 23754 23754 13111 14147 14295 14657 14667 15848 17086 17086 18453 19622 19822 25104 21787 ö 1957 4526 12208 8220 1217 3253 4506 7574 8908 99 11049 1540 1549 1920 28 3083 4347 2858 988 878 11084 STO 37 1400 4347 6707 6606 11084 307 6707 ö

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	Top Hit Descriptor	ANNA (HSF2BP), mRNA	Home sapiens neat strock transcription remaining the common partial cds.	Homo sapients mixing for Notice producting the 2 (2011) and nichathione Schausferase theta 1 (GST11)	Homo septents grunalitions of deliberation and allower.	Homo seplens chromosome 21 segment HS21C047	Homo saplens chromosome 21 segment HS21C047	Hamo septems Testis-specific XK-related protein on Y (XKRY), mRNA	Homo asplens Testle-specific XK-related protein on Y (XVRY), mRNA	W78h/1 x1 NCI CGAP Bm53 Homo septems cDNA clone IMAGE: 2824605 31	The series of the second HS21000	Train equals chamerone 21 segment HS21C049	From septembrain consistence of the control of the	ES I UZB/O From train, our analysis (Section 2) in the class providing report	Home septions A-linked shrinding occupanties dyspress in commercial sections.	regions	G.gorilla DNA for ZNI-80 gara nominal	RC3-HT0625-040500-022-509 HT0625 Home sapiens curving MRNA	Homo saplens DKFZP580M01ZZ protein (UKFZF380M01ZZ), IIIINUN	Homo sapiens DKFZP589M0122 protein (DKFZP589M0122), mRNA	ROZOZZOWAET NCI, CGAP, BIT67 Home septems cDNA clone IMAGE:4215039 5	ITILI BIT AREA TO LITTLE NOT COAP Sub3 Homo septens CDNA clone IMAGE:2722164 3'	GATTON A CALLES MADE NITT Homo sablens CDNA clone IMAGE:1754633 3' emiliar to SW:CYT_COTJA	P61061 CYSTATIN;	Homo septens mRNA for KIAA1169 protein, partial cds	Ret mRNA for short type PB-catherin, complete cds	H. septens mRNA for IFN-gemma (pKC-0)	Homo earliers KIAA0857 protein (KIAA0857), mRNA	Home saniers RGH2 cens, retrovirus-We element	VA, pertial cds	Α	mplets cds			.5 6060	
COLUMN PIGNIS	Top Hit Detabase Source			١	¥	Ž	Į	5	-	144641	MANUAL TOTAL	Į.	LN	EST HUMAN		NT	NT	EST_HUMAN	Ę	1	1444 E TOT	TOTAL HOMAN	ESI HOMAN	EST HUMAN	Έ	LZ.	Į		I.V.	Z	Z.	N	Z	LN 1	TN	ES! HOWAN
Sin Sin Sin Sin Sin Sin Sin Sin Sin Sin	Top Hit Acession No.		5901979	2.1	4 PE 00 AE240788 1	12.2	1 2	14449730	11410200	11418230	5	297	10.2	05087.1		1.0E-100 AF003528.1	(89631.1	1.0E-100 BE180809.1	TARTARENT	TARABANT	- 19	3F530735.1	W 207555.1	1 OE_100 A1200857 1	1 0E-100 AB032894 1	De2340 4	7000TE	ADZ-400. I	11478870 11	011078.1	×ι	4503792 NT	XΙ	5032104 NT	5032104 NT	BF244218.1
	<u>a</u> ≠ m	onis A	1.0E-99	1.0E-99 AB02322	V 00: 00 7	1.0E-88 At 4822/	C 00, 10.1	1.0E-100 IA-20.F	-1.0E-100	1.0E-100	1.0E-100 AWZ/52	1.0E-100 AL1632	1.0E-100 AL1632	1.0E-100 T05087.		1.0E-100	1.0E-100 X89631.	1.0E-100	4 20 420	1.051	1.05-105	1.0E-100 BF5307	1.0E-100 AW 207	4 05-400	1 OF 100	4 OF 400 De2240 4	1.0E-100 D00-10-1		-		1.0E-100 AF067		1.0E-100 AF036	1.0E-100		1.0E-100 BF244
	Expression Signal		1.8	277	8	0.00	08.0	1.53	\$	1.54	0.00	1.24	0.83	3.08		1.28	7.19	133	18				1.14	70 7						5.5	1.52	2.14	1.03	2.00		1.62
	ORF SEQ ID NO:		37088	37343			25443				25550	25618						25015			26419				0/807	\perp			7 28165		7 29558	22676	L			5 30637
	Escan SEQ ID	<u>-</u>	23808	24040		24525	12830	12830	12894	12894	12911	12979	13113	13135		13213	2 8	13200	_[13758	14163	14285	<u> </u>	_L	_1		15159	15417	15784	16927	<u> </u>	<u> </u>	1	L	Ш
	SEQ ID		11141	1350		198	-	2	8	8	88	185	300	35	3	127		4//	9	886	866	1415	1538		3	1856	82	2439	27.10	3018	4188	4211	4418	5031	5031	5207

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Table 4
Single Exon Probes Expressed in Brain

M37g08xf NCI_CGAP_Pr28 Homo sepiens cDNA clone MAGE:2489203's similar to contains element ae33b08.r1 Geesler Wilms turnor Homo sepiens cDNA clone IMAGE:897587 5' similar to TR:G487418 ae33b06.r1 Gessler Wilms furnor Homo expiens cDNA clone IMAGE:897587 5' straiter to TR:0487418 xa82f01.xf NCI_CGAP_CML1 Homo sepiens cDNA clone IMAGE:2573305 3' similar to gb:X12433 y38c08.s1 Sogres fetal liver spleen 1NFLS Homo septens cDNA clone IMAGE:129134 3 Homo sepiens Rho GTPese activisting protein 8 (ARHGAPS), transcript variant 4, mRNA 602020554F1 NCI_COAP_Bm87 Homo septens cDNA clone IMAGE:4166165 5 IMB3c11.y1 NCI_CGAP_QU1 Hamo sepiens cDNA clone IMAGE.2008396 57 IMB3c11.y1 NCI_CGAP_GU1 Hamo sepiens cDNA clone IMAGE.2008396 57 801847357F1 NIH_MGC_61 Hamo septens cDNA clane IMACE:3831310 5 Human mRNA for plasma inter-alpha-trypsin inhibitor heavy chain H(3) AU118182 HEMBA1 Homo sepiens aDNA dane HEMBA1003046 5" AU116951 HEMBA1 Homo septens cDNA clone HEMBA1000343 5' AU116951 HEMBA1 Homo septems aDNA done HEMBA1000343 5 Homo sepiens hect domain and RLD 2 (HERC2), mRNA AU140214 PLACE2 Homo sepiens GNA clone PLACE2000137 5 AU136800 PLACE1 Hamo sepiens aDNA alone PLACE1005089 51 AU127720 NT2RP2 Hamo septens cDNA dans NT2RP2001918 5 Human mRNA for Iddney epidermal growth factor (EGF) precursor Top Hit Descriptor MR1-TN0046-060600-004-b05 TN0045 Homo sepiens cDNA MR1-TN0046-080900-004-505 TN0046 Homo sapiens cDNA PM0-BND065-100300-001-008 BN0065 Homo sepiens cDNA G487418 ACTIN FILAMENT-ASSOCIATED PROTEIN.; G487418 ACTIN FILAMENT-ASSOCIATED PROTEIN.; Homo sapiens NF-E2-related factor 3 gene, complete cds AV732101 HTF Homo sepiens oDNA clane HTFBIG01 6 Homo sepiens ER to nucleus signaling 1 (ERN1) mRNA Homo sepiens ER to nucleus signalling 1 (ERN1) mRNA Homo espiene mRNA for KIAA1628 protein, partiel ods Homo septens mRNA for KIAA1485 protein, pertiel cds Homo sepiens mRNA for KIAA1626 protein, pertial ods Homo sepiens chromosome 21 segment HS21C003 PROTEIN PHPS1-2 (HUMAN); MER22 repetitive element; EST_HUMAN EST_HUMAN EST HUMAN **EST HUMAN** EST_HUMAN EST_HUMAN EST_HUMAN EST_HUMAN EST HUMAN EST HUMAN EST_HUMAN **EST HUMAN EST HUMAN** EST HUMAN EST HUMAN **EST HUMAN** Top Hit Detrabase EST_HUMAN EST HUMAN EST HUMAN Source 눋 4557588 NT 눌 上 눋 4657568 NT 5729867 Top Hit Acession 7382479 1.0E-100 AW075983.1 .0E-100 AU140214.1 1.0E-100 AWS08811.1 1.0E-100 AU118182.1 1.0E-100 AU136800.1 1.0E-100 AW630487.1 1.0E-100 AW630487.1 1.0E-100|AF135118.1 1.0E-100 AA496841.1 1.0E-100 BF376478.1 1.0E-100 AB040918.1 .0E-100 AU127720.1 1.0E-100|AA496841.1 1.0E-100 AL163203.2 1.0E-100 AU116951.1 1.0E-100 AU115951.1 1.0E-100 AB046846.1 .0E-100 AB046846.1 1.0E-100 BF376478.1 BF103853.1 1.0E-100 AV732101.1 1.0E-100 BF347519.1 1.0E-100 AI972388.1 1.0E-100 X14690.1 1.0E-100 R10887.1 1.0E-100 X04571.1 1.0E-100 1.0E-100 1.0E-100 1.0E-100 1.0E-100 #H (do L) **Jost Sinite** BLASTE 2. 8. 8. 0.8 9 1.19 0.04 1.67 5.64 1.19 0.76 0.08 1.97 1.37 0.68 3.62 1.82 211 211 1.88 0.40 0.9 1.13 7.17 4. 7.61 1.68 1.47 Expression Signal 31369 32558 31814 31815 32173 32224 32362 34746 ORF SEO 3149 32608 34747 36598 35749 32622 32009 34261 33520 35316 35599 34986 35317 ÖNQ \$28 828 18410 18455 18539 18850 18850 19113 19224 19340 19578 SEQ ID 19174 21603 22 848 19630 21158 21603 238 19587 19676 19530 19537 21123 21820 22136 22394 22554 T N Š ö 5614 888 8343 6742 6742 6783 5427 5747 6071 865 8430 8468 8812 SEO ID 6457 6588 0200 6786 6786 8912 9132 9210 9333 888 9483 9483 9743 9743 5000 10368 Š

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Homo sepiens glutathione S-transferace theta 2 (GSTT2) and glutathione S-transferace theta 1 (GSTT1) 988h03xf NCI_CGAP_LL24 Homo sapiens cDNA done IMAGE: 3' similar to TR:Q21997 Q21997 Homo eaplens phosphoribosylgiychamide formythansferase, phosphoribosylgiychamide synithetase, zk89e03.r1 Soeres_pregnent_uterus_NbHPU Homo sepiens oDNA done IMAGE:489964 5 zk89e03.r1 Scenes_pregnant_uterus_NbHPU Homo sepiens cDNA clone IMAGE:489964 5 Homo saplens pescadillo (zabrafish) homolog 1, containing BRCT domain (PES1), mRNA 999909.x1 Soarss_NFL_T_0BC_S1 Homo sapions cDNA clorps IMAGE:1843336 3* Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA 602156474F1 NIH_MGC_83 Hamo sepiens cDNA clane IMAGE-4297291 6 Homo sapiens 14q32 Jaggad2 gene, complete cds; and unknown gene Homo sepiens 14q32 Jegged2 gene, complete cds; and unknown gene Homo sepiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA Homo sapiens transcobalemin II; mecrocytic anemie (TCN2), mRNA Homo sepiens A kinase (PRKA) enchor protein 6 (AKAP9), mRNA Homo sepiens SH3-domain binding protein 1 (SH3BP1), mRNA Top Hit Descriptor Homo sepiens cerboxypeptidase A1 (pencreatic) (CPA1) mRNA RC3-ST0281-160600-016-h09 ST0281 Homo sepiens cDNA Homo sapiens SEC14 (S. cerewisias) #te 2 (SEC14L2), mRNA Homo sepiens SEC14 (S. cerevísies) illes 2 (SEC14L2), mRNA MR0-BN0070-270300-008-h11 BN0070 Homo sepiens cDNA QV2-PT0012-010300-070-d04 PT0012 Homo sepiens cDNA Hamo sepiens galgin-illes protein (GLP) gene, complete ads Homo sapiens KIAA0589 gene product (KIAA0589), mRNA Homo sepiens KIAA0509 gene product (KIAA0569), mRNA Homo sapiens ventral enterfor homeobox 2 (VAX2), mRNA Homo seplens ventral enterfor homeobox 2 (VAX2), mRNA phosphoribosyleminoimidezaie synthetese (GART) mRNA Homo sepiens of cardiac alpha-myosin heavy chain gene Homo sepiens mRNA for KIAA0446 protein, pertiel cds domo sepiens chromosome 21 segment HS21C047 Human endogenous retrovirus HERV-K, pol gene COSMID R151. [Z] TR:09UA08; H. sepiens EWS gene, expn 5 Single Exon Probes Expressed in Brain genes, complete ods EST_HUMAN EST_HUMAN EST_HUMAN HUMAN EST HUMAN **EST HUMAN** EST HUMAN EST_HUMAN Database Teo Source EST Ż Ę 7110714 NT 4503914 NT 7110714 NT 7057454 NT 5921460 NT 7862183 NT 11417974 NT 7110734 NT 7110734 NT 7862183 NT 5729892 NT Ż 5921460 NT 4502996 NT Top Hit Acession 11545732 1.0E-100 AL163247.2 1.0E-100 AW875464.1 1.0E-100 AF111170.3 1.0E-100|AF111170.3 AB007915.2 1.0E-100 AF286285.1 1.0E-100 AA115805.1 BE843070.1 1.0E-100 BF327292. 1.0E-100|AA115605.1 1.0E-100|AF240786.1 1.0E-100 BF446549.1 1.0E-101 BF081218.1 ģ AI221878.1 Z20656.1 1.0E-101 X72993.1 1.0E-100 1.0E-100 1.0E-101 1.0E-101 .0E-101 (Top) HIR BLAST E 1.0E-100 1.0E-101 1 0E-101 1.0E-101 1.0E-101 1.8-101 1.0E-101 1.0E-101 Acet Similar 1.0E-101 1.0E-101 1.0E-101 .OF-10. 1.0E-101 .OF-101 Value 4.52 2.11 1.59 5.88 6.88 14.28 1.62 8.27 6.67 5 3.67 1.62 1.63 1.46 1.52 1.52 28 Expression Signal 37319 37320 37806 37669 ORF SEQ 25443 37668 30908 25639 26087 28111 26112 28185 28398 28440 27012 27013 27182 27183 27510 31071 28335 27389 27808 28078 Ö N O 23349 12830 24230 24340 SEO ID 23104 24017 24278 24340 24471 25044 12902 12902 1347 13463 13463 13526 13603 13729 14324 14324 14482 25278 24668 13671 13790 14482 14673 14783 15332 15592 Ö 2401 SEQ ID 11356 11633 10458 11328 11328 11907 12200 12792 754 833 8 意覧 1740 1938 10658 11681 11749 12031 888 8 1577 1740 2050 2349 Ę

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K29g08.r1 Source_pregnent_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471998 5' stmiller to hh74g10.y1 NCI_CGAP_GU1 Homo sepiens cDNA clone IMAGE:2968578 5' similar to go:J03143 Homo septems Kruppel-type zinc finger protein (PEG3) mRNA, attenuative splice form 4, partiel cds hh74g10.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2988578 5' similar to gb:J03143 Homo sepiens Kruppel-type zinc finger protein (PEG3) mRNA, atternative spiloe form 4, partial ods INTERFERON GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN); INTERFERON GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN); wv58f12x1 NCL CGAP_Gee4 Hamo septens oDNA dane IMAGE:2833487 3' 801109217F1 NH_MGC_16 Hamo septens oDNA dane IMAGE:3349801 5' RC1-BT0313-220700-018-f12 BT0313 Hamo septens cDNA 801121621F1 NIH_MGC_20 Homo sepiens cDNA done IMAGE:3345869 57 801121621F1 NIH_MGC_20 Homo sepiens cDNA done IMAGE:3345869 57 601458531F1 NIH_MGC_66 Homo septens cDNA clane IMAGE:3862086 5 801784888F1 NIH_MGC_53 Hamp suplens cDNA clone INAGE:3928837 5 Homo sepiens ASHZL gene, complete cds, similar to Drosophila esh2 gene Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA Homo septens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA Homo sapiens hypothetical protein FLJ22087 (FLJ22087), mRNA **Top Hit Descriptor** EST377212 MAGE resequences, MAGI Homo sepiens cDNA EST377829 MAGE resequences, MAGI Homo sapiens cDNA Homo sepiens genme-glutemyltrensferase 1 (GGT1) mRNA Human mRNA for pencreatic gamma-glutamyltansferase Human mRNA for pencreatic gamma-glutamytransferase Homo septens mRNA for KIAA1351 protein, pertiel ods Homo sepiene mRNA for KIAA1361 protein, pertiel ods Homo sepiens cytoplesmic linker 2 (CYLN2), mRNA Homo sepiens cerbonic enhydrase VII (CA7), mRNA Homo sepiens cytopleamic linior 2 (CYLN2), mRNA PIR:S54640 S54640 YD8335.03c protein - yeast; Homo sapiens genomic downstream Rhesus box Homo sapiens RIBIIR gene (partial), excn 12 Homo sepiens RIBIIR gene (pertiel), excn 12 Homo sapiens RIBIIR gene (pertial), excn 12 Homo sapiens RIBIIR gene (partial), excn 12 Single Exon Probes Expressed in Brain EST HUMAN EST HUMAN **EST_HUMAN** EST HUMAN EST HUMAN **EST HUMAN** HUMAN EST_HUMAN EST HUMAN EST_HUMAN EST_HUMAN EST_HUMAN Detabase 西岸 Source EST 눋 E 눋 5921450 NT 토토 Ł F 7427512|NT 7427512 NT 11430734 NT 11545780 NT 5921400 Top Hit Acession AW965558.1 AW965139.1 BF035327.1 1.0E-101 AW630070.1 AJ237744.1 1.0E-101 AJ237744.1 1.0E-101 AB022785.1 1.0E-101 AW008475.1 .0E-101 BE257384.1 1.0E-101 AW630070.1 AJ237744.1 1.0E-101 AF208970.1 AF208970.1 1.0E-101 BF330759,1 1.0E-101 AB037772.1 AJ237744.1 AJ262312.1 1.0E-101 (BE276821.1 BE275821.1 1.0E-101 BF029174.1 1.0E-101 AA036800,1 1.0E-101 AB037772.1 X80069.1 1.0E-101 X00009.1 1.0E-101 1.0E-101 1.0E-101 1.0E-101 1.0E-101 .0E-101 1.0E-101 1.0E-101 1.0E-101 1.0E-101 1.0E-101 1.0E-101 6-10 1.0E-101 1.0E-101 (Top) 压 Most Simila BLASTE 3.69 1.09 1,98 1.16 3.68 1.09 227 £. 1.49 3.68 1.22 12 5.57 7.48 0.83 0.83 17.13 5 0.84 288 0.67 0.67 1.08 Expression Signa 28192 28193 28613 30304 30669 31651 ORF SEQ 31662 32978 33138 33398 34050 33563 32372 33632 33772 34051 34741 35080 35081 33554 33631 3297 Ö 15452 15452 16134 SEQ ID 15452 88 15961 16607 17697 18698 19905 20280 15721 15997 17697 18041 19358 19850 18905 20058 20147 20508 20649 2002 20915 <u>2589</u> 21908 21908 20432 20432 ÿ 2955 3375 2747 2747 3198 3396 88 SEQ ID 3235 3395 4074 5235 5033 6595 7173 822 7376 7623 7813 8008 8228 7220 7813 8229 9362 9362 3857 4974 8221 8221 7474 餐 ÿ

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	Top Hit Descriptor	1 (2011) transcript variant 3, mRNA	Homo sapiens gamme-gluzanymarsiorase 1 (500 1), usususip.	6014/2000 11411-mod	Home seriens releaseful Channel, subfamily K, member 10 (KCNK10), mRNA	Homo sentens, Jenus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA	POTERORESET NIH MGC 83 Home septens CONA clone IMAGE:3950887 5	ANTERORESET NIH MGC 83 Homo sepiens CDNA clone IMAGE:3950887 5	branched-chain alpha-keto acid dehydrogenase complex E1 alpha subunit [human, Genomic, 190 fft,	segment 8 of 9]	Homo separats mayor to the property of the property of the part of	HEPARIN-BINDING GROWTH FACTOR PRECURSOR 1 (HUMAN); HEPARIN-BINDING GROWTH FACTOR PRECURSOR 1 (HUMAN); OAAB Brook Living servings CONA done IMAGE:2162304 3' striller to gb:M13361	tmbacol xi Not Coar Entro Hairo Precursor 1 (HUMAN); HEPARIN-BINDING ROWHTH FACTOR PRECURSOR 1 (HUMAN);	RC-BT163-230499-Uco bi Tos Ironio september CONA	AVA OTROPE 240200 085-401 DT0068 Homo septems cDNA	4 - Constitution of the complete comple	Home services chromosome 21 segment HS21C103	Homo seplens down-regulated in adendria (DRA) mRNA	Human endogenous retrovinal DNA (4-1), complete retrovinal segment	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLUCAN), minuto.	Homo sapions solute certier femily 2 (facilitated glucose transporter), member 9 (000000),	Homo septens reelin (RELN) mRNA	601200082F1 NIH MGC 21 Homo saprens clara contentación de la sapriner to	amigocito.x; Johnston frantsi cartex Hamo sapians autiva crario invade.; Constant Co	amment of Johnston frontal cortex Homo sepiens cDNA done INAGE: 1539954 3' similar to	SW.GG95 HUMAN G08379 GOLGIN 95.	Home septents NAVA for process CNA done PLACE4000650 51	AUTHOUS LINE Homo septens oDNA dane PLACE4000650 5	Homo sapiens chromosome 21 segment HS21 0007	601107843F1 NIH MGC 18 Homo septens cDNA clone IMAGE:3343882 5	
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	Top Hit Aceseion No.		9845402 NT	<u>.</u>	·	10863960 N I	42912/	<u> </u>	E973648.1		1.0E-101 AB020828.1	\J590078.1	1.0E-101 AI590078.1	1.0E-101 AI908168.1	1.0E-101 AI908168.1	1.0E-101 AWS39051.1	AF012872.1	AL 163303.2	456/634 NT	M109/6.1	TA 4427448 INT	4826977 NT	4 OF 402 BF 408447.1		1.0E-102 AI124869.1	≥ x l	T061979 NT	1.0E-102 AU141005.1	1.0E-102 AU141005.1	1.0E-102 AL163207.2	1.0E-10Z BEZ31310.1
+	Most Similer (Top) Hit T	Vatue	1.0E-101	1.0E-101 BE619667	1.0E-101 BE61966	1.0E-101	1.0E-101	1.0E-101 BE97364	1.0E-101 BE97364	1.0E-101	1.0E-101	1.0E-101 AI500078	l		1.0E-101	1.0E-101	1.0E-102 AF0128			1	1.0E-102	1.0E-10.4	1			1.0E-102 Al12486				1	
+	Expression Sime	<u>.</u>	17.01	6.24	6.24	0.72	1.49	96.0	0.94	1.96	211	2.06			1.31	13.68	2		-			1.67			1.88	1.86		3 4.76			3 2.17
	ORF SEQ	<u>-</u>	35123	35506	35507	35850	36171	36323	36324	38713		<u> </u>	\		L		25485		26190				2007		2 27769						5 29748
	Exen SEQ ID	Ö	21050	22300	22309	22445	22965	23063	23093	22.474	23723	l	1_	24004		L	_	L	1_				_1	14145	15032	1		1_	1_	<u> </u>	8 17115
	Probe SEQ ID		37,4	7580	1298	76/6	10308	1947	10447	-	10/80	3	11.000	11398	478	12/6	38	332	758	1095	1245	1245	<u>\$</u>	1398	2307		200	3430	3130	4207	4378

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w163b08.x1 NCI_CGAP_KId12 Homo sapiens cDNA done IMAGE:2397971 3' similar to contains MER4.t1 er82f09.x1 Beretsed colon HPLRB7 Hamo septens cDNA clone IMAGE:2151785 3' similar to TR:Q13137 on57h04.s1 Soeres_NFL_T_GBC_S1 Hamp sapiens cDNA done IMAGE:1560823 3' similer to yd13d07.r1 Soares fetal liver spieen 1NFLS Home sepiens cDNA clone (MAGE:67021 5 yd13d07.rt Soeres fetal liver spieen 1NFLS Hamo sepiens cDNA clans IMAGE:67021 5 AU124629 NT2RM4 Hamo sepiens cDNA clane NT2RM4000309 5 Homo sapiens UDP giyoosytransferase 2 family, polypeptide B11 (UGT2B11) mRNA ak49h10.s1 Soares_bests_NHT Homo sapiens cDNA clone IMAGE:1408347 3' RC6-ET0072-150800-011-F01 ET0072 Homo sapiens cDNA Hamo sepiens UDP glycoeyltransferase 2 family, polypopiide B11 (UGT2B11) mRNA Homo septens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exam. Homo sepiens phospholipid acramblese 1 gene, even 1 and 5' flanking region Homo septens HSC54 mRNA for heat shock cognate protein 54, complete cds 801283770F1 NIH_MGC_44 Homo septens cDNA clone IMAGE:3805536 5 601283770F1 NIH_MGC_44 Homo septens cDNA clone IMAGE:3605638 5 801561505F1 NIH_MGC_20 Hamo septens cDNA clane IMAGE:3831241 5 801277215F1 NIH MGC 20 Homo septens cDNA clone IMAGE:3016243 5 901501107F1 NIH MGC_70 Homo septens cDNA clone IMAGE:3903145 5 Top Hit Descriptor QV3-NT0025-210600-236-h08 NT0025 Homo septens cDNA AV694817 GKC Homo sepiens aDNA dane GKCEEE11 6 AV694817 GKC Hamo sepiens aDNA clane GKCEEE115 AV755842 BM Homo suplems oDNA clone BMFAUD06 5' AV710738 Cu Homo sapiens cDNA clone CuAAKD03 5 Homo sepiens heat domain and RLD 2 (HERC2), mRNA Homo sepiens mRNA for KIAA0454 protein, pertial cds RC-BT074-280499-014 BT074 Homo septems cDNA RC-BT074-260499-014 BT074 Homo sepiens cDNA Homo sapiens histone descet/less 7 (HDAC7), mRNA Homo septens histone descet/lase 7 (HDAC7), mRNA Homo supjens mRNA for Centeurin-alpha2 protein SW:CAV2_HUMAN P51636 CAVEOLIN-2. [1] MER4 MER4 repetitive element; Single Exon Probes Expressed in Brain Q13137 NDP52.; EST HUMAN EST HUMAN EST HUMAN EST_HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST_HUMAN EST HUMAN EST HUMAN EST_HUMAN EST HUMAN EST_HUMAN Database Top I∓ Source ż 4507822 NI TN 8882077 11433046[N] 7705398 N 4507822 **rop Hit Acession** 1.0E-102|AA970786.1 1.0E-102 AAB68675.1 1.0E-102 BF359243.1 1.0E-102 BE388063.1 1.0E-102 BE388063.1 1.0E-102 AF153715.1 1.0E-102 AI905037.1 AU124629.1 1.0E-102 AI905037.1 1.0E-102 AB007923.1 1.0E-102 AV694817.1 1.0E-102 AV604817.1 1.0E-102 AI762859.1 1.0E-102 AV755842 1.0E-102 AV710738.1 BE763051.1 1.0E-102|AJ23894.1 BE910555. 1.0E-102|AF067133.1 1.0E-102 AB034951.1 1.0E-102 AI459825.1 BE728323.1 BE386106. 1.0E-102|T70393.1 T70393.1 1.0E-102 1.0E-102 1.0E-102 1.0E-102 1.0E-102 1.0E-102 1.0E-102 1.0E-102 1.0E-102 1.0E-102 1.0E-102 Vost Scraffer BLASTE 三(4) Value 2.58 3.55 2.55 2.28 3.79 3.67 12 9.52 238 0.69 3.67 2.48 1.32 5 8 <u>8</u> 221 8 823 221 0.75 3.91 2.84 2.83 2 28. 8.0 1.87 9.17 Expression Signa 37248 36295 36638 37287 35069 35070 36228 36229 36837 35049 35151 35017 34219 34335 33962 34218 34687 34668 33014 33288 34032 31954 32821 31414 31420 30753 ORF SEQ Ö 2 23074 23013 23680 23680 23951 21900 21978 23013 21900 21881 21851 888 21183 200 19756 19939 20195 20816 20895 21085 21085 18976 18402 19728 18492 18498 18092 18458 SEQ ID 11380 11290 10428 11008 11008 9150 10367 10367 8823 6238 9181 9221 8311 10281 8392 8501 9221 7065 8122 8392 7036 7255 7624 8201 5883 5898 2698 5704 6200 5287 SEQ ID

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ORF SEQ Expression (Top) Hit Top Hit Accession Databasee ID NO: Signal Value	37831 3.67 1.0E-102 U41302.1 NT	3.52 1.0E-102 AL163280.2 NT	31023 4.69 1.0E-102 AW 300862.1 ESI TOWAN	25528 1.19 1.0E-103 SESVOIDO:	25529 1.19 1.0E-103 BEW00136.1	25661 10.6 1,05-103 D51010 C	25650 1.19 1.0E-103 AJ278348.1 NT	29643 10.23 1.0E-103 BE877541.1 EST HUMAN	27028 3.76 1.0E-103 AF012872.1 NT	27354 1.75 1.0E-103 7857592 NI	27420 1.44 1.0E-103 4502428 NI	27421 1.44 1.0E-103 4502428 NI	27765 1.15 1.0E-103 AU134991.1 E31 HUMAN	27909 1.33 1.0E-103 AF-060698.1 N1	28066 1.23 1.0E-103 BF022878.1	28056 1.23 1.0E-103 B1-528378.1 EST HIMAN	2.68 1.0E-103 BE/147/22 EST HIMAN	28789 4.1 1.0E-103 AW 286245:1 E3121	28837 0.99 1.0E-103 ABOH0682.1	8.55 1.0E-100 Arocason	29165 1.23 1.0E-103 AA485883.1 EST HUMAN	29195 1.72 1.0E-103 11430876 NI	29367 3.47 1.0E-103 123983.1 ESI HUMAN	31567 0.96 1.0E-103 BF308027.1	31577 2.62 1.0E-108 AF179995.1	31923 0.89 1.0E-103 11439035 NT	31924 0.80 1.0E-103 11439035 NI	32132 0.75 1.0E-103 AW 954506.1 EST HIMAN	32133 0.75 1.0E-103 AW 9545000.1	32265 1.63 1.0E-103 AA/61442.	32304 0.94 1.UC-1Us r4 COSTOC
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Exan SEQ ID NO:	24305	┸	L	12896	7 12895		13016			L	<u></u>		L.	L	15316	33 15316	64 15830	74 16133		37 16490	4774 18526	1.		(5862 18639	L		L	6368 19137	6498 25092	6535 19301
Probe SEQ ID NO:	1,1	181	12450	8	19	8	8	8	122	190	198	198	2303	2452	2003	2803	3064	3374	3433	3737		; *	8	188	83	•	•			٩	8

Page 429 of 536 Table 4 Single Exon Probes Expressed in Brain

Single Exon Probes Expressed in Brain	. Top Hit Descriptor	tm58b05.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769 Q13709 ANONYMOUS.;	tm58b05.xf NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13789 Q13789 ANONYMOUS.;	Homo septens dystrophin (inuscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS200, DXS	Homo saplens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS2	mRNA	Homo sapiens ribosomal protein L3-like (RPL3L), mRNA	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene	EST377849 MAGE resequences, MAGI Homo sapiens cDNA	801571537F1 NIH_MGC_55 Homo septens cDNA clone IMAGE:3838545 51	tm88b05.x1 NCI_CGAP_Bm25 Hamo septens cDNA clone IMAGE:2162289 3' similar to TR:Q13789 Q13789 ANONYMOUS.;	tm88b05.x1 NCI_CGAP_Bm25 Homo septens cDNA clone IMAGE:2162289 3' similar to TR:Q13789 Q13789 ANONYMOUS.	EST27193 Human Brain Homo saplens cDNA 5' end similar to None	AU140344 PLACE2 Homo septems cDNA clone PLACE2000374 5	AU140344 PLACE2 Homo septens cDNA clone PLACE2000374 5	780603.X1 Sogres_NSF_F8_9W_OT_PA_P_S1 Homo septens CDNA clone IMAGE:3525984.3" similar to SW-PTNF HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1:	Homo septens trible functional domain (PTPRF interacting) (TRIO), mRNA	Homo septens triple functional domain (PTPRF interacting) (TRIO), mRNA	nd13-002.s.1 NCI_CGAP_Ov1 Homo sepiens cDNA clone IMAGE:800162.3' einitar to gb1.024.26.26S PROTEASE SUBUNIT 4 (HUMAN);	ae84d12.s1 Strategene achizo brain 311 Homo eaplens cDNA cione IMAGE:370871 3' similar to gb:X03747 cds1 SODIUMPOTASSIUM-TRANSPORTING ATPASE BETA-1 (HIMAAN)	QV2-NN0045-230800-322-b03 NN0045 Hamo septens cDNA	QV2-NN0045-230800-322-b03 NN0045 Hamo septens cDNA	H.saplens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)	EST375749 MAGE resequences, MAGH Homo septens cDNA
gle Exon Prop	Top Hit Database Source	EST_HUMAN (EST_HUMAN (П	EST_HUMAN	EST_HUMAN K	EST_HUMAN C	EST HUMAN	Г	Ι	П				T HUMAN		IΠ	EST_HUMAN		EST_HUMAN E
ais	Top Hit Acession No.	1.0E-103 AI580071.1	1.0E-103 AI690071.1	6032282 NT		5032282 NT	11431100 NT	880.1	1.0E-103 AW985778.1	1.0E-103 BE748158.1	1.0E-103 AIS90071.1	1.0E-103 AISB0071.1	T31080.1			1.0E-103 BF100244,1	6005921 NT	0005921 NT	8	1,080,1		1.0E-103 BE935842.1		П
	Most Similar (Top) Hit BLAST E Value	1.0E-103	1.0E-103	1.0E-103		1.0E-103	1.0E-103	1.0E-103 AJ289	1.0E-103	1.0E-103	1.0E-103	1.0E-103	1.0E-103 T31080.1	1.0E-103	1.0E-103	1.0E-103	1.0E-103	1.0E-103	1.0E-103 AA581	1.0E-103 AA77	1.0E-103	1.0E-103	1.0E-103	1.0E-103/
	Expression Signal	. 1.48	1.48	1.53		1.53	1.27	0.99	1.63	6.83	4.21	4.21	0.77	222	2.22	1.1	2.86	2.86	1.16	5.04	0.58	0.56	1.44	1.89
	ORF SEQ ID NO:	32396	32397	30579						32860	33446	33447		34354	34355	34430		34846	34891	34941	34995	34996	35811	35859
	Exen SEQ ID NO:	19380	19380	17918		-			19815	19918	20335	20335	20881			21298	21695	21695	21736	21777	21832	21832	22808	22847
	Probe SEQ ID NO:	6618	6618	6747	,	6747	8872	8835	7127	7233	7671	767.1	8187	8510	8519	8804	9002	9002	9046	8088	9162	9462	8968	888

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Table 4
Single Exon Probes Expressed in Brain

-			-	-	_	_	_	~	_		_				_	_		-			السا		N.	_		-	-	_	4	,# 4 ₁	
	Top Hit Descriptor	au51g04.71 Schneider fetal brain 00004 Homo septens cDNA clone IMAGE:2518326 5' similar to TR:O15046 O16046 KIAA0338	ODZIGOB. 55 NCI., OGAP. Lu5 Hamo septiens cDNA clone IMAGE:1522283 5' similar to TR:062084 Q62084 PHOSPHOLIPASE C NEIGHBORING;	Homo suplens AXL receptor tyrosine kinase (AXL), mRNA	Homo septens AXL receptor tyrosine kinese (AXL), mRNA	Homo sepiens NOD1 protein (NOD1) gene, excris 1, 2 and 3	Homo sepiens NOD1 protein (NOD1) gene, excrs 1, 2, and 3	Homo saplens mRNA for partial OCT/pleadn-A2 protein	Homo sepiens mRNA for partial OCT/bleadn-A2 protein	AU136283 PLACE1 Homo sepiens cDNA done PLACE1003923 5'	Hamo suplens polycystic Iddney disease (PKD1) gene, earns 27-30	7e88a10.x1 Source_NSF_FB_9W_OT_PA_P_S1 Homo capiens cDNA clone IMAGE:3287610 3' similar to contains MFR20 to MFR20 percent to contains MFR20 to MFR20 percent to	Hamo seciens hypothetical protein FL/20454 (FL/20454), mRNA	Homo septens gene for AF-6, complete cds	DKFZp684H1072_r1 684 (synonym: hfbr2) Homo sapiens cDNA clone DKFZp584H1072 5	DKFZp664H1072_rt 564 (synonym: htbr2) Homo septens cDNA clone DKFZp664H1072 5	Homo sapiens bane morphogenetic protein 8 (asteogenic protein 2) (BMP8) mRNA	2022008.s1 Strategene colon (#837294) Homo septens cDNA done IMAGE:587626 3' similar to ob.274116 met CD59 GLYCOPROTEIN PRECURSOR PHIMANY.	601577460F1 NIH MGC 9 Hamo septens cDNA clane IMAGE:3926438 5	RC1-CT0249-110000-214-f12 CT0249 Homo saplens cDNA	RC1-CT0249-110000-214-f12 CT0249 Homo sepiens cDNA	Homo septens ARP2 (softmelated protein 2, years!) homolog (ACTR2), mRNA	Homo seplens KIAA040 protein (KIAA0440), mRNA	Homo espiene KJAA0440 protein (KJAA0440), mRNA	Human Inniphocytic antigen ODS@MEM43 mRNA, complete cds	H. sepiene gene encoding phenylpyruvate tautomerase II	EST21658 Actenul gland tumor Homo sapiens cDNA 5' and	Homo sepiens mRNA for KIAA1276 protein, pertial cds	Homo sepiens mRNA for KIAA1276 protein, pertial cds		
	Top Hit Detabase Source	EST_HUMAN	EST HUMAN	1.	LN	LN	Z	LN	ĮN.	EST_HUMAN	N	EST HUMAN	LN.	LN	EST HUMAN	EST HUMAN	E	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	N.	N-	N.	NT	NT	EST_HUMAN	Ę	NT	NT	Ę
	Top Hit Acession . No.	1.0E-103 AI878956.1	AI792759.1	11424061 NT			AF149773.1	XB7831.2	X87831.2	AU136283.1	43610.1	3E644611.1	11526291 NT	1.0E-103 AB011399.1	1.0E-104 AL037549.3	1.0E-104 AL037549.3	4502428 NT	1.0E-104 AA132975.1	1.0E-104 BE744628.1	1.0E-104 BF334221.1	1.0E-104 BF334221.1	5031570 NT	7882125 NT		1.1	.1	VA319436.1			208.1	П
	Most Similar (Top) Hit BLAST E Value	1.0E-103	1.0E-103	1.0E-103	1.0E-103	1.0E-103 AF149	1.0E-103 AF1497	1.0E-103 XB7831	1.0E-103 X87831	1.0E-103 AU136;	1.0E-103 L43610.	1.0E-103 BE6446	1.0E-103	1.0E-103	1.0E-104	1.0E-104	1.0E-104	1.0E-104	1.0E-104	1.0E-104	1.0E-104	1.0E-104	1.0E-104	1.0E-104	1.0E-104 M34671	1.0E-104 Y11151	1.0E-104 AA3194	1.0E-104 AB0331	1.0E-104	1.0E-104	1.0E-104 X02781
	Expression Signal	9.2	3.56	2.04	2.04	222	222	1.3	1.3	2.8	10.74	2.41	2.11	2.83	3.73	3.73	2.18	3.68	2,57	1.38	1.38	1.08	1.11	1.11	7.41	2.74	2.04	0.79	0.79	0.76	3.93
	ORF SEQ ID NO:	32888	1998E	30008	3000	22998	8290E		36718	37340	36421	29928		31091	25676	25677		27853	27606	27820	27830	27893	27965	27066	28285			28986	28987	20315	29712
	Econ SEQ ID NO:	22786	23328	23424	23424	23434	23434	23476	23478	24037	23190	24339	24494	24620	13030	13039	14618	14919	14929	15091	15091	15158	15224	15224	15641	15683	16145	16341	16341	16674	17083
	Probe SEQ ID NO:	10138	10634	10737	10737	10748	10748	10793	10793	11347	11423	11748	11937	12128	227	122	1881	2190	2201	2360	2369	2438	2507	2507	2874	84	3388	3587	3587	3024	4344

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Single Extri Probes Expressed in Diairi	Top Hit Descriptor	Homo sapiens chromosome 21 unknown mRNA	Homo seplens chromosome 21 unknown mRNA	Homo sapiens death receptor 6 (DR6), mRNA	Human Down Syndrome region of chromosome 21 DNA	Human Down Syndrome region of chromosome 21 DNA	Homo septens alid mRNA for Aurora/Ip11-related kinase 3, complete cds	wj03b12.x1 NCI_CGAP_Kkl12 Homo sepiens cDNA clone IMAGE:2401727 3' similar to TR:Q14145 Q14145 KIAA0132 PROTEIN, pontains element LTR7 repetitive element;	wjo3b12.x1 NCI_CGAP_Kid12 Home septens cDNA clone IMAGE:2401727 3' stimiter to TR:Q14145 Q14145 KIAA0132 PROTEIN, contrains element LTR7 repetitive element;	Homo sapiens PDZ domain-containing guentine nucleotide exchange factor i (LOC51735), mRNA	301150451F1 NIH_MGC_19 Homo saplens cDNA clone INAGE:3503220 5'	601150451F1 NIH_MGC_19 Homo septens cDNA clone IMAGE:3503220 5	Homo sepiens adeptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA	UI-H-BI4-aow-b-09-0-UI s1 NCI_CGAP_Sub8 Homo sepiens cDNA clone IMAGE:3086176 3	ned16g11.x1 NCL_CGAP_Lu24 Homo septens cDNA clone IMAGE:3365948 31	2/98b05.s1 Source_febal_fiver_spleen_1NFLS_S1 Homo septens cDNA clone IMAGE:462897 3'	yc83f02.r1 Soares infant brain 1NIB Homo sepiens cDNA clone IMAGE:22440 5"	Homo sepiens Tho Isoform mRNA, complete cds	Homo sepiens Trio Isoform mRNA, complete ods	IL3-HT0619-080900-249-F07 HT0619 Homo sepiens cDNA	L3-H70619-080900-249-F07 H70619 Homo septems cDNA	xd78d02x1 Sogres_NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:2803523 3' similar to TR:Q24116 Q24116 HYPOTHETICAL 29.4 KD PROTEIN.;	xd78d02xt Soares NFL_T_GBC_S1 Homo sepiens cDNA clone IMAGE:2003523 3' similar to TR:Q24116 024116 HYPOTHETICAL 29.4 KD PROTEIN :	Homo sapiens histone acetyltransferase MORF mRNA, complete ods	977.5		AV728070 HTC Hamo septens aDNA clane HTCBYA07 5'		24 and 25		RC0-HT0885-310700-021-b09 HT0885 Homo saplens cDNA
מסויין וויסאם פונ	Top Hit Database Source	Į.	NT	Σ	Z	7	M	EST_HUMAN	EST HUMAN		EST_HUMAN	THUMAN		EST_HUMAN	EST_HUMAN	EST HUMAN	T_HUMAN	NT	M		EST_HUMAN	EST_HUMAN		Z	EST_HUMAN	EST_HUMAN		T_HUMAN			EST_HUMAN
JIIC	Top Hit Acession , No.	1.0E-104 AF231920.1	1.0E-104 AF231920.1	7857038 NT	U43379.1	U43379.1	1.0E-104 AB017332.1	1.0E-104 AI768797.1	1.0E-104 AI768797.1	7706512 NT	BE314182.1	BE314182.1	11425572 NT	1.0E-104 BF509244.1	3F448230.1	AA682308.1	T74219.1	1.0E-104 AF001395.1	1.0E-104 AF091395.1	1.0E-104 BF352841.1	3F352841.1	1.0E-104 AW103848.1	1.0E-104 AW103848.1	¥	1.0E-104 BE79/713.1	1.0E-104 BE79/1713.1	70.1	55.1	1	11427757 NT	3E720191.1
	Most Similar (Top) Hit BLAST E Value	1.0E-104	1.0E-104	1.0E-104	1.0E-104 U43379.1	1.0E-104 U43379	1.0E-104	1.0E-104	1.0E-104	1.0E-104	1.0E-104 BE3141		1.0E-104	1.0E-104	1.0E-104 BF4482	1.0E-104 AA6823	1.0E-104 T74219.	1.0E-104	1.0E-104	1.0E-104	1.0E-104 BF3528	1.0E-104	1.0E-104	1.0E-104 AF11351	1.0E-104	1.0E-104	1.0E-104 AV7280	1.0E-104[AU1307	1.0E-104 U66535.	1.0E-104	1.0E-104 BE72018
	Expression Signal	1.23	1.23	1.06	1.28	1.26	1.12	9.51	9.51	0.75	3.31	3.31	2.03	0.83	5.23	0.5	1.31	4.27	4.27	4.4	4.4	0.85	0.85	0.71	2.83	283	1.29	4.61	4.41	0.82	2.07
	ORF SEQ ID NO:	29832	29933	30441	31573	31574	31630	32141	32142	32322	32663	32864	32881	34330	34915	34897		35060	35061	33529	33530	35503	35504	35698	35852	35853	36160	36204	36327		37221
	Exen SEQ ID NO:	17305	17305	17824	18637	18637	18682	19144	19144	19316	19621	19621	19813	21187	21754	21833	21854	21893	21893	20412	20412	22306	22306	22497	22641	22841	22946	22986	23096	23110	23930
	Probe SEQ ID NO:	4570	4570	5106	5850	5850	5897	6375	6375	6551	6706	8708	7125	8495	5065	भक्ष	9184	9214	9214	8341	9341	9654	9654	9847	9993	6000	10239	10339	10450	† 1946	11268

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	Top Hit Descriptor	250 Linear 34070 LOS HOBBS Homo saplens cDNA	ACCEPTIONS OF THE MAN SECTIONS CON CHARGE 4302507 6	OUCHAIGHT THE MOC OF Home serving CDNA clone IMAGE:3841081 5	SUI 3008U0F1 NIT MISC. AT FRAID SENIER CONA COME IMAGE:3841681 5	601506800-1 Nin_mcc_k1 I wild appearance (RPS6KA5), mRNA	Profits september 12 AM Homo september CONA clone IMAGE: 3958676 51	0015151911 1 1 1 1 1 1 1 1 1	Homo sepiens smylold bets (A4) precured protein (protesse nextr-II, Alzheimer disesse) (APP), mKNA	Homo seprens mess (microsof) notices (microsoft) microsoft complete cds	Trans services proceeding channel subunit (HERG-3) mRNA, complete cds	Hollis equals powered to account HS210080	TUTION SERVICE STREET SERVICE SERVICE OF SERVICE SERVI	FETTANDO SALAM I Homo seniens CDNA 5' end similar to autoimmune anigen Ku, p70/p80 subunit	EST 2000 Spread I Trick Spread Constitution of the IMAGE 3919511 6	001434491F1 11tt _mooAnd	Linear series bromotomein adlacent to zinc finger domain, 28 (BAZ2B), mRNA	Home services homodomain adjacent to zinc finger domain, 28 (BAZ2B), mRNA	FST373781 MAGE resouverces, MAGG Homo septens cDNA	ANALASSOCIAL MAC OF Home septens CDNA clone IMAGE:3850156 5'	ANTALGAZZET NIH MIGC 65 Homo sabiens cDNA clone IMAGE:3850166 5	Homo earliers chromosome 21 segment HS21C008	Library services mRNA for KIAA0796 protein, perfiel ods	EST378088 MAGE resquences, MAGI Homo septems cDNA	Home seniors FB.AP ublaufilth-proben ligase (UBE3A) gene, each 2	Home services Retire-derived POU-domain factor-1 (RPF-1), mRNA	PAYACHONET NIH MGC 19 Homo sepiens cDNA clone IMAGE:4130334 5	ANADADADARET NIH MIGC 19 Homo septems CDNA clone MAGE:4130334 5	Home serviers GTPase activating protein the (GAPL), mRNA	Home carriers GI Pass scribating protein #ee (GAPL), mRNA	ESTAGAGE RESCUENCES, MAGE Homo septens cONA	ANARTOTOFI NIH MGC 21 Hamp septents aDNA done IMAGE:3980019 5	Home enjene platochin 4 (PKP4), mRNA	Human mRNA for dbi prote-progene	
	Top Hit Detabese Source	Т	Т	Т	П	HUMAN		EST HUMAN	Ę	뉟	Ę!	Į.	Z	L	EST HUMAN	EST HUMAN	L _N	N.	N I	EST HOWAY		ESI HUMAN	Z	Net Linksh	ESI TOMOTI	12	N A A A A A A A A A A A A A A A A A A A	TANK I	EST TOWARD	2 2	NAME TO T	TOT IN TANK	באו חטשעון	Z Z	
	Top Hit Acession No.		E720191.1	1.0E-104 BF684288.1	1.0E-104 BE731978.1	E731978.1	11434720 NT	E393892.1	4502166 NT	4505150 NT	1.0E-105 AF032897.1	1.0E-105 AF032897.1	1.0E-105 AL163280.2	50918.1	1.0E-106 AA318360.1	BE891766.1	1.0E-105 AJ228041.1	73040ZZINI	7304822 IN I	AW961688.1	BE86881.1	BE86881.1	AL163208.2	1.0E-105 AB018339.1	1.0E-105 AW 988016.1	AF016704.1	11420134 IN	BF314302.1	1.0E-105 BF314302.1			AW951634.1	BE90261	CASERS 4	1.0E-105/X12550.1
- 	Most Similar (Top) Hit I BLAST E	an a	1.0E-104 BE720191.1	1.0E-104 B	1.0E-104 B	1.0E-104 BE7319	1.0E-104	1.0E-104 BE3938	1.0E-106	1.0E-105	1.0E-105	1.0E-105/	1.0E-105/	1.0E-105 D50918.1	1.0E-105	1.0E-105 BE8917	1.0E-105	1.0E-105	1.0E-105		1											1		1	
	Expression Signal		2.07	4.96	1.75	1.75	1.42	238	11.13	8.99	1.92	1.92	16.0	1.03	1.29	1.44	2.80	0.88	0.88	2.07		0.74	424				1.07								0.97
-	ORF SEQ ID NO:		37222	37259	_		37712		25722		25987	25988						28759	28760	29447	L	30059				30681	3	32485	32486	30515	30516	3 32709	32944		4 33579
Ī	SEQ ID		23930	23960	24189	24189	24381	L	15514	L	<u>l</u>		14554	L	_	L	١.	16106	16105	16821	1_	L.	17613	17762	17810	18053	18118	19465	19465	17961	17961	7 19963	_	L	Ш
	Probe SEQ ID	:	11268	1,200	150	11500	1479	12702	373	410	280	280	1814	1919	2186	2322	3008	33.46	3348	407	4694	466	4886	5043	505	5247	6312	980	6804	6885	5885	6927	7184	7722	7758

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	EST02975 Fetal brain, Stratagene (cat#936208) Homo septens cDNA clone HFBCR32	W850c10.x1 NCI_CGAP_Bm25 Homo septions cDNA clone INAGE:2500626 3' similar to SW:ACSA_PENCH P36833 ACETYL-COENZYME A SYNTHETASE	RC1-CN0008-070100-011-e05 CN0008 Hamp septens cDNA	UI-H-Blop-abl-b-12-0-UI s1 NCI CGAP Sub2 Homo sepiens cDNA clone INA GF 2711782 3	QV2-010062-140300-063-409 OT0062 Hamo septens cDNA	QV2-0T0062-140300-083-d09 OT0062 Hamo septens cDNA	601443755F1 NIH_MGC_65 Homo sepiens cDNA done IMAGE:3847884 5	601443755F1 NIH MGC 66 Hamo septens cONA clone IMAGE:3847894 51	Homo sapiens SMARCA4 lacform (SMARCA4) care, complete cds, attenuatively splined	Homo sepiens COLAAB gene for e8(IV) collagen, expn 31	Homo eaplens Ran binding probein 11 (1.005/144) mRNA	w/74f07x1 Soeres_thymus_NHFTh Homo sapiens cDNA clone IMAGE:2535301 3' similar to TR-P87892 P87892 PROTEASE	7018c10.x1 NC_CGAP_Kd411 Homo sepiens cDNA clone IMAGE:3574291 3' similer to TR:P97680 P97680 PIN4	Homo seriens days for Strain 3 series 2 series 2	Homo seciens cere for Smark 3, even 2 and 3.	UI-HE-BNO-ald-0-07-0-UI-1 NIH MGC 50 Home services CONA city MA DE-80788348 FT	1979-01.xf NCI CGAP Uti Homo septems cONA clame IMAGE-22150A8 3'	EST377629 MAGE resequences, MAGI Homo sabiens cDNA	Human dihydrofolate reductace pseudogene (psi-hd1)	Human dihydrofolate reductase pseudogene (psi-hd1)	Homo sapiens soluble neuroplin-1 mRNA, complete cds	Human epidermal growth factor receptor (EGFR) precursor-mRNA, exon 4, partial cds	ng41c05.s1 NCI_CGAP_Co3 Homo sepiens cDNA clone IMAGE:837352 3' similar to contains element LTR3 recettible element:	ng41c05.e1 NCI_CGAP_Cc3 Homo sepiens cDNA clone IMAGE:837352 3' similar to contains element	L.I.R.3 repotitive element;	MR0-H10165-140200-008-d10 HT0165 Homo sepiens cDNA	Homo septens glubathione S-trensferese thete 1 (GSTT1), mRNA	601149783F1 NIH_MGC_19 Hamo sapiens cDNA clane IMAGE:3502481 5	qi76h10.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1878307 3'	Homo saplens glutathione S-transferase theta 1 (GSTT1), mRNA
gie Exon Proc	Top Hit Darkabase Source	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	Į.	אַז	Z	EST HUMAN	1	T		T HUMAN	Т	П		NT	IN	TN	EST HUMAN	П	Т	THOMAN		┒	6.1 EST_HUMAN (\neg
150 H	Top Hit Acessian Na	T05087.1	AW007194.1	AW840817.1	1.0E-105 AW016879.1	1.0E-105 AW882372.1	1.0E-105 AW882372.1	BE867793.1	BE867793.1	1.0E-105 AF254822.1	D63548.1	7705936 NT	1.0E-105 AW027554.1	3E430001.1	24.1	7.7		1.0E-106 AJ565065.1	556.1	Ļ		2.1	1	6.1		Ī	1.0E-106 BE144286.1	4504184	E280201.1	1276526.1	4504184
	Most Similar (Top) Hit BLAST E Value	1.0E-105 T05087	1.0E-105 AW007	1.0E-105 AW840	1.0E-105	1.0E-105	1.0E-105	1.0E-105 BE8677	1.0E-105 BE8677	1.0E-105	1.0E-105 D83548	1.0E-105	1.0E-105	1 0F-105 BF4300	1.0E-105 AB0049	1.0E-105/	1.0E-106 AW503	1.0E-106	1.0E-106 AW985	1.0E-106 J00146.	1.0E-106 J00148.	1.0E-106 AF14571	1.0E-106 U48724	1.0E-106 AA52744	10,	1.0E-100 AA02/4	1.05-105	1.0E-108	1.0E-106 BE28020	1.0E-106 AI27652	1.0E-106
	Expression Signal	6.55	1.41	0.68	2.82	0.0	6.0	99.0	89.0	5.73	1.59	2.38	2.58	87	1.7	1.73	1.30	1.79	2.68	0.75	206	1.33	3.48	4.71	7	4.71	231	2.89	1.82	3.24	1,91
	ORF SEQ ID NO:	33750	34129	34663		34054	34055	35247	35248	36778	37146	37204	37494	37592	37753	37754		25954	25947	28000	28000	26948	27138	27245	277248	27578	0/0/7	2///8	28064	28210	20842
	Econ SEQ ID NO:	Z290Z	20991	21518		21791	23	22077	22077	23531	23860	23912	24179	24270	24415	24415	12962	13013	13313	13371	13371	14262	4 4 6	14536	14598	74840		OF C	13322	15,08	14138
	Probe SEQ ID NO:	7927	8297	8828	8948	9103	8	9467	9467	10850	11195	11250	11580	11675	11831	11831	147	200	223	501	285	1515	1607	1796	1708	2 2	21.12	3 8	DIE?	2761	5262

Page 434 of 536 Table 4 Single Exon Probes Expressed in Brain

•	1/3/2/3		~	~	_	_	-	_	_	_		_							4.	ر ح			دے			<u> </u>	20		24	. OU	
The state of the s	Top Hit Descriptor	Homo saplens glutathione S-transferase theta 1 (GSTT1), mRNA	Hamo septens mRNA for KIAA1328 protein, partial cds	Hamo septens mRNA for KIAA1328 protein, pertiel cds	Homo saplens hypothetical protein FLJ11273 (FLJ11273), mRNA	Homo saplens hypothetical protein FL11273 (FL11273), mRNA	Homo saplens gene for activin receptor type IIB, complete cds	Homo septens mRNA for KIAA1278 protein, pertie cds	Homo septens mRNA for KIAA1278 protein, pertial cds	EST389875 MAGE resequences, MAGN Homo septens cDNA	EST388375 MAGE resequences, MAGN Homo septems cDNA	Homo saplens APIS-like ((APIS-1), mRNA	MR0-HT0185-140200-008-410 HT0165 Hamo septens cDNA	H.septens mRNA similar to D29763 mouse mRNA for seizure-related gene product 6. Shares domains with BMPs, Toflod, Sushi repeat profeins	H.saplens mRNA similar to D29763 mouse mRNA for seizure-related gene product 6. Shares domeins with BMPs, Tolloid, Sushi recent profesia.	el24b09.s1 Socres_testis_NHT Home septens cDNA done 1391225 3' similar to gb:X12433 PROTEIN PLPS1-2 0-II MANN	AL130113 NT2RP3 Home services ANA Alexa NT20D2000224 Et	AU130113 NTZRP3 Home senders cDNA clone NT2RP3nnn774 5	2W28d12.s1 Soares overy turnor NOHOT Homo seniens CDNA rights (MACZE-77) 615.9	AU143428 Y79AA1 Homo sapiens CDNA clone Y79AA1001912 5	AU143428 Y79AA1 Homo appiens cDNA clone Y79AA1001912 5	602154012F1 NIH_MGC_83 Hamp suplens cDNA clone IMAGE:4285067 5	601439670F1 NIH_MGC_72 Homo septens cDNA clone IMAGE:3924641 67			spiens cDNA clone IMAGE:9897323' similar to gb:X65873	57108) mRNA	Alone MARCH: DOBROAFE			HEMBA1000129 5'
BIG LAGIT FIG	Top Hit Database Source	호	NT	F	F	LN LN	N.	Į.	Į	EST HUMAN	EST HUMAN	N-	EST HUMAN	N.	Į.	EST HIMAN	EST HIMAN	EST HUMAN	Т	Г	EST_HUMAN		EST_HUMAN			EST HUMAN	ı	Т	11425503 NT	Т	THUMAN
5	Top Hit Acession No.	4504184 NT	17.1	17.1	R922985 NT	FN 5222965 NT	AB008681.1	1.0E-106 AB033104.1	1.0E-106 AB033104.1	1.0E-106 AW974650.1		9729	1.0E-106 BE144296.1	1.	Σ.		Ī	3.1	Γ	Γ	8.1		1.0E-106 BE897112.1	11545913	11545913 NT		28617	E292722.1	11425503	11425503 NT	<u> </u>
	Most Similar (Top) Hit BLAST E Value	1.0E-106	1.0E-106 AB03774	1.0E-108 AB03774	1.0E-108	1.0E-106	1.0E-106 AB00868	1.0E-106	1.0E-106	1.0E-108	1.0E-106	1.0E-106	1.0E-108	1.0E-106 AL05025	1.0E-106 AL050253	1.0E-106	1.0E-106 AU13011	1.0E-106	1.0E-106	1.0E-106	1.0E-106	1.0E-106 BF67957	1.0E-106 B	1.0E-106	1.0E-106	1.0E-106 AA663779,1	1.0E-108	1.0E-106 BE292722.1	1.0E-106	1.0E-106	1.0E-106 AU116850
	Expression Signal	1.91	5.23	5.23	2.18	2.18	0.81	1.18	1.18	7.95	7.95	1.05	4.1	1.09	1.09	2.61	0.58	0.58	0.58	1.3	1.3	4.80	0.77	17.66	17.68	5.18	5.33	1.21	82.6	9.29	0.67
	S G	26843	28357	28358		28589			28839	28391	28382	29410	20024	30469	30470	30750	31480	31481	31533	31637	31638	31756	31800	32083	32084	33031	33084	33161	33275	33276	33481
	Ø]		15707					16190	16783	16763	16780	17297	17853	17853	18090	18555	18555	18605	18689	18680	18792	18892	19095	19095	19955	20002	20090	20182	20182	20378
	Probe SEQ ID NO:	2828	2942	2942	3176	3178	3367	3434	3434	4017	4017	4035	4562	5135	5135	5285	5764	5764	5816	3904	2005	8	888	8325	8328	727	7324	7402	7511	7511	71.14

Page 435 of 536 Table 4 Single Exon Probes Expressed in Brain

	Top Hit Descriptor	Т	T	1		Ī	Γ		CO5084 69 KD ISLET CELL AUTOMATICEN ,	Т	Т	Т	cn03a04.y1 Normal Human Trabecular Bone Cells Home sapiens cDNA clone NHTBC_cn03a04 random Cn03a04.y1 Normal Human Trabecular Bone Cells Home INACE: 2167600.31 similar to contains MSR1.83		TAR1 PTR5 reporting element; TAR1 PTR5 reporting element; TAR2 PTR5 reporting element; TAR3 PTR5 reporting element;		1 (601282387F1 NIH MGC 44 Hamb septens durk dure IMAGE:3054403 5	- 1	- 1	Т	T	┰	Τ	Т	T	Т	Harmen namodine receptor mRNA complete cds	Т	Т	Т	T	Т	7
	Top Hit Detabase Source	MANUEL TOT	NOMOL ICI	ESI HOMAN	EST HUMAN	EST HUMAN	EST HUMAN		EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN		EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	ESI HUMAN	EST HIMAN	2	ECT UIMAN	EST HIMAN	133	2 12	I N	ESI TOMAN	TOT TOWN	FOT LI MAN	EST HIMAN	
	Tap Hit Acession No.		1.0E-106 BE /41408.1	1.0E-108 BE741408.1	4 OE-406 A1523088.1	4 OE-106 RE387850 1	4 OF-108 RE387950.1		1.0E-106 AI654123.1	1.0E-106 AW838831.1	1.0E-106 AA825307.1	AA825307.1	1.0E-108 AT750447.1		1.0E-108 AI479569.1	1.0E-106 AI479569.1	1.0E-106 BE389234.1	1.0E-106 BF027310.1	1.0E-106 BF027310.1	1.0E-106 AAG04417.1	1.0E-106 AA604417.1	1.0E-106 AW363299.1	1.0E-106 ALLOSEGO. I	1.0E-106 AL 163202.2	1.05-106 BH-032/55.1	1.0E-106 BFW3Z/33.1	1.0E-106 J05200.1	1.0E-106 J06200.1	1.0E-106 BE25/385.1	1.0E-106 BE010882.1	1.0E-106 BE010882.1	1.0E-106 AW 410405.1	1.0E-106 BE884466.1
	Most Similar (Top) Hit BLAST E Value		1.0E-106	1.0E-108	10 t	4 OF 405	401-101-101-101-101-101-101-101-101-101-		1.0E-108	1.0E-106	1.0E-106	1.0E-108	1.0E-106		j									┙	1	1	1		j			_	
	Expression Signed		6.44	6.44	00.7	000	27.0	2	3.64	0.58	3.28	3.28	1.28		1.8	18	1.10	1.09	1.09	622	6.22												3.32
	ORF SEQ ID NO:		33707	33708	70000		3430T		34443				35021		35169	25470	Ŀ			39003									37202		2 37437		31068
	Exan SEQ ID NO:		20579	20579	l _	.1	21219	21218	21299	L	L	L	<u> </u>	ı	21996	l	1_		L	1_	_						5 23668		23991	<u> </u>	24132	1 25194	3 24664
	Probe SEQ ID NO:		7884	7884		80/4	8527	897/	8607	988	9045	9045	8	8	8329	8	8000	1000	8984	19141	10141	10185	10356	10479	10812	10812	10995	10995	11384	11532	11532	11981	12193

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		T	T		T	T	T	T		T	T		T	T	Τ	Τ	Τ	T	Τ	Ī	Ī	Ī	T	Ť	֓֟֟֟֟	Τ	T	T	Ī	T	T	Ť
Oligie Extil Flobes Explessed III blann	Top Hit Descriptor	601433087F1 NIH_MGC_72 Hamo septens cDNA done IMAGE:3918524 51	RC1-CT0249-090800-024-d05 CT0249 Homo serviens cDNA	Homo saciens Xg pseudoautosomal region; segment 1/2	Human IFNAR gene for interferon alpha/beta receptor	Homo septens neuronal cell achesion molecule (NRCAM) mRNA	Homo sabiens NY-REN-25 antigen mRNA, pertial cds	Human IFNAR gene for interferon alpha/beta receptor	Homo saciens sodium-dependent Noh-effinity dicerboxyleis transcorter (NADC3) mRNA complete cits	Homo seplens BAZ18 mRNA for bromodomein adiacent to zinc finger domain 18, complete over	QV2-HT0540-120900-358-a05 HT0540 Homo sepiens cDNA	Homo sapiens cathepsin Z precursor (CTSZ) gene, expn 3	Homo sepiens mRNA for KIAA0453 protein, pertial cds	Homo septems mRNA for KIAA0463 protein, pertiel ods	Human dipeptidyl peptidase IV (CD28) gene, exxn 20	PM1-CN0031-190100-001-d03 CN0031 Homo septens cDNA	PM1-CN0031-190100-001-d03 CN0031 Homo septens cDNA	801567619F1 NIH_MGC_21 Hamo septens cDNA clane IMAGE:3842309 5'	601567619F1 NIH_MGC_21 Hamo suplens cDNA clane IMAGE:3842309 57	PM1-CN0031-190100-001-d03 CN0031 Homo septens cDNA	PM1-CN0031-190100-001-d03 CN0031 Homo sepiens cDNA	Homo septens SMT3 (suppressor of mif two 3, yeast) homolog 2 (SMT3H2), mRNA	Homo sapiens myotubularin (MTM1) gane, exon 9	EST381115 MAGE resequences, MAGK Homo sapiens cDNA	601442558F1 NIH_MGC_65 Homo sapiens cDNA done IMAGE:3846494 5	Homo saplene general transcription factor IIIC, polyceptide 1 (alpha subunit, 220kD.) (GTE3C1), mRNA	Homo septens general transcription factor IIIC notweentide 1 (alche auteus especial transcrip	UI-HE-BNO-GI	UHIF-BNO-eff-08-0-U.H NIH MGC 50 Hamp septems cDNA clara IMAGE-3070830 ST	wh56h04.x1 NCI CGAP Kid11 Homo sepiens cDNA clone IMAGE:23847x1 3'	fh09d11.x2 NIH MGC 17 Hamo septens cDNA dane IMAGE:2884624 5	A I 1992/80 LANAMAK U.
	Top Hit Detabase Source	EST HUMAN	EST HUMAN	IN	¥	Ę	Į.	Į.	¥	NT	EST HUMAN	N	NT	L.	L L	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	Į.	Ę	EST_HUMAN	EST_HUMAN			T HUMAN	Т	Т	Т	HIMAN
	Top Hit Acession No.	1.0E-106 BE894488.1	1.0E-106 BE095905.1		-	4826963 NT	83.1	T-	1.0E-107 AF154121.1			75.1		1.0E-107 AB007922.2			51.1	30.1	50.1	51.1	151.1	5902097 NT	71.1	1.0E-107 AW969038.1	1.0E-107 BE867489.1	11431489 NT	11431489 NT	1.0E-107 AW503013.1	Γ	Γ	-	T
	Most Similar (Top) Hit BLAST E Vælue	1.0E-106	1.0E-108	1.0E-107	1.0E-107 X80459.	1.0E-107		1.0E-107 X80459		1.0E-107	1.0E-107	1.0E-107 AF136Z	1.0E-107	1.0E-107	1.0E-107 U13729.1	1.0E-107 AW8424	1.0E-107	1.0E-107 BE7324	1.0E-107 BE7324	1.0E-107 AW8424	1.0E-107 AW8424	1.0E-107	1.0E-107 AF0206;	1.0€-107	1.0E-107 E	1.0E-107	1.0E-107	1.0E-107	1.0E-107	1.0E-107 AI765078.1	1.0E-107	4 OF-407 A
	Expression Signal	3.32	4.6	4.42	1.20	4.03	1.89	1.52	11.55	67.0	3.77	1.55	0.00	00.0	0.95	1.45	1.45	1.2	1.2	3.80	3.89	2.63	5.14	0.66	3.2	1.45	1.45	1.42	1.42	1.46	9.0	0.055
-	ORF SEQ ID NO:	31069					25028	26305	26379	26673	26996	27187	27283	27284	27671	27822	27823	27991	27982	28421	28422	28502	29190	31242	31495	32506	32507	33023	33024	33193	33469	35213
	Exan SEQ ID NO:	24664	24791	13040	13066	13385	13394	13635	13714	14004	14309	14488	14571	14571	14833	l	- 1	\perp	_ [15773	15773	15861	16558	18335	18566	19484	19484	19947	19947	20106	20354	22041
	Probe SEQ ID NO:	12183	12408	822	258	607	616	866	948	1255	1562	1746	1832	1832	2205	2362	2362	2535	2535	3007	3007	3080	3806	5537	5775	8823	8823	7263	7263	7429	7690	9287

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Table 4
Single Exon Probes Expressed in Brain

Single Exon Probes Expressed in Brain	Exp Most Similar Top Hit Acession Top Hit Acession Top Hit Acession Top Hit Acession Top Hit Descriptor NO: Signal BLASTE No. Source Source	36537 3.18 1.0E-107 AIS62850.1 EST_HUMAN	36794 14.26 1.0E-107 LA9141,1 NT	23560 36807 1.71 1.0E-107 BF986511.1 [EST_HUMAN 602123863F1 NIH_MGC_56 Homo sepiens cDNA clone IMAGE:4281039 6	37252 6.86 1.0E-107 BE540550.1 EST_HUMAN	38405 5.97 1.0E-107 11419701 NT	23178 36406 5.97 1.0E-107 11419701 NT Homo sapiens HSPCX49 protein (HSPCX49), mRNA	37768 1.36 1.0E-107	37769 1.36 1.0E-107 4506970 NT	5.88 1.0E-107 AA001415.1 EST HUMAN	28367 2.66 1.0E-108 BE296042.1 EST HUMAN	28857 1.87 1.0E-108 Y18000.1 NT	27883 4.97 1.0E-108 BE209694.1 EST HUMAN	28755 0.71 1.0E-108 AF032897.1 INT	28766 0.71 1.0E-108 AF032897.1 NT	1.14 1.0E-108 AW68438.1 EST HUMAN P55194 SH3-BINDING PROTEIN 3BP-1.1	29853 2.18 1.0E-108 U72981.1 NT	29854 2.18 1.0E-108 U72861.1 NT	30113 1.74 1.0E-108 7881979 NT		30883 1.16 1.0E-108 AW384084,1 EST HUMAN	30954 1.7 1.0E-108 BE868016.1 EST_HUMAN	30955 1.7 1.0E-108 BE869016.1 EST_HUMAN	0.99 1.0E-108 AF012823.1 NT	31790 6.13 1.0E-108 AF264717.1 NT	1.0E-108 AF264717.1 NT cds Cds Cds Cds Cds Cds Cds Cds Cds Cds C
	Exan ORF (•				24427 3	24427 37	25328		13991 20	15149 27	16103 28	16103 28						Н			18626	18828 31	18828 31
	Probe SEQ ID NO:	10003	10886	10880	11293	11367	11387	11843	11843	12043	88	1242	2428	3344	3344	4136	4480	4480	4752	4896	6391	5440	5440	5837	6048	8048

PCT/US01/00667

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Sirgie Exort Probes Expressed in Drain	Top Hit Descriptor	Homo sepiens caveolin-1/-2 locus, Contig1, D75522, genes CAV2 (exons 1, za, and zb), CAV (exons 1 and zb), CAV (exons 1), 2, and 2 (exons 1), CAV (exons 1),	PM4-CT0403-240700-001-c10 CT0403 Home septens cDNA	Homo eaplers Ed-AP unquint-growing gase (out) gale, won the real three (1953) here each 4	Homo septents to Art unsquitted months demand of manner B (GPROSB), mRNA	HOTTO Septents G promit receiption, remain of strong of many of the septents of the PANA TABLE OF THE STRONG T	HOTTO sappens of the July and constitution of the Constitution of	SOUTH 1547 IF I NIT CAMP BINEZ Homo services CDNA clone IMAGE: 4181037 5	ACASSAGE NCT COAP Brind? Homo sections cDNA clone IMAGE:4181037 5	COLORS SORT I NO COLO LOS CONTROL DE CONTROL MANA CONDISTA CONTROL CON	Homo septens connective users grown receives of the construction o	ULATE-BIND-608-6-12-C-DLIT NAT MICC SO HOME CONA CIONE INACE:3062878 5	ULHT-BMC-408-4-12-4-Ci. I I II I MCC 30 I GII S GARANDA COMPINE CAS	Homo eaplens in 10-ferrity delicarpoon technologies (Lin) in section 273/23 57 similar to PIRA45773	AST-10.r1 Soares melanogys ZNBrIM Homo saperis cultiva dara mandellar communications of the communications and the communications of the communications and the communications are communicated to the communications and communications are communicated to the communications are communicated to the communications are communicated to the communications are communicated to the communications are communicated to the communications are communicated to the communications are communicated to the communications are communicated to the communications are communicated to the communications are communicated to the communications are communicated to the communications are communicated to the communications are communicated to the communications are communicated to the co	RATARRAPASET NIH IMGC 10 Homo sections CDNA clone IMAGE:3445361 5	W. Pool Control of Cold associated internative binding protein (GMAP-210)	Homo expens minner for our resource in the CACNA1F) generally and partial cds, alternatively	Homo septens carcium chemical espira in second (Chica Chica) second septens carcium chemical second	EST378268 MAGE resequences, MAGI Homo septens cDNA	AV708790 ADC Homo septiens cDNA clone ADCAEE03 6	AV708750 ADC Homo serviers cDNA clone ADCAEE03 5	Homo sepiens G protein-coupled receptor 48 (GPR48), mRNA	Home servious COL4A6 cens for e8/IV) colleges, exch 23	Homo seniens mRNA for FL.00037 protein, pertial cds	R2018571F1 NCI CGAP Bm87 Homo seciens aDNA done IMAGE:4154297 5	19 21 MAN 77 - 260400-079-D08 UM0077 Homo septens cDNA	Limman DNA for KIAAAAAA nedal cds	FIGURE 118 CAN TANGET STORY FOR THE PROPERTY CHARGE (RON) MRNA	Idino sayens reportation (1) Li High Control of Transportation (1) MANAGER (1)	Home eaplers tetrestroppeder repeat content 2 (1 102) this ex	Home sapiens mytha tor Klaatueed progen, parties as	Homo sapiens mRNA for KIAAUSES protein, perda cos	TOTIO BENDETE ILLUCTURE PITOSPINAPIONE LA COMPANIONE LA CO
B EXOLI PIODE	Top Hit Database Source	Ho TN	T HUMAN					Т	Т	HUMAN	┪	T	LOWAN	Ė			LICENSE	Ę	5	T HIJMAN	Т	Т	A CAROLL		Z	TO INVAN	Т	אויייטרר ו כבו	Į.	LN.	NT	M	N.	L
Sing	Top Hit Agession No.	1.0E-108 AJ133289.1		06.1	8.1	11431857 NT	4758333 NT	1.0E-108 BE252807.1	1.0E-109 BF528912.1	1.0E-108 BF528912.1	1.0E-108 AF083500.1	1.0E-108 AW 408694.1	1.0E-108 AW408694.1	AF203977.1		144974.1	1.0E-108 BE535227.1	Y12490.1	A E777401 1	ALLORATOR 1	1.0E-109 AW SOULD: 1	AV /08/80.1	1.0E-108 AV /US/50.1	IN COLUMN	D63539.1	1.0E-108 AK024447.1	1.0E-108 BF346350.1	AWB03116.1	ŦІ	11438391 NT	4507712 NT	1.0E-109 AB023216.1	1.0E-109 AB023216.1	M28699.1
	Most Similar (Top) Hit 1 BLAST E Velue	1.0E-108	1.0E-108	1.0E-108 AF0187	1.0E-108 AF0167	1.0E-108	1.0E-108	1.0E-108 E	1.0E-108	1.0E-108	1.0E-108	1.0E-108	1.0E-108	1.0E-108		1.0E-108 N44974	1.0E-108	1.0E-108 Y12490	4 05 400 45222	1.00-100	1.01	1.05-108	1.05-108	1.0E-108	1.0E-108 De353	1			1.0E-109 D8697					
	Expression Signal	121	0.92	0.63	0.63	5.82	3.55	1.18	0.84	0.84	1.68	0.48	0.48	0.75		25.0 25.0	1.73	1.98	7	BC.T	3.82	22	2.2	1.6/	1.68	2.41	8.32	0.87		1.59				10.97
	ORF SEQ ID NO:	898		32280	32291	32811		33137				33838	33839		L			30597					37254			31072		25488	25623	25687				3 26598
	SEQ ID	18048	18897	19287	19287	19748	20020	20057	20082	20082	L	1_	l_	1	1_	1	20368	L_	<u> </u>	_	_ !							12869	12800	L	L			13933
	Probe SEQ ID NO:	8	8285	128	8521	1902	7339	7377	7406	7405	7983	8014	8014	8045		8984	10585	10731		10998	11239	11204	11294	11343	11405	12204	12583	41	8	220	154	282	584	1180

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Top Hit Descriptor	B23 (NPM1) mRNA, complete cds	lens CUNA date IMAGE: Assesso o	tens cDNA cone IMA(JE:2838630 3	ten, partial cas	THS/TICKS	Homo sepiens SNF5/IN/1 gene, exon 6	ATHODIC ANTIGEN ;	owesen1x1 Source_fetal_liver_spleen_1NFLS_S1 Hamo septens d.N.A. dans invoce_1031000_0 sillines to TR:002197 CIRCULATING CATHODIC ANTIGEN.	tor 1A (resina) (GUCA1A) manna	J2816F Human fetal heart, Lambda ZAP Express Homo sapiens curn come 32010 o summer anno 37816F PROTEIN ZNF43	9 Homo sapiens cDNA	Homo sapiens CDNA	Homo sapiene retinal dehydrogenese namado Borama (RCLT) minuty, compress com	Homo sapeins adenosine monophosphilite dearningsee 1 (AMPDA) para winns 8-10	Homo espelins adenosare monoprospriate designates of 1 (20mm), control o	Train agree to control	occur, per use cue	Homo appens mixed to No. 10. And the Linear service Anna IMA(3E:2238330 3' similar to WP:F53A2.8	* NEW INC. TO SERVICE STORY OF THE PROPERTY OF	MANGE 12 19202 S BRITISH IN CONT. C. 1 22 10 MILES	mg3c12.s1 NCL_CGAP_P722 Home septens cDNA clone IMAGE:1216262.5 strings to 571.011.2_1101674.1 Pengapangan matangkan satangsperase THETA 2:	itor 1A (retire) (GUCA1A) mRNA	(KJA40377), mRNA	kme IMAGE:53057 5'	VARIOUS IN COMES BINEIN MEN IN IN INC. ACTION CONTRACTOR IN INC. 1950-1950 5	6011 608 ZZZ Z NRT MOC TO TOTAL SEPTEMBER OF A COMPANIE OF TOTAL SEPTEMBER S	Nik close PI ACE1006159 5	AU13/222 FLAUCT Fully agreeme contribution of the IMAGE:4272922 6	
	Homo sepiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds		П	Homo sapiens mRNA for KIAA0018 protein, pertial ods	Homo sapiens chromosome Z1 segment HSZ1009	Homo sapiens SNF5/INI1 gene, exon 6			П		Γ	П	Homo sapiens retinal dehydrogenese h	Homo sapeins adenosine monophospin	╗	П	Homo sepiens miKNA for KIAAUOUS procent, per use cus	Homo septens mixing for London			_	T	Long serions KIAA0377 came product (KIAA0377), mRNA	Т	Т	Т	Т	T	7
Top Hit Deterbase Source	NT	EST_HUMAN	EST_HUMAN	NT	Ę	NT L	EST_HUMAN	8.1 EST_HUMAN	Ν	EST HUMAN	EST HUMAN	EST HUMAN	NT	N	노	EST HUMAN	호	Ę	EST_HUMAN	EST_HUMAN	3 7 7 7	121		I NI	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN
Top Hit Acession No.		3.1	3.1		1.0E-109 AL163284.2		A1022328.1	A1022328.1	4504208	N85190.1	AW8831921	AW8931921	1.0E-109 AF240698.1	M37928.1	M37928.1	1.0E-109 BE140144.1	1.0E-109 AB011181.2	AB011181.2	1.0E-109 AI655417.1	1.0E-109 AA682274.1		1.0E-109 AA662274.1 ES		7062083 IN	1.0E-109 R15400.1	1.0E-109 BE293673.1	1.0E-109 BE293673.1	1.0E-109 AU137282.1	1.0E-109 BF673718.1
Most Similer (Top) Hit BLAST E Vatue	1.0E-109 M28089.1	1.0E-109 BE29367	1.0E-109 BE28367	1.0E-109 D13843.2	1.0E-109	1.0E-109 Y17123.1	1.0E-109 A1022328	1.0E-109 Al022328	1.0E-109	1 0F-100 N85190.	1.0E-109 AW8831	1.0E-109 AW8831	1.0E-109	1.0E-109 M37928.	1.0E-109 M37828.	1.0E-109	1.0E-109	1.0E-109	1.0E-109	1	1		1		1.0E-109				1
Expression	1	334	3.31	3.3	1.78	1.88	3.98	88,	207	,	3 14	3,14	124	60	0,0	2.59		1.42	3.88						1.27	1.30			1.06
ORF SEQ ID NO:	26508	28087	88	27315	27705			28085	28082	<u> </u>						L	20357		79497							30320			30503
SEQ ID	13023	200	14280	14605	4085	14976	15340	1	1			18142	1	1_	L		1_		1	1	1_		17109	17298	17595	L	<u>i_</u>		17988
Probe SEQ ID NO:	4484	4634	1 2 2	1887	73.27	2248	acac.	8090		38	5000	2982	3508	3548	3548	3873	3074	3974	4427	777		4141	4371	4581	4867	4692	4002	5167	6179

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Single Exon Probes Expressed in Brain

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Top Hit Descriptor	Homo sapiens placental protein 11 (serins proteinass) (P11) mRNA	RC1-HT0615-200400-022-d04 HT0615 Homo sepiens cDNA	CM/1-UT0038-060900-300-h07 UT0038 Homo sepiens cDNA	RC1-HT0815-200400-022-404 HT0615 Hamo septens cDNA	Homo seplens mRNA for KIAA1591 protein, pertial cds	Homo sepiens AT-binding transcription factor 1 (ATBF1), mRNA	601808495F1 NIH_MGC_18 Hamp septens cDNA clone IMAGE: 4040279 5'	801809485F1 NIH_MGC_18 Hamo sapiens cDNA clane IMAGE: 4040279 5	801145017F2 NIH_MGC_19 Hamo sepiens cDNA dane IMAGE:3160229 5'	Novel human gene mapping to chomosome 13	PM0-BT0340-091299-002-e05 BT0340 Homo septens cDNA	7818H01 Chromosome 7 Fetal Brain cDNA Library Homo sepiens cDNA clone 7818H01	601478417F1 NIH_MGC_68 Homo septens oDNA clone IMAGE:3882124 5	801479417F1 NIH_MGC_68 Hamo septens cDNA clone IMAGE:3882124 5	ILOHT0205-07/199-142-g01 HT0205 Hamo sepiens dDNA	ys00308.r1 Soares refine N2bGHR Homo septens cDNA done MAGE:222110 5' similar to SP.A53491 A53491 BUMETANIDE-SENSITIVE NA-K-CI COTRANSPORTER - SPINY	601289780F1 NIH MGC_8 Homo sepiens cDNA clone IMAGE:3620030 5	601289780F1 NIH MGC 8 Homo saplens oDNA clone IMAGE:3620030 67	HSC1EC121 normalized infant brain cDNA Homo septens cDNA clone c-1ec12	601063030F1 NIH_MGC_10 Homo sepiens cDNA done IMAGE:3446599 5'	601063030F1 NIH_MGC_10 Homo septens cDNA clone IMAGE:3449599 5"	802080724F2 NIH MGC_81 Homo sapiens cDNA clone IMAGE:4245341 5	Homo sapiens KIAA0744 gene product; histone deacetylese 7 (KIAA0744), mRNA	Homo sapiens KIAA0744 gene product; histone deacetylese 7 (KIAA0744); mRNA	AU121370 HEMBB1 Hamo septiens cDNA clane HEMBB1002890 5"	Homo sapiens Chediak-Higashi syndrome 1 (CHS1) mRNA	2508512.rt Sceres fedal Jung NbHL19W Homo sepiens cDNA clone IMAGE:301439 5' similar to	PIR:S43866 S43860 p54-beta strees-activated protein kinases - rat;	Homo sepiens single-minded (Drosophile) homolog 1 (SIM1), mRNA	802039003F1 NCI_CGAP_Bm84 Home septens cDNA clone IMAGE:4186753 6	602036003F1 NCI_CGAP_Bm64 Homo sepiens cDNA clone IMAGE:4186753 5'	Homo sapiens SNF5/INI1 gene, exxn 6	Homo sepiens SNF5/NI1 gene, exon 6
Top Hit Detablesse Source	N.	EST_HUMAN	EST_HUMAN	EST_HUMAN	Z	Z	EST_HUMAN	EST_HUMAN	EST_HUMAN	Ę	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	NT	NT	EST_HUMAN	M		EST HUMAN	Z	EST_HUMAN	EST HUMAN	NŦ	N-
Top Hit Acession No.	5174622 NT	1.0E-109 BE179356.1	1.0E-109 BF379688.1	1.0E-109 BE178358.1	1.0E-109 AB046811.1	11432574 NT	BF182707.1	BF182707.1	1.0E-109 BE263297.1	AL040784.1	AW749130.1	1.0E-109 AA077498.1	1.0E-109 BE787540.1	1.0E-109 BE787540.1	1.0E-109 BE145672.1	184860.1	3E397068.1	1.0E-109 BE397068.1	-09804.1	1.0E-109 BE540909.1	1.0E-109 BE540909.1	3F694831.1	7862279 NT	7862279 NT	10121370.1	4502838 NT		W16510.1	11418618 NT	3F33D540.1	1.0E-109 BF339540.1	17123.1	17123.1
Most Striller (Top) Hit BLAST E Value	1.0E-109	1.0E-109	1.0E-109	1.0E-109	1.0E-109	1.0E-109	1.0E-109 BF1827	1.0E-109 BF1827	1.0E-109	1.0E-109 ALC497	1.0E-109 AW749	1.0E-109	1.0E-109	1.0E-109	1.0E-109	1.0E-109 H84860	1.0E-109 BE3970	1.0E-109	1.0E-109 F08804.	1.0E-109	1.0E-109	1.0E-109 BF6948	1.0E-109	1.0E-109	1.0E-109 AU1213	1.0E-109		1.0E-109 W 10510.1	1.0E-109	1.0E-109 BF3395	1.0E-109	1.0E-109 Y17123.1	1.0E-109
Expression Signel	3.09	1.11	79'0	1.6	76.0	3.99	6.28	5.28	0.67	1.48	66'0	2.77	8.42	8.42	99.0	181	0.63	0.63	264	1.71	1.71	15.79	1.55	1.55	1.8	272		11.0	1.46	1.27	1.27	2.1	273
 	30662		31580				33232			96888	34014		34468	34467	34711	34990	35101	35102		9099E			36818	36819	37013	37336		37291	37602	37773	37774	27714	277.14
· Exen SEQ ID NO:	18036	18318	25078	18318	19827	20138	20140	20140	20338	20787	20877	21247	21325	21325	21567	21825	21929	21929	22046	23364	23384	23399	23588	23568	23739	24032		23880	24280	24432	24432	14978	14976
Prabe SEQ ID NO:	0623	220	5838	2003	7140	7464	7468	7466	7674	8073	8183	8555	8633	8633	8876	9H37	8250	9250	8384	10673	10673	10710	10888	10888	11069	11342		11383	188	11848	11848	12112	12328

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Top Hit Descriptor	Homo saplens gene for AF-8, complete cds	Homo septens deloginates, todostyratine, type II (DIOZ), usilisaty visualisaty in the septens deloginate in the septens de	Homo sapiens reticate zupor ano manetario and ano ano ano ano ano ano ano ano ano ano	Homo septents lettoring that a familiar injudical regulations (American SAHC3467	CO4468 Human reservation (Trisecularies) Forms September 2 mRNA	HOMO BEDICATE STATE AND THE CONTRACT OF THE CO	Human dyeutuk everi (U.11) seria, everi zeria.	Harris equals to the complete of a second to the finger domain 18, complete of a second to the finger domain 18, complete of a second to the finger domain 18, complete of a second to the finger domain 18, complete of a second to the final	HOURS SELECT IN MICH. ALL Home sections CDNA clone IMAGE:3809883 5	001237 SHORT INTO MICE TO COMP SUIDS HOME SEDIENS CON COMP IMAGE:3085784 3'	UST BIT ENGLOSS TO THE STATE OF	HOTO SECTION CONTROLL TO THE PROPERTY (PZP) TIRNA	Trans separation for the property (PZP) mRNA	Harno supports programmy to the process of the constant of the	KIAA0500 PROTEIN;	out32b10.x1 Soeres_NPL_T_GBC_S1 Hamp septiens cDNA clone IMAGE:1627ecs 3 semiliar to	SW:N(21_RAT P62991 NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN FOM 121;	AU117812 HEMBAT Hamp supering Color Color Telegram Color Col	ACKARAGA NILL MAC 17 Home seriens CINA clane IMAGE:3028538 5	ANTALANATZES NIH MGC 70 Homo sapiens cDNA clone IMAGE:3895795 5	Homo earliens hypothetical protein FLJ10300 (FLJ10300), mRNA:	Home serians handhelical protein PL/10300 (FL/10300), mRNA	Human cystic fibroeis transmembrane conductance regulator (CFTR) gene, exch 7	Himmen GS2 pena. econ 2	Himan (SS) dens. mon 2	LACADA MINISTER DE BROSS Homo septems CDNA clone IMAGE:2167407 3' similar to SW:ETV1_HUMAN	PS0549 ETS TRANSLOCATION VARIANT 1;	AV7714276 DCB Hamp septems aDNA clane DCBCGE01 6"	AV714276 DCB Homo septems cDNA clone DCBCGE01 5"	Homo sepiens mRNA for KIAA0888 protein, partial cds	AU137923 PLACE1 Hamp sepiens aDNA dans PLACE1007511 5	
Top Hit Database Source	Ę	N	ᅜ	Ę	EST HUMAN	Į.	<u>ا</u>	Į.	LN	EST HUMAN	EST HUMAN	<u>ل</u> ا	Į.	뉟	EST HUMAN		EST HUMAN	EST HUMAN	IN.	ESI HUMAN	ESI HUMAN	- L	ž į	2	Z	Z	EST HUMAN	EST HUMAN	EST HUMAN	Ę	EST HIMAN	
Top Hit Acessian No.	AB01.1389.1	7549804 NT	5803073 NT	5803073 NT	٠. ١	7549804 NT		5031620 NT	AB032263.1	BE379477.1		4503008 NT	11436041 NT	11436041 NT	4 0F-410 BE018556.1		A1017213.1	1.0E-110 AU117812.1	7862441 NT	BE299406.1	1.0E-110 BE621069.1	IN COSTALL	IN CASUALT	L'ZLLOCM	1.0E-110 U08888.1	1.0E-110 U08888.1	1 OE-110 AIBB0280 1	AV744278.1	4 DE-440 AV714276.1	4 0E 440 AR020875 1	4.0E-110 AUGUSTON 4	AU13/863.1
Most Similar (Top) Hit BLAST E Value	1.0E-109	1.0E-110	1.0E-110	1.0E-110	1.0E-110 C04498.	1.0E-110	1.0E-110 U84550.	1.0E-110	1.0E-110 AB0322	1.0E-110 BE3794	1.0E-110 BF50888	1.0E-110	1.0E-110	1.0E-110	4 OF-410		1.0E-110 A101721	1.0E-110	1.0E-110	1.0E-110 BE2994	1.0€ 110	1.0E-110	1.0E-110		4							
Expression	2.08	1.85	4.71	4.71	0.7	2.28	1.54	0.8	9.0	1.19	1.6	+	1.49	1.49	100	2	2.14	3.9	2.7	2.63	0.8	8.61	8.04	808	0.8	0.8	72.0					28.0
ORF SEQ ID NO:	31047	25444	25482	25483	25543	25444		28675		27361			28603) N	29951			30642						32747						33235
Bean SEQ ID NO:	24813	12831	12864	12864	12905	12831	13298	13912	14005	14651	14784	15613	15052	15962		2//01	17326	1_	17844	18020	18434	18451	18451			19894		1.				20143
Probe SEQ ID NO:	12443	6	8	8	2	101	514	1157	1258	1914	2851	2845	3180	3189	1	13	7	4908	4916	5212	5630	5656	5656	6817	7002	7002		7224	7325	7325	7355	7469

Page 442 of 536 Table 4 Single Exon Probes Expressed in Brain

				Τ-	τ-	т	_	-			_	_	Т	Т	T	Т	Т	Т	7	Т	Ţ	T	1	T	T	Ť	Т	_	Т	T	T	T		7	
	Top Hit Descriptor	LAGSAN ANIM MICC 20 Homo sablens cDNA clone IMAGE:2905581 5' similar to TR:077298 077258	E0:114D9.2 PROTEIN.;	QV2-LT0053-020400-119-e04 LT0063 Homo septems curva	Homo sapiens galactokinase 2 (GALK2), mrtwA	H. sepjens mRNA for myokanic dystrophy protein kinase ilke protein	ANTARGOLD NIH MGC 21 Home subjens CDNA clone INAGE:3840433 5	ANTERSANTET NIH MGC 21 Hamp septens cDNA clone INAGE:3840433 5	ACTION OF Some traffs, NHT Homo saplens CDNA clone IMAGE:781298 5' similar to TR:G1145816	G1145816 FKBP54;	601439784F1 NIH_MGC_72 Hamo appears convenient management of the convenient of the c	ILO-BT0163-040889-094-010 B10103 From Saprans Cuito	Hamo septiens gene for AF-6, complete an	qc31c12.x1 Soeres, pregnant, uterus, NDHPU Homo saperis curvo cure invocir, reconstruction	IPMS-NN1082-140900-006-f12 NN1082 Homo sepiens cDNA	I II H. Bld. ecs-b-05-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085784 3	Limes discorne problem 123a mRNA, complete ods	Liven entire res GTPase activating protein-like (NGAP) mRNA	ANALYSECATE ANIH MIGC 88 Homo septems cDNA clone IMAGE:3862096 5	Home serions not one sundrame critical region gene 1 (CECR1), mRNA	Human cardiac alpha-myosh heavy chain (MYH6) gene, exons 32 to 34	Homo sepjens KIAA0555 gene product (KIAA0555), mRNA	Home senions colladen type IX abha 1 chain (COL9A1) gene, exons 29, 30, 31, and 32	Homo sepiens DKFZP434D156 protein (DKFZP434D166), mRNA	Human enkechalin B (enkB) gene, exon 4 and 3' flank end complete cds	Homo sepiens phosphorylese kinase, alpha 1 (muscle) (PHKA1), mRNA	80144380E1 NIH MGC 65 Homo septems oDNA done MAGE:3847655 5	and South A Communication of the Communication of t	RELATED PROTEIN RAL-A (HUMAN);	DKFZp434C1815_r1 434 (synonym: hasa3) Homo septens Cutyk codie Livit Arthur Codies	UITH BWO-#II-4-03-0-UI.s.1 NCI_CGAP_Sub6 Home explains cutvA clone IMM CE.ZI 25020 3	2-NT0101-280700-114-E03 NT0101 Homo septens cDNA	wiesdot x1 NCI CGAP Kid12 Homo sepiens cDNA clone IMAGE:2398465 3' similar to gb:J04813	CYTOCHROME P450 HIA5 (HUMAN);	
,	Top Hit Deftabase Source		EST_HUMAN	EST_HUMAN	1	TIV	707 (1) 14/4h/	ESI HOMAN	LSI HOMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	LX.	EST HUMAN	Cet LIMAN	TOWN IN TOWN	NAMOR I CH	Z.	Z	ESI DOMAIN	Z	Z	Z	Z	17	2 12	EST UINGAN	LOUIS INCINITION OF THE PROPERTY OF THE PROPER	EST HUMAN	EST HUMAN	EST HIMAN	ECT LI IMAN	TOWN TOWN TOWN TOWN TOWN TOWN TOWN TOWN	EST HUMAN	
	Top Hit Acession No.				1432732	, 2000			1.0E-110 BE734357.1	1.0E-110 AA446529.1	1 0E-110 BE897218.1	1.0E-110 AW062258.1	Γ			وَاعِ			4758807 NI	3F035327.1	8393092 N	1.0E-111 MZ014Z.1	IN//1299/	AF036126.1	TIME TOOLOGY	KUZZOS.1	ol lenet	1.0E-111 BE867808.1	A1344679.1	4 OF 444 At 0407R9 4	A14/20/4440 4	1.0E-111 AW 284046.1	BF300228.1	1.0E-111 AI761228.1	
	5 111	2012	4 0F-110 BE302504.1	1 0E-110 AW8383	100 1	21-20:1	1.0E-110 Y1Z337.1	1.0E-110 BE73435	1.0E-110 B	1.0E-110	1 0E-110 E	1.0E-110	4 OE-410 4	7 06 440 7	1.0=1.10	1.0E-110 t	1.0E-110 BF5088	1.0E-111 U43701	1.0E-111	1.0E-111 BF0353	1.0E-111	1.0E-111			1.0E-111	1.0E-111	_		4 DE-414 AI3446		_1	1	١	}	
	Expression Signal		1 88	3, 6	346	3.40	3.04	3.75	3.75	2.45	7 7	11 71		F	1.35	3.25	1.45	10.84	1.05	2.38								1.00					2.99	0.62	
}	ORF SEQ ID NO:		25007	33087	0000	36081	36578	36816	36817	20110	1	1							25845			26338	27080					31249					8 33104	33198	
	SEQ ID	<u> </u>		21913	27.22	22869	23330	23567	23567	11		\perp	_1	1	24753	25339	14784	1_	13004	L	L	13673	14371	14962	16892		17425	18341	ł	- 1	18343	19624	7 20028	3 20110	
	Probe SEQ ID			9234	24/8	10221	10648	10887	10887		11420	11838	12061	12280	12346	12420	12701	18	Į.	718	726	8	1624	2234	4150	4295	6	5544		26	6580	80/9	7347	7433	

Page 443 of 536 Table 4 Single Exon Probes Expressed in Brain

		apopiosis infibitiony	r to 1K:G1200410	r to TR:G1256410						RNA, complete cds					ter to gb:L09235	0;	13545 5			TBC_cn07a11 random						3086023 3'	3086023 3'			
	Top Hit Descriptor	Homo septems basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apopiosis inflibitory protein (naip) and survivel motor neuron protein (smn) genes, complete cds	2879g03_r1 NCI_CGAP_GCB1 Homo septems cDNA clone IMAGE:703732 5' similar to TR:G1286410	G1256410 11-ZINCH-INGER INGARACAIF IION I DOLON IN INGERTO3732 5' similar to TR:G1256410	2879903.11 NCL CCAP_GCD1 FORD SEPTER CLICA COMP.; G1256410 11-ZINC-FINGER TRANSCRIPTION FACTOR.;	Homo sepiens protein x 0001 (LOC61185), mRNA	Human beta4-Integrin (ITGB4) gene, exon 13	Homo septems nuclear ractivity of section 1 costs, cyresting of the costs of the co		Homo sepiens cone sodium-celclum potassium exchanger splice varient (NCXC) mRNA, complete cds	601847132F1 NIH MGC 66 Hamo septens curve curie livrocurve cons	Human mRNA for integrin alpha-2 subunit	Human mRNA for megan appla-2 subulifit	Home separation and the Ether's Home separation of the State of the St	UVZ-BIUGIT-Z/VBUC-SECTION CONTRACTOR INACE RZB170 3' similar to gb:L09235	VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, UBIQUITOUS (HUMAN);	Homo septembrition of the control of	231701.fl Sold by Judy and Judy Johns excess 12.3.4,5 and 6	בותונים חוומיות התיחור ופתפלים ליום ב'/ אתים	on07a11.x1 Normal Human Trabeculer Bone Cells Homo sapiens cDNA clone NHTBC_cn07a11 random cn07a11.x1 (NN1) mRNA	Homo agracia and Line and the Angel Ange ADCAOBO8 5	AV 708462 ALDO From separate Control Complete cds	11. Company Company & Controviese bote (ACACB), mRNA	HOTIO BEDIENTS BLOOKING AND THE STANDING (STAR) GETS. BOOT 5	Thursan security and the secretary profession (StAR) cane. extra 5	THE BY AND THE TANK CAN SUB HOME SECTIONS ON A CONTRACT SUBSECT ST	THE DIA THE PARTY OF THE STABLE HOME SEPTENS CONT. HOME STABLES CONT. HANDE STABLES CONT. HOME STABLES CONT. HANDE STABLES CONT. CON	Homo serviers HTRA serine professe (PRSS11) gene, complete ous	ZINC FINGER PROTEIN 135	
	Top Hit Dafabase Source	5	1	EST_HUMAN	EST HUMAN	N.	NT	<u>L</u>	Ż	NT	EST_HUMAN	NT	NŢ	LN.	EST HUMAN	EST HUMAN	ᅜ	EST HUMAN	¥	EST HUMAN	본	EST HUMAN	<u>L</u>	LN T	Z	LN.	EST HUMAN	EST HUMAN	NI POSCODOT	OWIGOTIN:
, 	Top Hit Acession No.	100017.4		\A278868.1	1A 278868.1	11431896 NT		11420516 NT	AK024453.1	1.0E-111 AF177987.1	1.0E-111 BF214902.1	X17033.1	1.0E-111 X17033.1	1.0E-111 AF091395.1	1.0E-111 BF333210.1	AA604160.1	D10083.1	1.0E-111 AA131248.1	U68159.1	1.0E-111 AI751071.1	11417901 NT	AV708482.1	ö١	4501854 NT	1.0E-112 U29103.1	1.0E-112 U29103.1	BF509039.1	BF509039.1	AF157623.1	1.0E-112 P52742
	Most Similar (Top) Hit BLAST E Value	1	1.000	1.0E-111 AA2788	4 0F-414 AA2788	10E-111	1.0E-111 U66533	1.0E-111	1.0E-111 AK0244	1.0E-111	1.0E-111				1.0E-111	1.0E-111 AA6041			1.0E-111 U68150											⅓
	Expression		9.0	57.0	2	200	3.28	0.79	0.73	1.57	8.65	12.0	12.9	2.8	0.40				4.25	274	3.72			1.29	12.55	12.56				22
	ORF SEQ ID NO:		33279	33815	_	2000		1				34620			35086		L		36902				30599					5 28030		0 26458
	Exan SEQ ID NO:		20185	20688		20088	1.	1_	\ _	74.30	L		1_	1_	L	١ _	L		1_	<u></u>	<u>L</u>	L			1.	I_	7 13395	L		0 13800
	Probe SEQ ID NO:		7514	7993		7903	8088	8579	9674	9707.2	200	278	8782	898	9217	10052	10080	10172	10973	11465	11807	12424	12672	\$	Š	8	917	617	981	1040

Page 444 of 536 Table 4 Single Exon Probes Expressed in Brain

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	Top Hit Descriptor	Homo sepiens KIAA0440 protein (KIAA0440), mRNA	Homo sapiens KIAA0440 protein (KIAA0440), mRNA	WISOTOSX1 NCI_CGAP_Kid12 Home sepiens cDNA clone IMAGE:24006113	801442874F1 NIH_MGC_65 Homo sapiens cDNA clane IMAGE:3848858 5'	Homo sepiens glutamate receptor, tonotropic, kalhate 1 (GRIK1) mRNA	wk45b12x1 NCI_CGAP_Pr22 Homo eaplens cDNA done IMAGE;2418335 3' similar to gb:M81650_ma1 SEMENOGELIN 1 PROTEIN PRECURSOR (HUMAN);	MR2-BT0580-060300-113-f09 BT0390 Homo sapiens d2NA	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA	Homo sepiens mRNA for KIAA1411 protein, perties cds	Homo sapiens mRNA for KIAA1411 protein, partial cds	yyS5d07.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:273229 5'	Homo sepiens NOD1 protein (NOD1) gene, excres 1, 2, and 3	801594717F1 NIH_MGC_8 Homo saplens cDNA clone IMAGE;3948557 5	802152849F1 NIH_MGC_81 Hamp saplens cDNA clone IMAGE:4283420 5	601142755F1 NIH_MGC_14 Hamp sapiens aDNA dane IMAGE:3506508 5'	801142755F1 NIH_MGC_14 Hamo septens cDNA clane IMAGE:3506508 51	802/31405F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4270921 5'	Homo sepiens solute cerrier family 8 (neurotransmitter transporter, L-proline), member 7 (SLC&A7), mRNA	Homo sapiens solute cerrier family 8 (neurotransmitter transporter, L-profite), member 7 (SLCSA7). mRNA	801845089F1 NIH_MGC_55 Hamp septens cDNA clane IMAGE;4070302 5	AU118051 HEMBA1 Hamo septents cDNA clone HEMBA1002773 5	601443151F1 NIH_MGC_65 Hamp sepiens cDNA clane IMAGE:3847285 5'	601443151F1 NIH_MGC_65 Hamo sepiens aDNA done IMAGE:3847285 57	730g07.x1 Sogres, NSF_F8_9W_OT_PA_P_S1 Homo septens cONA clone IMAGE:3523020 3' similar to TR:09VW35 Q9VW35 CQ8743 PROTEIN	MR3-SN0009-100400-108-b12 SN0009 Hamo espiens cDNA	Homo sepiens mRNA for secreted modular calcium-binding protein (smoc1 gene)		ak24c08.y6 NCI_CGAP_Ktd3 Homo septens cDNA clone IMAGE:1888802 5' similar to TR:064362 Q64362. FUSED TOES;	
מון וומש מופּי	Top Hit Detabase Source	NT	NT	EST HUMAN	EST HUMAN	LN	EST HUMAN	EST_HUMAN	N.	IN	LNT	EST_HUMAN	, LN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	TN	M	T HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	Г	П	F.	EST_HUMAN	EST_HUMAN	
	Top Hit Acession No.	7662125 NT	7062125 NT	1.0E-112 AI766925.1	BE86859.1	4504116 NT	AI825511.1	BE076073.1	4504116 NT	32.1	32.1	N46046.1	AF149773.1	BE741666.1	1.0E-112 BF672815.1	1.0E-112 BE273103.1	1.0E-112 BE273103.1	1.0E-112 BF574235.1	11416777 NT	1141 <i>6777</i> NT	1.0E-112 BF213358.1	4U118051.1	1.0E-112 BE867635.1	1.0E-112 BE867635.1	3.1	1.0E-112 AW863327.1	1.0E-112 AJ249900.1		2	
	Most Similar (Top) Hit BLAST E Value	1.0E-112	1.0E-112	1.0E-112	1.0E-112 BE8688	1.0E-112	1.0E-112 AIB2851	1.0E-112 BE0760	1.0E-112	1.0E-112 AB0378	1.0E-112 AB0378	1.0E-112 N46046.	1.0E-112 AF1497	1.0E-112 BE74160	1.0E-112	1.0E-112	1.0E-112	1.0E-112	1.0E-112	1.0E-112	1.0E-112	1.0E-112 AU1180	1.0E-112	1.0E-112	1.0E-112 BF11141	1.0E-112	1.0E-112	1.0E-112	1.0E-112 AI792603	
	Expression Signal	4.39	4.39	1.37	1.1	1.15	.0.7	0.74	1.30	4.9	4.9	40.71	1.04	1.43	0.68	17.0	0.71	1.13	1.87	1.87	0.56	1.73	2.09	2.09	2.15	286	3.37	1.92	1.59	
	ORF SEQ ID NO:	27117	27118	27867	27969		02.28	29253	12862	89008	30069			31889	32134	32308		32607	32995	32996	33507	33919	34894	34695	35849	36611	36796	36981	37053	
	Esan SEQ ID NO:	14423	14423	14923	15229	15842	16115	10614	17300	17437		i		18832	19138	19304	19304	19575	18921	12861	25120	20787	21547	21547	22444	23368	23548	23711	23779	
	Probe SEQ ID NO:	1679	1679	2194	2512	3078	3355	3864	4565	4704	4704	5581	5985	6155	6369	6639	6239	6741	7236	9224	7729	8083	8856	8856	9783	10877	10868	11040	11109	

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i able 4 Single Exon Probes Expressed in Brain	Top Hit Descriptor	qk24008.y5 NG_CGAP_Kid3 Homo septems cDNA clone IMAGE:1806902 5' straller to TR:Q64362 Q64362 FUSED TOES;	PM0-CT0237-141099-001-h02 CT0237 Homo septens cDNA	qk24c08.y5 NG_CGAP_Kd3 Hamo sepiens cDNA clone IMAGE:1868802 5 similer to TR:Q64362 Q64362. FUSED TOES ;	ok24c08.55 NCI_CGAP_Kd3 Homo sepiens cDNA clone IMAGE:1869902 6' similer to TR:Q64362 Q64362. FUSED TOES;	ao85f01.x1 Schiller meningiome Homo sepiens cDNA clone INAGE:1983625.3"	ax95f01.xt Schiller meninglome Homo seplens cDNA clone IMAGE:1953625.3"	Human X-linked phosphoglycerate kinase gene, exon 8	8085f01.x1 Schiller meringtoma Homo saplens cDNA clone IMAGE:1953625.3'	Homo sapiens elF4E-transporter mRNA, complete cds	UI-H-BW 1-ent-f-03-0-UI:s1 NCI_CGAP_Sub7 Home sepiens oDNA cione IMAGE:3082876 3'	Homo sapiens PLP gene	Homo septems mRNA for putative RNA helicase, 3' end	Homo seplens gene for cholecystokinin type-A receptor, complete ods	Homo septems activating transcription factor B (B-ATF), mRNA	Homo sepiens activating transcription factor B (B-ATF), mRNA	601469465F1 NIH_MGC_67 Hamo septens cDNA clane IMAGE:3872536 5	AU127214 NT2RP2 Hamo sepiens aDNA clane NT2RP2000807 5"	AU140291 PLACE2 Homo saplens cDNA clone PLACE2000274 6"	Homo sapiens P-glycoprotein (mdr1) mRNA, complete cds	Homo septens UDP-N-acety-lepha-D-gelactosamine:polypoptide N-acetygelactosaminytransferase 8 (GaNAc-T8) (GALMT8), mRNA	Homo sepiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), transcript variant B, mRNA	Homo sepiens ATP-binding ceasette, sub-family B (MDR/TAP), member 4 (ABCB4), transcript variant B, mRNA	Homo sepiens gluterinate receptor, fonotropic, N-methyl D-aspertate 24 (GRIN2A) mRNA	(2A) mRNA				Homo sapiens hypothetical protein FLJ11008 (FLJ11009), mRNA
le Exon Prob	Top Hit Detablesse Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	Г	NT	THUMAN		EST HUMAN	TN	NT	NT					T HUMAN							EST_HUMAN	T HUMAN	T_HUMAN	
Sing	Top Hit Acession No.	1.0E-112.AI792603.1	1.0E-112 AW377870.1	1.0E-112 AI792603.1	1.0E-112 AI792803.1		1.0E-113 A/365586.1			5.1	18.1	6.1	18.1	1	5453562 NT	3562	28.1			1.0E-113 AF016635.1	1 11525737 NT	9961249 NT	9961249 NT	6006002 NT	9009002 NT	1.0E-113 BE262161.1	1.0E-113 BE282181.1	1.0E-113 AW958980.1 ES	8922819 N
	Most Similer (Top) Hit BLAST E Vælue	1.0E-112	1.0E-112	1.0E-112	1.0E-112	1.0E-113	1.0E-113	1.0E-113 M11985.1	1.0E-113	1.0E-113	1.0E-113 BF61521	1.0E-113 A.100697	1.0E-113	1.0E-113 D85808.	1.0E-113	1.0E-113	1.0E-113	1.0E-113 AU1272	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.05-113	1.0E-113
	Expression Signal	1.59	6.6	1.92	1.92	5.37	5.37	7.99	2.06	1.44	1.02	26.34	1.92	10.0	2.16	2.16	2.97	7.66	4.17	1.47	262	99:0	9.0	9.0	9.0	0.78	0.78	0.56	0.48
	ORF SEQ ID NO:		37085	37734	37735	28152	26153	28362	28906	27382	27551	27913	28536	30300	30335	30336		30909	31554	31589	31725	31806	31807	31974	31975	32979	32980	33347	34629
	Exan SEQ ID NO:	23779	23806	24399	24399	13499	13499	13688	14279	15524	14820	15174	15892	17891	17731	17731	25178	18205	18621	18848	18781	18843	18843	18908	18998	19906	19906	20242	21482
	Probe SEQ ID NO:	11109	11139	11810	11810	725	725	921	1532	1832	2088	2456	3127	4966	5008	5008	5165	5405	5832	5861	5979	606	200	6224	6224	1221	7221	7573	8790

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	Top Hit Descriptor	601297709F1 NIH_MGC_19 Homo sepiens cDNA clone IMAGE:3627554 5'	601297709F1 NIH_MGC_19 Hamo sapiens cDNA clone IMAGE:3627554 5	RC1-FT0134-280800-021-d02 FT0134 Homo sapiens cDNA	Homo sepiens transmembrane probbin 2 (TMEM2), mRNA	Human erg protein (ets-related gene) mRNA, complete cds	Homo sepiens RAN binding protein 7 (RANBP7), mRNA	Homo septens RAN binding protein 7 (RANBP7), mRNA	UI-HF-BN0-akt-b-10-0-UI.r1 NIH_MGC_50 Hamo sapiens cDNA clane IMAGE:3077322 5	602247740F1 NIH_MGC_62 Homo sepiens cDNA clone IMAGE:4333280 5'	602247740F1 NIH_MGC_62 Homo sepiens oDNA clone IMAGE:4333280 5'	UI-HF-BN0-ekt-b-12-0-UI.r1 NIH_MGC_50 Homo sepiens cDNA clone IMAGE:3077326 5	hh81a09.y1 NCI_CGAP_GU1 Homo seplens cDNA done IMAGE:2989176 5' similar to TR:060327 060327 KIAA0584 PROTEIN;	hh81e08.y1 NCI_CGAP_GU1 Homo septiens cDNA done IMAGE:2889176 5' strailer to TR:060327 060327	NIPONOOT LINE	Homo saplens glutamate receptor, londeropic, N-methyl D-aspartate 2A (GRIN2A) mRNA .	Homo sepiens glutamete receptor, tonotropic, N-methyl D-espertate 2A (GRIN2A) mRNA	601105529F1 NIH_MGC_15 Homo saplens cDNA clone IMAGE:2988366 5'	nc80b03.r1 NCI_CGAP_GC1 Homo sepiens dDNA clone IMAGE:797069 5' eimiter to SW:FEN1_HUMAN P39748 FLAP ENDONUCLEASE-1;	m380b03.r1 NCI_CGAP_GC1 Homo septems dDNA clone IMAGE:797069 5' stmiter to SW:FEN1_HUMAN P39748 FLAP ENDONUCLEASE-1;		yd15c01.s1 Scares fetal liver spiecn 1NFLS Homo sapiens CDNA cione IMAGE:106288 3' similiar to ob:A21187 ALPHA-2-MACROGLOBULIN PRECLISSOR (HUMAN)contains Alumentitue element:	Homo septens hypothetical protein FLJ20080 (FLJ20080), mRNA	Homo sepiens rhabdold fumor deletion region protein 1 (RTDR1), mRNA	Homo sepiens nucleoportnHike protein 1 (NLP_1), mRNA	Homo sepiens mRNA for KJAA1276 protein, partial cds	Homo sepiens mRNA for KIAA1276 protein, partial cds	Human gene for catalase (EC 1.11.1.6) exon 2 mapping to chromosome 11, band p13	601869932F1 NIH MGC_19 Homo sapiens cDNA clone IMAGE:4100214 5	Homo sepiens NOD1 protein (NOD1) gene, exons 1, 2, and 3	Human Interferon-alpha receptor (HulFN-elpha-Rec) mRNA, complete cds
	Top Hit Database Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	F	Z	۲ <u>۷</u>	N	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN		NAMODE 1 CT	Ł	MT	EST_HUMAN	EST_HUMAN	EST HUMAN	i	EST HIMAN	Σ	F	Ę	Þ	NT	NT	EST_HUMAN	NT	١
	Top Hit Acession No.	1.0E-113 BE382842.1	1.0E-113 BE382842.1	1.0E-113 BE772987.1	11428367 NT		5453997 NT	5453997 NT	1.0E-113 AW500517.1	1.0E-113 BF691687.1	1.0E-113 BF691687.1	1.0E-113 AW500519.1	1.0E-113 AW630291.1		v	6006002 NT	6006002 NT	3E292968.1	AA580720.1	AA580720.1		170551.1	B023087 NT	7857529 NT	TN 679073	\B033102.1	\B033102.1	004086.1	3F206374.1	4F149773.1	103171.1
	Most Similar (Top) Hit BLAST E Value	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113 M21535	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1.0E-113	1,0E-113	277	LUC-113 AWGSU	1.0E-113	1.0E-113	1.0E-113 BE2929	1.0E-113 AA5807	1.0E-113 AA5807		1.0E-114	1.0E-114	1.0E-114	1.0E-114	1.0E-114 AB0331	1.0E-114 AB0331	1.0E-114 X04086	1.0E-114 BF2063	1.0E-114 AF1497	1.0E-114 J03171
	Expression Signal	3.06	3.06	0.93	4:1	0.45	0.81	0.81	0.61	0.55	0.55	1.83	2.84		#07	.30	1.39	2.81	1.32	1.32		60	17	5.09	4.27	1.28	1.28	2.75	1,02	2.61	0.72
	ORF SEQ ID NO:	34830	34831		35583		35802	35803	36386	36387	36388	37011	37019	200	07076	31974	31975	37177	37393	37394		28045	28468	26712	27104	25401	25492	28537	28581	28377	29731
	Exan SEQ ID NO:	21682	21682	21968	22381		22598	22598	23160	23161	23161	23737	23746	l	1.	18008	18698	23890	24082	24082		13400	13808	14039	14413	12871	12871	15883	15932	18745	17096
	Probe SEQ ID NO:	8992	8992	9301	9730	9830	9950	9950	10514	10515	10515	11067	11078	60,7	0/0	11181	11181	11227	11481	11481		88	1049	1290	1667	2807	2807	3128	3169	3997	4358

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PCT/US01/00667

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Top Hit Descriptor	Homo sepiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and parbal cds, afternatively	people's	AV733454 cdA Homo septens cDNA clone cdAlbAus o	AV733454 odd Home septens citing carbane o	Homo seplens LIM HOX gene 2 (LHX2) mRNA	Homo sepiens clethrin, heavy polypeptide-like 1 (CLTCL1), mRNA	Homo eaciens TNF-Inducible proben CG12-1 (CG12-1), mRNA	Homo serviers hypothetical protein (DJ1042K10.2), mRNA	Homo seciens hypothetical protein (DJ1042K10.2), mRNA	Homo sepiens HLA-B associated transcript-1 (D6S81E) mRNA	Company Polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA	TOTILO SEPTIMO DE VICETA D	Home seprens was and 10 (12 to 10) (12 to 10) (12 to 10 to 1	10 4 - University Co. A. D. Co. Homo, earlier & Charle IMAGE: 1948809 3' similar to TR: 000536 000536	GROSTOLIN NO. CONT	LIP-IN LEAVE INC. CARE GOA Home sections CDNA clone IMAGE: 1948309 3' similar to TR: 000536 000536	QUOTO INC. COM CONTROL OF THE LINE BARTING PEPTIDE 5:	United Hall Committee on the Second Section (TABS), mRNA	Home services transforming growth factor beta activated kinase-binding protein 1 (TAB1), mRNA	Lines engine fertilin heavy polyoeolide 1 (FTH1) mRNA	Trout Septemble Institut, incomplete the synthese mRNA, complete ods	Home services arithmenting digital semialdehyde synthase mRNA, complete cds	Homo surione Bruton's tyrosine kinase (BTK), alpha-D-galectosidase A (GLA), L44-like ribosomal protein	(L44L) and FTP3 (FTP3) genes, complete ods	Homo sepiens Kirkhovetz mixtviv, partier oue	Homo expens tostocar-1 mixtury, cumplicar cus	QV4-UM0094-300300-136-508 UM0094-normo saprana contra	Homo sapiens micha for epine-tubulin o (Tipas gara)	Homo septens mRNA for septer subulin 8 (1 USAs gene)	Homo explens pertial TTN gene for thin	Homo septens mRNA for KIAA0350 protein, partial cds	Homo saplens st2-like 3 (SIRT3), mRNA	Hamo sepiens EphA4 (EPHA4) mRNA	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes	
Top Hit Databese Source		K	EST HUMAN	HUMAN	1	5		1	12		Z	L	Ł	EST HUMAN		EST HUMAN	1	S.1 IEST HUMAN	LN!	Į.	Į.	EN!	ž	Ŋ	Ŋ	L	EST HUMAN	<u>F</u>	7	12	1 _N	Į.	IN C	Į.	
Top Hit Acession No.	+	Ψ.	2	2	4759673	14526347 NT	1 10200 (1)	11410041 140349E0 NT	11034650T	DCO450LL	4758111 N	4506938 N	<u>2</u>	1.0E-115 AW804759.1		1339206.1		U338206.1	5174702	5174702INI	4503794 NT	1.0E-115 AF229180.1	1.0E-115 AF229180.1	178027.1	4B007902.1	4F231124.1	AW804759.1	AJ245922.1	4 0F-115 A 1245922 1	4 OE 445 A 1977909 4	4 DOM2248 2	TOPOCO	TN 0758274	AT CORDET 4	1.0E-113[ALU90037.1
Most Similar (Top) Hit Te BLAST E		1 0F-114 AF223391	1 0E-114 AV73345	4 DE-114 AV73345	100	1.05-114	1.05-	1.01-114	1.0E-114	1.0E-114	1.0E-115	1.0E-115	1.0E-115	1.0E-115		1.0E-115 AI339200		1.0E-116 AI33920	1.0E-115	1.0E-115	1.0E-115	1.0E-115	1.0E-115	1.0E-115 U780Z7.	1.0E-115 AB0079	1.0E-115 AF2311;		1	1	1	1		1.05-113	1	
Expression Signal		- 2	- 6	3	**************************************		1.32	3.42	88.	4.93	2.89	2.03	2.33	2.23		0.99		0.99	1.36	1.36	40.4		1.26	101											204
ORF SEQ ID NO:		20745	307.10				37759				25464			25733		25939	L	25940		28202	L		26986	27285	١			00518						29768	
Esan SEQ ID NO:		9	274(2	71967	23812	24386	24418	25402	24902	24902	12840	12942	1_	L		13307	1_	13307	L	L	L	<u>l_</u>	14298	44670		L	L	L	ᆚ		i			_ 1	8 17363
Pobe SEQ ID NO:			10789	1113	11145	11796	11834	12334	12577	12577	72	127	131	388		523		623	769	260	7.	1552	1552		250	200		8	3113	3113	3466	4021	4369	4403	4628

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v	1/3/2/3			-													4	.	-	_e `	-	مبياح	-		Ľ		Ψ,	2017	1000	P 1944
	Top Hit Descriptor	Novel human mRNA from chromosome 1, which has strill grities to BAT2 genes	Homo sepiens chromosome 21 segment HS21C068	Homo sepiens chromosome 21 segment HS21C068	EST382416 MAGE resequences, MAGK Hamp septens cDNA	802118348F1 NIH_MGC_56 Hamo septens cDNA clone IMAGE:4276738 51	Homo sepiens similar to ER to nucleus signaling 1 (H. sepiens) (LOC63433), mRNA	Homo sepiens similer to ER to nucleus signaling 1 (H. sepiens) (LOC63433), mRNA	au84g01.x1.Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519588 3' similar to gb1.07807 DYNAMIN-1 (HUMAN);	au84g01x1 Schneider fetal brain 00004 Homo sapiens cDNA clone INAGE:2519568 3' similar to gb1.07807 DYNAMIN-1 (HUMAN);	Homo septens sperm surface protein (HSS), mRNA	Homo seplens sperm surface proben (HSS), mRNA	Homo septens similar to ribosomal protein S28 (H. septens.) (L.OC63436). mRNA	Homo saplens KIAA0054 gene product; Helicase (KIAA0054), mRNA	Homo sepiens KIAA0054 gene product, Helicase (KIAA0064), mRNA	yd80b08.r1 Soeres febal liver spieen 1NFLS Homo sapiens cDNA clone IMAGE:116095 5' similar to SP:DPOG_YEAST P16801 DNA POLYMERASE GAMMA	0231a08.x1 Soares total fetus Nb2HF8 9w Homo sabiens cDNA-clone IMAGE:1676914.3*	0231806x1 Sogres, total fetus, Nb2HF8, 9w Homo septens cDNA clone IMAGE:16769143'	Homo sapiens mRNA for KJAA0895 protein, partial cds	RC8-ET0081-130700-011-301 ET0081 Homo septens cDNA	RC8-ET0081-130700-011-G01 ET0081 Homo septems cDNA	Homo sapiens eukaryotic translation initiation factor 48 (EIF4B), mRNA	601816352F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:4050108 5"			1989e09 xf Sogree_NFL_T_GBC_S1 Homo septens cDNA clone IMAGE:1843336 3*		tr:016129 016129	s CDNA clone IMAGE:2838239 3' elmiter to SW:CAYP_CANFA	Homo sepiens UDP-glucose: glycoprobain glucosyftransferase 1 (HUGT1), mRNA
	Top Hit Detabase Source	NT	NT	NT	EST HUMAN	EST HUMAN	LN.	둗	EST HUMAN		1426786 NT	¥	Ł			EST HUMAN	EST HUMAN	EST_HUMAN	뉟		EST HUMAN		EST_HUMAN			EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	
	Top Hit Acession No.	AL096857.1	1.0E-115 AL163268.2	1.0E-115 AL163268.2	1.0E-115 AW970335.1	1.0E-115 BF865387.1	11425128 NT	11425128 NT	A1928799.1	AI928799.1	11426786	11426786 NT	11426038 NT	7861883 NT	7881883 NT	T86774.1	1.0E-115 AJ076598.1	1.0E-115 Al076698.1			1.0E-115 BE830187.1	77					1	1.	1.4	8910279
	Most Similar (Top) Hit BLASTE Value	1.0E-115 AL09895	1.0E-115	1.0E-115	1.0E-115	ŀ	1.0E-115	1.0E-115	1.0E-115 Al928796	1.0E-115,AI928796	1.0E-115	1.0E-115	1.0E-115	1.0E-115	1.0E-115	1.0E-115 T86774.1	1.0E-115	1.0E-115	1.0E-115 AB02321	1.0E-115	1.0E-115	1.0E-115	1.0E-115	1.0E-116	1.0E-115/	1.0E-115	1.0E-115 AI221878	1.0E-115 AJ524687	1.0E-116 AW6715	1.0E-115
	Expression Signal	2.64	3.51	3.51	1.62	0.78	1.98	1.98	1.34	1.34	78.0	70.0	9.84	204	2.04	0.83	1.54	1.54	8.22	13.71	13.71	2.15	0.8	2.26	226	1	1	0.82	7.62	1.33
	ORF SEQ ID NO:	28682			96906	30802	31143	31144	31313	31314	31916	31917	32061	32198	32199	32521	32835	32936	33068	33885	33886	34548	35522	35743	35744	36284	36285	36293	36549	36797
	Exam SEQ ID NO:	17363			18069		18253	18253	18400	18400	18945	18945	19075	19202	19202	19497	19864	19864	19991	20754	20764	74 404	22327	952 22	22540	23064	23064	23072	23310	23549
	Probe SEQ ID NO:	4628	4848	4848	5283	5338	5454	5454	5604	5604	6168	6168	6302	6434	6434	8835	7178	7178	7308	8080	88	8712	8678	8	888	10418	10418	10428	10617	10800

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Onigio LAUI FIODOS LAPIOSSOU III DIGIII	Top Hit Descriptor	hq54c10.x1 NCI_OGAP_Pan3 Homo sapiens cDNA clone IMAGE:3123186 3' sknillar to TR:O88378 O88378 PRP4 PROTEIN KINASE HOMOLOG;	hq54c10.x1 NCI_CGAP_Par3 Home sapiens cDNA clone IMAGE:3123186 3' similar to TR:O88378 O88376 PRP4 PROTEIN KINASE HOMOLOG;	Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E) mRNA	601111744F1 NIH_MGC_16 Hamo septens aDNA clane IMAGE:3352379 5'	QV3-OT0065-200300-137-h12 OT0065 Hamo sepiens cDNA	Homo septions glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) cornes. complete cds	901121347F1 NIH MGC 20 Homo septens cDNA clore IMAGE:2988875 5	Homo sepiens synaptojanin 1 (SYNJ1), mRNA	Homo sepiens synepolojenin 1 (SYNJ1), mRNA	Homo sepiens pericentrin (PCNT) mRNA	Homo explens pericentrin (PCNT) mRNA	Human apolipoprotein B-100 (apoB) gene, exans 17 and 18	Human apolipoprotein B-100 (apoB) gene, exons 17 and 18	Homo saptens protein phosphatese, EF hand calcium-binding domain 1 (PPEF1) mRNA	Human offactory receptor offr17-201-1 (OR17-201-1) gene, offactory receptor offr17-32 (OR17-32) gene and offactory receptor pseudo offr17-01 (OR17-01) pseudocene, complete cds	Homo saplens mRNA for KIAA0700 protein, partial cds	601513337F1 NIH_MGC_71 Homo septens cDNA clone IMAGE:3914600 5'	Hamo saplens DiGearge syndrame critical region, centrameric end	Homo sapiens DiGeorge syndrome critical region, centromeric end	Homo septiens sodium phosphete transporter 3 (NPT3) mRNA	PM-BT135-070499-016 BT135 Homo saplens cDNA	qn19d04.x1 NCI_CGAP_Lu5 Homo saplens cDNA done IMAGE:1898995 3' similar to contains element. MER26 repeditive element:	similar to	NASE, MITOCHONDRIAL PRECURSOR;			GE:3636764 5	MR2-HT0379-210200-102-b04 HT0379 Homo sapiens cDNA
מום דיומץ פול	Top Hit Detabase Source	EST_HUMAN	EST_HUMAN	보	EST_HUMAN	EST_HUMAN	Ŀ	EST HUMAN	N	LN.	NT	LN.	LN	L	L	LN	NT	EST_HUMAN	TN	IN	NT	EST_HUMAN	EST HUMAN		HUMAN	L	NT		EST HUMAN
5	Top Hit Acession No.	BE045890.1	BE045890.1	4502528 NT	BE255549.1	1.0E-115 AW884375.1	1.0E-115 AF240786.1	BE275502.1	TN 4507334 NT	TN 4507334 NT	5174478 NT	6174478 NT			5453941 NT		3.1	1.0E-116 BE889256.1	-77570.1		5031954 NT	AI907096.1	1.0E-116 A1302062.1						1.0E-116 BE158133.1
	Most Similar (Top) Hit BLAST E Value	1.0E-115 BE04586	1.0E-115 BE04580	1.0E-115	1.0E-115 BE2555	1.0E-115	1.0E-115	1.0E-116 BE27550	1.0E-118	1.0E-116	1,0€-116	1.0E-116	1.0E-116 M19824.	1.0E-116 M19824.	1.0E-116	1.0E-116 U78308.	1.0E-118 AB01833	1.0E-116	1.0E-116 L77570.1	1.0E-116 L77570.1	1.0E-116	1.0E-116 AI907096	1.0E-116	i i	1.0E-110 W 42822.	1.0E-116/	1.0E-116/	1.0E-116	1.0E-118
	Expression Signal	1.54	1.64	2.27	2.53	1.63	2.16	1.98	2.21	1.76	2.55	2.66	2.6	2.6	1.95	1.36	2.84	1.53	4.87	4.87	2.43	1.57	0.87	;	*	1.8	1.8	0.76	1.55
	ORF SEQ ID NO:	37174	37175	37281	37699	37767		25060	26216	-	27447	27448	27552	27563	27787		27015	28183	28582	28583	29713	30156	30627	-	ALOLS	31862	31863	31034	
	Exan SEQ ID NO:	23888	23888	23981	24366	24426	24481	13341	13555	13609	14728	14728	15585	15585	15030	15083	15178	15533	15934	15834	17084	17534	18005	1	8	18895	18895	18961	19189
	Probe SEQ ID NO:	11225	11225	11374	11775	11842	11920	550	783	839	1990	1990	2090	2090	2306	2340	2458	2738	3171	3171	4345	4803	5197	Ş	8 3	a 14	917	9184	6421

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Single Extri Frones Expressed in ordin	Top Hit Descriptor	C02944 Human heart cDNA (YNakamura) Homo sapiens cDNA done 3NHC0567	AV716314 DCB Hamo sepiens cDNA clone DCBBCG06 5	EST62885 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to keratin 2	EST62885 Jurkart T-cells V Homo eapiens cDNA 5' end similar to similar to keratin 2	CM-BT043-090299-075 BT043 Homo septens cDNA	601338268F1 NIH_MGC_53 Homo saplens cDNA clone IMAGE:3680680 5'	ph09c05.x1 Soares_NFL_T_GBC_S1 Home sepiens cDNA done IMAGE:1844168 3' similer to gb.X53741_me1 FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);	Homo sapiens laminin, alpha 2 (merosin, congenital muscular dystrophy) (LAMA2), mRNA	Homo sepiens partiel mRNA for xylosyltransferase I (XT-1 gene)	Homo sepiens partial mRNA for xylosyltransferase I (XT-I gens)	QV4-HT0401-281289-063-c09 HT0401 Homo septens cDNA	CM2-CT0482-300800-349-e06 CT0482 Homo sepiens cDNA	qq41e04.xt Sogres_NhHMPu_S1 Homo sapiens cDNA done IMAGE:1935102.3' similer to WP:B0495.7 CE01785 :	DKFZp76211110_r1 762 (synonym: hmel2) Homo septems cDNA clone DKFZp7621,1110 5	Homo sapiens acetyl-Coerzyme A carboxylase alpha (ACACA), mRNA	Mus musculus fragile-X-related protein 1 (Fx1h) gene, exons 13a through 15	Homo saplens lymphocyte activation-associated protein mRNA, complete cds	Human apolipoprotein B-100 (apoB) gene, exon 10	EST369769 MAGE resequences, MAGE Homo septens cDNA	0932c11.81 Soures_NFL_T_GBC_S1 Homo septens dDNA done IMAGE:1578548 3'	EST188414 HCC cell line (matestasis to liver in mouse) II Homo septens oDNA 6' end similar to ribosomal protein L29	Homo sepiens collegen, type IV, alphe 5 (Alport syndrome) (COL4A5), mRNA	DKFZp434C1120_r1 434 (synonym: https:// Homo sapiens cDNA clane DKFZp434C1120 5	H. sepiene mRNA for TPCR16 protein	H. seplens mRNA for TPCR16 protein	Homo septens Scar 2 (SCAR2) gene, partial cds	Homo sapiens Scar 2 (SCAR2) gene, partial cds	Homo sepiens mRNA for KIAA0866 protein, complete cds	Homo sepiens strophin-1 interacting protein 1; activin receptor interacting protein 1 (KIAA0705), mRNA	601562657F1 NIH_MGC_20 Hamo septens cDNA done IMAGE:3832214 5'
פום בצמוו בינמ	Top Hit Detabese Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	LN	N⊤	LN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	N.	LN	NT	N F	EST_HUMAN .	EST_HUMAN	EST HUMAN	Ę	EST_HUMAN	Į.	N	Ę	Z.	TN		T_HUMAN
(III)	Top Hit Acession No.	C02944.1	1.0E-116 AV716314.1	AA354258.1	AA354258.1	1.0E-116 Al904151.1	1.0E-116 BE585507.1	Al216352.1	11418646 NT		41.1	1.0E-116 BE158913.1	1.0E-116 BF335849.1	Al367140.1	1.0E-116 AL134889.1	4828636 NT	1.0E-117 AF124383.1	20.1	7.	AW957699.1	AA978114.1	23.1	8059564	AL042120.1			Г	1.0E-117 AF134304.2		2461	1.0E-117 BE730508.1
	Most Similar (Top) Hit BLAST E Value	1.0E-116 C0294	1.0E-118	1.0E-116 AA354;	1.0E-118 AA354;	1.0E-118	1.0E-116	1.0E-116 A12163	1.0E-116	1.0E-118 AJ2774	1.0E-118	1.0E-116	1.0E-116	1.0E-116 AB6714	1.0E-116	1.0E-117	1.0E-117	1.0E-117 AF1233	1.0E-117 M19816	1.0E-117 AW957	1.0E-117 AA9781	1.0E-117 AA3167	1.0E-117	1.0E-117	1.0E-117 X89870.1	1.0E-117 X89670.1	1.0E-117	1.0E-117	1.0E-117	1.0E-117	1.0E-117
	Expression Signal	1.19	5.74	1.37	1.37	96.0	1.86	1.61	1.52	0.74	0.74	0.78	2.4	2.85	1.86	1.67	0.96	1.02	1.51	1.54	1.64	2.1	2.03	2.95	1.27	1.27	10.03	10.03	3.57	0.73	3.01
	ORF SEQ. ID NO:	32672	32855	34101	34102	34209	34674	34837	35411	36036	38037	36104	36519	37025		25059	28474	27188	27274	27674	28674	28355	28674	28605	30043	30044	30119	30120	30233	30471	30699
	SEQ ID NO:	19544	19790	20961	20061	21071	21528	21687	22228	22818	22818	22894	23281	23750	25267	13328	15559	14489	14562	14936	16024	16720	17040	17273	17408	17408	17491	17401	17614	17854	18070
	Probe SEQ ID NO:	6844	7102	8267	8267	8378	8836	8007	. 8573	10170	10170	10246	10586	11080	12625	545	1055	1747	1823	2208	3262	3971	4310	4538	4874	4874	4729	4750	4887	5136	5264

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	Top Hit Describiar	1111 Annual Control of Service C	EST26111 Cerebeltum II Hamo septents Curus of an amount of the septents (who) bene. 3 end of ods	Hamo saprans inches inches receptor (sho) gare, 3' and of cds	HOTTO BEGINS INVIORATION CONTRACTOR CONTRACT	AV /1/700 DCD FIXING Service CONA CONE DC8BAE01 5	AV 11768 DOD 1000 THE TOTAL BRIDE Home explans a DNA clone IMAGE: 2468629 3' similar to TR: 075085	O75065 KIAA0477 PROTEIN :	Homo sepiens neural cell adhesion molecule 1 (NCAM1), m.c.o.	Harro septens incure on animates.	CM-BI UAS-CAUZAS-VI 3 BI 1920 FORMS SEPTENTS CONA	Unaversities of the service density incorded receptor, exon 11	ANA EACH ATE A NIH MICE 21 Home sapiens CONA clone IMAGE:3843748 5	University of the Computation of the Bracetor 2 (GABABR2) mRNA, complete cds	Hours series Drosobile Kelch III/e protein (DKELCHL), mRNA	Thin separate the KIAA0191 gene, pertial ode	Homo earlies proben (peorbly-proty dis/trans isomerase) NIMA-Interacting 1 (PIN1), mRNA	Home series probin (people) proty distrans isomerase) NIMA-interacting 1 (PIN1), michael	Home earliers mRNA for MEGF8, pertial cds	Lives services mRNA for MEGF8, pertial cds	And 1882/1251 NIH MGC 8 Hamp septems cDNA clane IMAGE:3544298 6	Homo seniens ATP-binding cessette, sub-family A (ABC1), member 3 (ABCA3), mRNA	Homo saciens ATP-binding cassette, sub-family A (ABC1), member 3 (ABC43), mktvA	Homo saplens HSPC161 mRNA, complete cds	DKFZp43056 r1 434 (synonym: https://domo.eaplens.cin/A.come.DMFZph341056 r1	Homo sepiens hypothetical protein (D.328E19.C1.1), mRNA	Homo explens sine coults homeobox (Drosophile) homolog 1 (SIX1) mixture	801281947F1 NIH MGC 44 Homo saplens cDNA clone IMAGE:3604019 5	601281947F1 NIH MGC 44 Homo septems CDNA clone IMAGE:3604019 5	801281947F1 NIH_MGC_44 Hamp septens CDNA clone IMAGE:3604019 b	EST383789 MAGE resequences, MAGB Homo septems cDNA	Human breakpoint cluster region (BCR) gene, complete cds	Human breakpoint cluster region (BCR) gene, complete cds	Hano septens PRKY exam 7	
	Top Hit Database		EST HUMAN	L'A		EST_HUMAN	EST HUMAN	EST_HUMAN	N	Ę	EST HUMAN	EST_HUMAN	۲.	EST HUMAN	Z	N.	LN.	<u> </u>	Z.	ž!	IN	ES! HOMAN	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	N IN	EST LEIMAN	-1.	12	CCT LIMAN	EST HIMAN	ENT HIMAN	NAN LI	TAN TAN			
בייים בייים	Top Hit Acession No.		8.1				1.0E-117 AV717788.1	N950145.1	10834689 NT	10834989 NT		AI904151.1	D16524.1	1.0E-117 BE733922.1	1.0E-117 AF090033.1	11420222 NI		11628424FT	11424836 N	1.0E-117 AB011541.1	1.0E-117 AB011541.1	1.0E-117 BE269856.1	FN 6464024	4.0E-117 4501640 NT	100000	ALM45054.1			BE389/00.1	BE308/03	BE389/00.1	1.0E-118 AWBOT (20.1	1.0E-118 U0/000.1	1.0E-118 U07000.1	1 1000 1
-	Most Similar (Top) Hit BLAST E	Value	1.0E-117 A	1.0E-117 L78571.1	1.0E-117 L76571.1	1.0E-117	1.0E-117	4 DE-117 AI950145	1.0E-117	1.0E-117	1.0E-117 AI904151	1.0E-117 AI90415	1.0E-117 D16524.	1.0E-117	1.0E-117	1.0E-117			1.0E-117	$ \cdot $					1	1.0E-118 ALD456			1		_	\perp			
	Expression		0.86	5.01	5.01	1.75	1.75	Sic 6	228	220	0.58	0.56	225	2.07	29	1.11	1.77	2.68	2.68	3.32	3.32	14.73										1.08			4.64
	ORF SEQ		30574	33108	33109	33212	33213	2000				L				36345		36861	36802	37196	L		3 37501									4		0 28190	4
ļ	Exon SEQ ID	ÿ	47027	20031	2003	1_	1_	L_	205/3	L	1_		1_	L			1_	<u> </u>	丄	L	1_	L	7 24186	$oldsymbol{ol}}}}}}}}}}}}}}}}}}$		1	13288	4 15555	7 14955	7 14955	7 14055	15054	4 15450		15867
	Probe SEQ ID	ÿ	0000	382	322	7448	7446		7878	200	83.10	8340	2 8	9898	9846	10469	10765	10984	1080	11243	11243	11369	11587	11687	88	Z	504	\$	1222	7227	7227	2329	2744	2744	3102

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	Top Hit Descriptor	ARBE - I NOT COMP KINS Home septems CDNA clone IMAGE: 1916769 3'	Applications of the North Property of the INA GE 1916769 3	doublook i Not Joseph Darker Complete Cds	Full Mary 10 1000011 From Product (KIAA0478), mRNA	Home separate calcium channel camma 4 subunit (CACNG4) gene, exen 3	Hadib serial accessing parameter a structure (CACNG4) gene, exten 3	TOTIO SECOND CARCILLY OF IN MANA	Horno services males (RELN) mRNA	Lines could filmost transmembrare conductance regulator (CFTR) gene, expn 4	Louis Cycle Ind (1874) mRNA	Homo employs T-box 4 (TBX4), mRNA	Lance series francient recently botonitial channel 5 (TRPC5), mRNA	nome separate management control factor beta binding protein 2 (LTBP2) mRNA	Home sapients mean transforming growth factor beta binding protein 2 (LTBP2) mRNA	Harrie Saprella recont transcrivers # 1 Percentage Control Con	IDN 40-00-01-21 - 1-434 (surveyum Hencs) Home against oDNA clone DKFZ043400127 5	UKFZPASŁOUIZI JI SZY (SPIROTIFIE) (CZORFS), mRNA	PACHALIENET NIH MIGC 46 Homo explore cDNA done IMAGE:4302749 5	ANA 4804 50F1 NIH MAGE 67 Homo septens cDNA done IMAGE:3872247 5	OC 1200 CO. 1000 CO. 1000 BT 10203 Homo sepiens cDNA	OVA BTOOCH DECOMPOSE PROSES Hamo sepiens CDNA	CONTROL Spares NIHMPL ST Hamp septens cDNA done IMAGE:811789 5	208407 rt Soares Nit-HMPu St Hamo septens cDNA clone IMAGE:811789 5	Hirman mRNA for KIAA0383 gene, perties cds	Human mRNA for KIAA0363 gene, partial cds	Home services latent transforming growth factor beta binding protein 2 (LTBP2) mRNA	Home serious latent transforming growth factor beta binding protein 2 (LTBP2) mRNA	PART 1449R3E2 NIH MGC 19 Hamo septens CDNA clone IMAGE:3160502 5	TAKETARSAK 1824 rt. 586 (synchym; huter) Homo septens cDNA clone DKFZp586K1824	Home enviews hypothetical profesin (DJ328E18.C1.1), mRNA	TOKETARATORITY H 647 (synonym: http:// Hamo saplens cDNA clane DKFZp5470017 5)	22-12-00-4 NCI CGAP BITZ3 Hamo sapiens aDNA clone IMAGE:3564785 3' similar to SW:ZP3A_HUMAN	P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR;	
	Top Hit Database Source	Т	Т	HOMAN	5	5!	Ž	EZ.			Į.	Z	Į,	Z	Ł	. 1	EST HUMAN	EST HUMAN	N.	ESI HOMEN	ES! HUMAN	ESI HOMAIN	ESI HUMAN	TOTAL LINAN	FIN FIN	12			N I	ESI HUMAIN	ESI HUMAN	N. C. C. C. C. C. C. C. C. C. C. C. C. C.	ESI HUMAN	EST HUMAN	
	Top HR Acession No.			-		1425793	-	F142624.1	11422054 NT	1114C02Z411	٠	11425900 N	11425900 N	11420784 NT	4557732 NT	4667732 NT	1.043761.1	1.0E-118 AL043761.1	11431050 NI	3F 68 5272.1	3E781223.1	1.0E-118 BE062855.1	BE062855.1	AA443024.1	AA443024.1	1.0E-118 AB002381.1	0.1	4001132	4667732 N I	BE263134.1	- 1	185/015 N	AL 138321.1	BF196407.1	
	Most Similar (Top) Hit BLAST E		1.0E-118 AI347694	1.0E-118 Al347694	1.0E-118 D23050.1	1.0E-118	1.0E-118 AF14262	1.0E-118 AF14262	1.0E-118	1.0E-118	1.0E-118 M55109	1.0E-118	1.0E-118	1.0E-118	1.0E-118	1.0E-118	1.0E-118 AL04376	1.0E-118	1.0E-118	1.0E-118 BF08527	1.0E-118 BE781Z	1.0E-118	1.0E-118 BE0628	1.0E-118 AA4430	1.0E-118 AA4450	1.05-118	1.0E-116 ADVUZS	1.0E-118	1.0E-118	1.0E-118 BE2631	1.0E-118 AL0484	Į	1.0E-118 AL1383	1.0E-118 BF1964	
	Expression Signet		4.67	4.67	4.77	0.9	1.87	1.87	76.0	0.94	1.24	0.83	0.83	1.49	1.44	1.44	1.12	1.12	5.63	0.86	2.17	6.58	6.58	1.37	1.37					4.95		1.53	86'0	1.88	
	ORF SEQ ID NO:		28805	28606	29439	30028	30800	30901	31247	31248	31395	31491	31402	31578	32368		32738		33264	33512	33083	34116	34117		1		1		34456	34767	34806	35327	35731	36134	
İ	Esca SEQ ID NO:		15953	15953	16811	17393	18140	18140	18340	18340	18477	18563	18583	18640	19355	19355	19689	19689	20172	20397	20567	20976	20976					_	21313	Ļ	21655	22146	22536	22822	١
•	Probe SEQ ID NO:		3190	3180	4067	4650	5837	5337	5543	5543	2684	2112	5772	5853	6592	6592	7009	6997	7500	7733	7872	8282	8282	8288	8288	8573	8573	8621	8621	8833	8084	8483	9886	10274	

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Single Exoll Flores Expressed III Diali	Top Hit Descriptor	xa46a10.x1 NGL CGAP_Kid11 Homo sepiens dDNA done IMAGE:2772888 3' skriller to SW:BODG HUMAN 075636 GAMMA-BUTYROBETAINE 2-OXOGLUTARATE DIOXYGENASE	UI-H-BW0-80-8-07-0-UI:s1 NCI CGAP Sub6 Homo sepiens cDNA clone IMAGE:2729772.3	802141528F1 NIH_MGC_48 Hamo sapiens cDNA clone IMAGE:4302798 5	Homo septens protein with polyglutamine repeat, calcium (ca2+) homeostasis endoplasmic redoulum protein (ERPROT213-21), mRNA	EST186814 HCC cell line (matestasis to liver in mouse) il Homo sepiens cDNA 5' end similar to dynein, light	Contact I, cyclyssering 601499514F1 NIH M.C. 70 Home seglens of NA close IMA DE Soutses R	801499514F1 NIH MGC 70 Hamo sapiens cDNA clone IMAGE:3901563 51	QV0-UM0091-120600-385-b12 UM0091 Homo sapiens cDNA	QV0-UM0091-120600-385-b12 UN0091 Homo saplens cDNA	Homo sepiens chloride channel CLC4 (OC4) mRNA, complete cds	Homo sapiena CGI-105 protein (LOC61011), mRNA	Homo sapiens mRNA for KIAA0930 protein, partial ods	Homo sepiens hypothetical protein FLJ10052 (FLJ10052), mRNA	on10b05.s1 NCI_CGAP_Lu5 Homo septens cDNA done IMAGE:1556241 3' similar to WP:E04F6.2 CE01214;	Homo sepiens glutamate receptor, tonotropic, kainete 1 (GRIK1) mRNA	AU133399 NT2RP4 Homo sepiens cDNA clone NT2RP4001991 5'	Human neurofibromin (NF1) game, complete cds	RC1-NN0073-250800-018-g08 NN0073 Homo septens cDNA	AV693731 GKC Homo saplene cDNA clone.GKCDHB03 57	DKFZp782M0710_r1 762 (synonym: hmel2) Homo sepiens cDNA clone DKFZp762M0710 5	DKFZp762M0710_J1762 (synonym: hmel2) Homo septens cDNA clone DKFZp762M0710 5	qb77c0cx1 Soarse_febti_heart_NBHH19W Homo espiens cDNA clone IMAGE:1706128 3' similar to SW +4C1 MONISE prover KEDATIN TYDE I CYTOCKE ETAL 40	T		21574513'				
אום ביצחון גווחד	Top Hit Detabase Source	EST HUMAN	EST HUMAN	EST_HUMAN	Ę	MAN III FOL	EST HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	N.	N	TN.	N.	EST_HUMAN	LN TN	EST_HUMAN	L	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HIMAN	Т	Z	EST_HUMAN	NT	EST_HUMAN	EST_HUMAN	EST HUMAN
	Top Hit Acession No.	1.0E-118 AW271289.1	1.0E-118 AW296351.1	BF686214.1	11065988 NT	440	1.0E-118 BE008678 1	BE908676.1	1.0E-118 BF093687.1	1.0E-118 BF083687.1	1.0E-119 AF170492.1	TN 50807	1.0E-119 AB023147.1	8922205 NT	1.0E-119 AA916780.1	4504116 NT	20.1					1.0E-119 AL134903.1	Ţ	<u></u>	1.0E-119 AF315683.1	1.0E-119 AI476732,1		23.1	4.1	1.0E-119 BE615150.1
	Most Similar (Top) Hit BLAST E Value	1.0E-118	1.0E-118	1.0E-118 BF68621	1.0E-118	4 05 440	1.0E-118	1.0E-118 BE90867	1.0E-118	1.0E-118	1.0E-119	1.0E-119	1.0E-119	1.0E-119	1.0E-119	1.0E-119	1.0E-119	1.0E-119 M89914.	1.0E-119	1.0E-119	1.0E-119	1.0E-119	1 OF-419 A 1450703	1.0E-119	1.0E-119	1.0E-119	1.0E-119 X06292.	1.0E-119	1.0E-119 BE79661	1.0E-119
	Expression Signal	0.48	0.65	1.61	1.8	200	188	1.68	1.61	1.61	0.07	1.61	5.97	1.57	0.8	1.42	2.5	24.82	3.11	1.83	0.63	0.63	7.67	0.92	26'0	98.0	2.62	4.69	1.5	1.19
	ORF SEQ ID NO:	36227	36300	37165	37186	37201		37458	37461	37462	28173	28433	27374	28606		28325				30630	31201	31202	31778	31940	31941	31987	32135	32148	33070	34390
	SEO ID NO:	23012	23077	23869	23899	23008				24150		•		15864	15996			ı	Į		18301	18301	18816		18967	19013	19139	19140	19993	21252
	Probe SEQ ID NO:	10365	10431	11206	11236	11248	11548	11548	11551	11551	741	1014	1926	3099	3234	3934	5253	99239	6270	5347	5503	5503	903	6190	6190	6239	8270	8380	7310	8290

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Chigh Lyons Lybrossed III Digili	Top Hit Descriptor	Homo sapiens KIAA0477 gene product (KIAA0477), mRNA	qf43er11.x1 Soeres, testis, JNHT Homo saplens cDNA clone IMAGE:1752764 3' similer to TR:Q13458 Q13458 GUANINE NUCLEOTIDE EXCHANGE FACTOR PROTEIN TRIO	8432705.11 NCI CGAP GCB1 Hamo eaplens oDNA clane IMAGE:814977 5	Homo saplens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exons 16-17	Homo sepiens hypothetical protein FLJ10206 (FLJ10206), mRNA	Homo sepiens hypothetical protein FLJ10206 (FLJ10206), mRNA	Homo sapiens Scd mRNA for etearcy-CoA desaturase, complete cds	Homo sepiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, excrs 16-17	Homo sepiens pertial II,-12RB1 gene for IL-12 receptor beta1 chain, excrts 16-17	602:188072F1 NIH_MGC_45 Hamo sapiens aDNA dane IMAGE:4310833 5"	RC3-CT0212-240898-011-f03 CT0212 Homo sepiens cDNA	Homo sepiens syneptojanin 1 (SYNJ1), mRNA	Hama sepiens intersectin 2 (SH3D1B) mRNA, complete cals	Homo septens intersectin 2 (SH3D1B) mRNA, complete cds	yy40g12.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:273769 51	Homo sepiens cysteine-fich repeat-containing protein SS2 precursor, mRNA, complete cds	Homo sepiens distribution and metalloprotesse domain 10 (ADAM10) mRNA	Homo expiens gene for AF-8, complete cds	Home septems gene for AF-8, complete ads	Homo sepiens equeporth 4 (AQP4), splice variant b, mRNA	Homo sepiens synaptojanin 1 (SYNJ1), mRNA	Homo septems cAMP-specific phosphodiostenase 8A (PDE8A) mRNA, partial cds	Homo sapiens cAMP-specific phosphodiestenese 8A (PDE8A) mRNA, partial cds	Homo sapiens stannicoalcin (STC) gene, partial cds	Homo septiens stanniocalch (STC) gene, partial cds	Homo saciens glutamate receptor, brodropic, kainate 1 (GRIK1) mRNA	3981 3					Human TBXAS1 gene for thromboxene synthese, even 7	
21.	Top Hit Detabase Source	LN.	EST HUMAN	EST HUMAN	Ę	E	ĮŅ.	¥	TN	NT	EST_HUMAN	EST_HUMAN	L.	Ę	LN	EST_HUMAN	Į.	LN	TN	LN LN	ŢN	IN	NT	NT	NT	NT.	NT	EST_HUMAN	EST_HUMAN	EST_HUMAN	LN	N _T	L	L
	Top Hit Acession Na.	11036643 NT	1.0E-119 AH49798.1	VA465124.1		11425837	11425837 NT	1.0E-119 AB032261.1	J.297701.1	1.0E-119 AJ297701.1	3F569571.1	1.0E-119 AW847519.1	4607334 NT	NF248540.1	NF248540.1	444873.1	\F167706.1	4557250 NT	(B011399.1	\B011399.1	4755124 NT	4507334 NT	1.0E-120 AF056490.1	\F056490.1	(F098463.1	1F098463.1	4504116 NT	1.0E-120 AI190903.1	F568222.1	1.0E-120 BF568222.1	129428.1	1	1	1
	Moet Shnilar (Top) Hit BLAST E Value	1.0E-119	1.0E-119	1.0E-119 AA4851	1.0E-119 AJ2977	1.0E-119	1.0E-119	1.0E-119	1.0E-119 AJ2977	1.0E-119	1.0E-119 BF5695	1.0E-119	1.0E-120	1.0E-120 AF2485	1.0E-120 AF2485	1.0E-120 N44873.	1.0E-120 AF1677	1.0E-120	1.0E-120 AB01130	1.0E-120 AB01130	1.0E-120	1.0E-120	1.0E-120/	1.0E-120 AF05640	1.0E-120 AF09846	1.0E-120 AF09646	1.0E-120	1.0E-120	1.0E-120 BF56822	1.0E-120 E	1.0E-120 M29428	1.0E-120 M29428	1.0E-120 D34619.	1.0E-120 Y00067.
-	Expression Signal	1.15	0.55	3.35	1.29	0.71	0.71	4.18	2.38	2.38	6.31	2.16	1.43	2.49	2.49	2.31	3.08	1.21	0.02	0.92	5.24	1.50	1.95	1.95	2.22	2.22	1.36	0.0	16.61	10.01	0.57	0.57	1.77	5.22
	ORF SEQ ID NO:	35683	35867	36008	36263	36317	36318	36390		36914			26741	26439	26440	26832	27033	27250	27585	27586	27985	25741	28682	29083	20083	29964	30401	30468	31357	31358	32110	32111	33236	33812
	Ean SEQ ID NO:	22458	22854	22794	23047	23089	23080	23163	23660	23980	23828	25326	13100	13778	13778	14152	14343	14539	14831	14831	15247	13100	700	7084	1340	17340	17784	17851	18444	18444	19120	1920	20 44	20490
	Probe SEQ ID NO:	9807	10008	10146	10401	10443	10443	10517	10985	10985	11159	12198	ğ	1018	1018	1405	1597	1799	28	2100	žš	3302	4325	4326	4814	494	3065	5133	6840	5649	8350	8350	7471	7795

PCT/US01/00667

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Most Similar (Top Hit Acession Detabose BLASTE No. Source Value	Z	EST HUMAN	Z	Z	N.	i Z	NAME TO T	TOT WINAN	1.0E-120 BE362102.1 E.S.I. DOMEN	1.0E-120 BF308641.1 EST TOMAN	1.0E-120 AU133205.1 EST FIORMAN	1.0E-120 AL040801.1	1.0E-120 Al904151.1 EST_FIUMAN	1.0E-120 AB029000.1 NI	1.0E-120 BE298387.1 EST HUMAN	1.0E-120 BE867619.1 EST HIMAN	1.0E-120 BEB67619.1	1.0E-120 U94774.1 NT	1.0E-121 Y18000.1	1.0E-121 AU134963.1 ESI HUMAN	1.0E-121 503Z19ZINI	1.0E-124 AB011133.1	1.0E-121 4765139 NT	1.0E-121 4755130 NT	1.0E-121 M95988.1 NT	1 OF-121 M95988.1	IN 124 (178891 4	1,05-12-12-12-12-12-12-12-12-12-12-12-12-12-	1.05-121 1 15coot 1	1.0E-121 11920B.1	4.0E-121 AB03/706.1	1.0E-12! AB03//38.1	4.0E-121 AF150150.2
	1.0E-120 YO	1.0E-120 BF	1.0E-120 AB	1.0E-120 AE	1.0E-120 AE	1.0E-120 AE	1.0E-120 AE	1.0E-120 BE	1.0E-120 BE	1.0E-120 BF	1.0E-120 A	1.0E-120 A	1.0E-120 A	1.0E-120 A	1.0E-120 BI	1.0E-120 B	1.0E-120 B	1.0E-120 U	1.0E-121 Y	1.0E-1211A	1.0E-121	1.0E-121	1.0E-121			l	l					1	
Expression Signal	5.22	2.43	0.85	0.85	2.33	2.33	1.17	5.28	5.28	3,75	8.25	0.79	0.54	2.55	3.72	2.06	2.06	1,38				2.81	1.33	22,									7.35
ORF SEQ ID NO:	33613	34063	34135	34136	34138	34139	34182		35234	35492	35510	35525		35831	37015	37311	37312	37567	25534	26808		5 27001	27407						_]				9 29090
SEQ ID	20,490	20824	20907	20997	21001	21001	21045	22063	22063	72227	22312	22329	L	L.	1_		24007		12898	13165	15549	14315	14694	١	1	_1	_1		15844	15844	16281	5 16281	18419
Probe SEQ ID NO:	2,00	8230	8303	8303	8307	8307	8352	1046	2076	9845	0986	7780	9792	9768	11071	11316	11316	11850	7	388	707	1568	1958		200	<u>8</u>	1984	2085	3079	3079	3525	3525	3888

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	Top Hit Descriptor	FTN-01 - NOT CGAP Part Home septens cDNA clone IMAGE:2005417 3'	H amiens ECE-1 cone (excm 17)	Hudging x1 NCI CGAP Lu24 Hamo sapiens cDNA clane IMAGE:31861193	PRY 401485F1 NIH MGC 9 Homo sapiens cDNA clone IMAGE:3049820 5	Himan oktobe transporter (GLUT4) gene, complete cds	Lower serious You meuticountering region; segment 2/2	RC3-NN0086-270400-011-f02 NN0088 Homo septens cDNA	RC3-NN0086-270400-011-f02 NN0086 Homo expiens cDNA	Homo septens demme-eminobutyric acid (GABA) A receptor, alpha 2 (GABKAZ), mixing	Horno septens DNA for prostacyclin synthasa, exon 8	Homo saciens DNA for prostacyclin synthase, each 8	Inches of Human Perception isless Homo septens con Significanto TR: 075457 075457 CT1 USOLIO	PHOSPHOLIPASE A2-GAMMAA.; PHOSPHOLIPASE A2-GAMMAA.; Long-onk of Human Pancreatic laters Homo septens cDNA 6' similar to TR:075457 075457 CYTOSOLIC	PHOSPHOTORICASE A2-GAMMA. PHOSPHOSPHOTORICASE A2-GAMMA. PHOSPHOSPHOTORICASE A2-GAMMA.	Home services UDP-discussors/stransferase 284 precursor (UGT284) mRNA, UGT284*E458 elible,	complete cds	Hamp sayens clining in the plant was expected to the plant of the control of the	A1119320 HEMBA1 Homo sepiens cDNA done HEMBA1005638 5	Homo septens T-cell (imphome invesion and metastasis 1 (TIAM1), mRNA	Homo sepiens intersectin short isoform (ITSN) mRNA, complete cds	Homo sepiens T-cell lymphoma invasion and metastasis 1 (11AM1), micro	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cas	(I) actually (in second section of the section of t	Human kappa-immunoglobulin germline pseudogene (Chrizz 4) variable region (aubgroup v region ry Homo saplens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds	Homo saplens collegen, type XII, eighe 1 (COL12A1), mRNA	Home seciens collegen, type XII, aipha 1 (COL12A1), mRNA	ANTAGO032F1 NIH. MGC 70 Home sapiens cONA clone IMAGE:3898358 5	Inchese 73F1 NIH MGC 19 Home explens cDNA clone IMAGE:4125234 5	601896173F1 NIH_MGC_19 Hamo saplens dDNA clane IMAGE:4125234 5	
<u>}</u>	Top Hit Detabase Source	Т	EST HUMAN	Т	7	HOMAN		NAME IN	Т	NO.	12	2	i.	EST HUMAN	EST_HUMAN	¥	ᅜ	NAME TO TOTAL	TOT TOWN	TOWNER TO THE	Z	LV.	1		TN FA		2 2	TOT TOT	FOT LIBITAN	EST HUMAN	
	Top Hit Acession No.		<u>-</u>				1	1	20.1	W 898086.1	114302411	384122.1	384122.1	1.0E-121 AW583858.1	1.0E-121 AW 583858.1	11427788 NT	1.0E-121 AF064200.1	7330334 NT	N50624.1	1.0E-121 AU119320.1	TN 0/10/2011	1.0E-142 AT 11-100.	110201	1.0E-122 AFT 14400.1	1.0E-122 M20707.1			11478424 [7]	1.0E-122 BE906024.1	1.0E-122 BF316170.1	leraioiva.
	<u>≱</u> = ⊔	Value	1.0E-121 AI26329	1.0E-121 X91937.	1.0E-121 BE2222	1.0E-121 BE271424.1	1.0E-121 M91463.	1.0E-121 A	1.0€-121	1.0E-121 AWB98	1.0E-121	1.0E-121 D84122	1.0E-121 D84122	1.0E-121	1.0E-121	1.0E-121	1.0E-121	1.0E-121	1.0E-121 N5962	1.0E-121	1.05-122	1	1	1							╛
+	Expression Signal		2	3.24	76.0	0.85	16.0	0.68	1.78	1.78	211	2.45	2.45	1.21	1.21	2.95	821	3.46	2.53	283	2.28	263	2.14			1.28		1.35			22
-	ORF SEQ ID NO:		20863	30259	30510					30638		33664	33885				36616		36844	3 37269				1 28302	0 28614	2 27128	0 27150	0 27151	7 27262		2 27955
	SEQ ID	<u>-</u>	17035	17647	1	I.	1_	1_	L	17943	20533	<u> </u>	L	l	1	1	·	1_	<u> </u>	1_		7 13128	13147	13631	8 13950	8 14432	١.		1_		5 15212
	0	j Z	4296	6019	5188	5474	\$525	6788	9889	888	7838	7842	7842	9768	84/20	10875	4000	10880	10917	11308	18	327	348	862	1198	1688	1201	17071	1807	2485	2495

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	Top Hit Descriptor	Homo sapiens FYVE domain-containing dual specificity protein protein prospirates FTVE domain-containing dual specificity protein protein protein cols	Homo sapiens amyold bets (A4) precured protein (protesse nextral, Azheimer disease) (APP), mRNA	ULAH-ENCAR-A-CI-T NIT MSC_ OF FORM SAFETY CONTRACTOR SAFETY NIT 14/07 AB LICENS SAFETY NIT 14/07 AB LI	60111366/F1 NRT MCC 10 full september CONA clone IMAGE:3354232 5	SAGNO S. Soeres testis NHT Homo sepiens dDNA done IMAGE:1408339 3'	Home services mRNA for doublesest and math-3 related transcription factor 1 (DMRT1)	Homo eachans lethel client larvae (Drosophile) homotog 2 (LLGL2), mRNA	Trick or program of the Party Home sendens CDNA clone IMAGE:2013767 3' similar to	SW:MTA1_HUMAN Q13330 METASTASIS_ASSOCIATED PROTEIN MTA1.:	4)52h07x1 NCI_CCAP_Brit23 Horito explens CLINA CLITE INTOCLITED SW:MTA1.; SW:MTA1_HUMAN Q13330 METASTASISASSOCIATED PROTEIN MTA1.;	Novel human gene mapping to chomosome A, acroning of up, (propositional)	EST367904 MAGE resequences, mage intuition estrates control	Homo septens gand for 5124, even 10	Homo septems prosporomentromuses 1 (Trimin I), illingo September 100 OCAD Brief Homo septems CDNA clone IMAGE:4153670 5	SUZUTBUCOFT INC. COMP. PAINS THAT Home september CONA clone IMAGE:4153870 5	U.C. Lackers chromosoms 21 segment HS21C049	Home services inner membrane protein, mitochondrial (mitofilm) (IMMT), mRNA	incinction of the state of the	products products products	Home septens prosprintingstrostations of the contract of the c	Homo sepiens pertial mRNA for immunoglobulin kappa chain variable region (IGVK gene), sample GN02	Human amelogenin (AMELY) gene, 3' end of cds	Human amalogenin (AMELY) gene, 3' end of ods	Human amelician'in (AMELY) cene. 3' end of ode	Home seeins RABO-like protein (LOCS1209), mRNA	Homo seriens duteminy-peoide cyclotrensferese (gluteminy cyclese) (QPCT), mRNA	Homo sapiens retinalderryde-binding protein (CRALBP) gene, complete cds	
חווחים פוחוות	Top Hit Detebese Source	N		HUMAN	П	EST HUMAN	TOWN.	N.	Ž	EST HUMAN	EST_HUMAN	Ę	EST_HUMAN	Ę	L'A	EST HUMAN	EST HUMAN	I N	Z	Ę	LN	5	1	L L	į t	Z	- Z	5	
	Top Hit Acession No.	-	4502188 NT	5.1	2	<u>.</u> ,		1	11424216 NI	J359618.1	1.0E-122 Al359618.1		1.0E-122 AW955834.1	1.0E-122 AB024068.1	11418187 NT	3F345Z74.1	3F345274.1		5803114 IN	4505818 NT	4505818 NT	١ ÷		1.0E-123 MOO418.1	1.0E-123 M30418.1	IN 1.814CCM	- 1	N 102100	1.84218.1
	Most Shrilar (Top) Hit BLAST E Value	1.0E-122 AF264717	1.0E-122	1.0E-122 AW5046	1.0E-122 BE25803	1.0E-122 BE25803	1.0E-122 AAB080/1	1.0E-122 /	1.06-122	1.0E-122 Al359618	1.0E-122/	1.0E-122	1.0E-122	1.0E-122	1.0E-122	1.0E-123 BF345Z7	1.0E-128 BF345Z		1.0E-123	1.05-123	1.0E-123						┙	1,05-123	╛
	Expression Signal	1.41	5.04	1.46	1.38	7.1	0.73	0.65	121	1.10	1,19	1.05	217	1.88	6.8	1.74	,		2.5	5.58			7						1.56
	ORF SEQ ID NO:	28280	30148		31170			34530	34761	35073			Ŀ			20181			20422	29634						3 27557			30847
	SEQ ID	15612	17528	17658	18275	18275	19801		21617	<u>ا</u>	1	L	1_	L	L		<u>_</u>	13754	13781	13966	1	1	_1						18163
	Probe SEQ ID NO:	84	4705	883	27.73	9868	7113	8695	8028	0333	2000	10034	10008	11358	11958	751	751	885	, 8	126	2		1438	2002	2082	2082	2313	3245	5361
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	Top Hit Descriptor	Homo sepiens retinaldehyde-binding protein (CRALBP) gene, complete, cds	901591108F1 NIH MGC 7 Hamo suplems cDNA clone IMAGE:3946433 5'	AU118435 HEMBA1 Hamo seplens cDNA clone HEMBA1003591 5"	YQ84603.11 Soares fetal liver spleen 1NFLS Homo suplens cDNA clone IMAGE:202444 5' similar to SP:YAK1 YEAST P14680 PROTEIN KINASE YAK1	Human growth hormone releasing hormone gene, expn 7	Human hBRAVO/Nr-CAM precured (hBRAVO/Nr-CAM) gene, complete cds	Homo septems heperan suffate (glucosarnine) 3-O-suffotransferase 2 (HS3ST2), mRNA	Homo septens 2-50/goadeny/ate synthetase 2 (OAS2), mRNA	601152815F1 NIH_MGC_19 Homo sepiens cDNA clone IMAGE:3508162 5'	AU131881 NT2RP3 Homo septems cDNA done NT2RP3003409 5'	AU131881 NT2RP3 Homo septiens CDNA clone NT2RP3003409 5	RC4-BT0311-261109-012-a07 BT0311 Homo septens cDNA	Homo sepiens mRNA for KIAA0454 protein, pertlal cds	Oryctologus cuniculus New Zeeland white elongation factor 1 slibhs (Rabeflaz) mRNA, complete cds	602086791F1 NIH MGC 83 Homo saplens cDNA clone IMAGE-4250879 5'	602086791F1 NIH_MGC_83 Hamp saplens cDNA clone IMAGE:4250879 51	Homo sepiens T-cell lymphoma invesion and metastasis 1 (TIAM1) mRNA	Homo sepiens T-cell lymphome investor and metastrais 1 (TIAM1) mRNA	Homo sepiens DNA for emyloid precursor protein, complete cds	Homo saplens chromosome 21 segment HS21C046	281504.r1 Strategere achtzo brain 311 Homo eaplens dDNA clone INAGE:728719 5 similar to TR:G300482 G300482 POL#REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT)	281b04.r1 Strategere echizo brain S11 Homo espiene CDNA clone INAGE:728719 5 striitar to TR:G300482 G300482 POL-REVERSE TRANSCRIPTASF HOWN OG RETTROVIRAL ELEMENT.		metastasis 1 (TIAM1) mRNA		and complete cds	npiete cds		E:3893954 5	Homo sapiens giutamata receptor, lonotropic, kainata 1 (GRIK1) mRNA
	Top Hit Database Source	IN	EST HUMAN	EST_HUMAN	EST HUMAN	N	N	Z	L'N	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	П	Z	T HUMAN	Г			Ā	F	EST_HUMAN	1	Ę						24.1 EST_HUMAN	П
	Top Hit Acession No.	1	BE799746.1	1.0E-123 AU118435.1	H53196.1	-	1	11525833 NT	11436439 NT	2.7	1.0E-123 AU131881.1				1 -	1.0E-123 BF677292.1		4507500 NT	TN 002209		6.2	1.0E-124 AA397551.1	1.0E-124 AA397551.1		7500	7705446 NT	2.1	2.1	1.0E-124 AJ131712.1	1.0E-124 BE879524.1	4504116
	Most Similar (Top) Hit BLAST E Value	1.0E-123 L34219.	1.0E-123 BE79974	1.0E-123	1.0E-123 H53198.	1.0E-123 U42224	1.0E-123 U55258	1.0E-123	1.0E-123	1.0E-123 BE2630	1.0E-123	1.0E-123	1.0E-123	1.0E-123	1.0E-123 U09823.	1.0E-123	1.0E-123	1.0E-124	1.0E-124	1.0E-124 D87675.	1.0E-124 AL16324	1.0E-124	1.0E-124	1.0E-124 /	1.0E-124	1.0E-124	1.0E-124	1.0E-124 AF27489	1.0E-124	1.0E-124	1.0E-124
	Expression Signal	1.58	1.62	2.59	1.2	1.25	287	1.62	1.3	2.18	29.0	79.0	1.13	243	15.48	4.60	4.66	2.19	2.19	290	284	2.68	2.08	7.84	1.61	1.94	4.95	4.95	220	3.05	0.85
	ORF SEQ ID NO:	30848	31191	32145	32688	32698	32849	33061	33312	33324	33836	33637		35183	35230	37637	37638	25708	25709		25898	26092	20083	26174	26223	26321	26747	26748	27263	27512	28774
	Exan SEQ ID NO:			19146	19643	19652	19783	19985	20212	20221	20511	20511	21126	22023	22067	24314	24314	13070	13070	13076	13259	13450	13450	13515	13562	13653	14074	14074	14548	478	16118
	Probe SEQ ID NO:	5361	5494	6377	6905	6915	7094	7302	7642	7661	7816	7816	8433	9269	9405	11720	11720	282	262	268	473	675	676	742	2007	88	1325	1325	88	88	3358

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Homo sapiens ubiquitin specific protesse 9, X chromosome (Drosophila fat facets related) (USPQX), mRNA hg94a09x1 NCI_CGAP_Kid11 Homo sepiens cDNA done IMAGE:2953240 3' similar to TR:095162 ng94409.x1 NCI_CGAP_Kid11 Homo sepiens cDNA clone IMAGE:2353240 3' similar to TR:095162 Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6BIR1) gene, exch Hamo sepiens ATP-sensitive Investity realthing K-chennel subunit (KCNJ9/BBIR1) gene, each UHIF BNO-skz-b-04-0-UI.r1 NIH_MOC_60 Homo sepiens cDNA clone IMAGE:3078846 5' ac08h05.s1 Stratagene HeLa cell s3 937216 Homo saplens cDNA clone IMAGE:855897 3 H. saplens lactate dehydrogenase B gene exen 1 and 2 (EC 1.1.1.37) (and joined CDS) hj05c08.x1 Source_NFL_T_GBC_S1 Homo septens cDNA clone IMAGE:2980906 3 Homo sepiens IQ motif containing GTP ase activating protein 1 (IQGAP1) mRNA wc43g03.x1 NCI_CGAP_Pr28 Hamo sepiens cDNA clane IMAGE:2321428 31 wc43g03.x1 NCI_CGAP_Pr28 Hamo sepiens cDNA clane INAGE:2321428 31 WIGSTOZIKI NCI_CGAP_KId12 Homo septens cDNA clone IMAGE:2400891 3 WIGSTOZIKI NCI_CGAP_KId12 Homo septens cDNA clone INAGE:2400891 3 096162 PEROXISOMAL SHORT-CHAIN ALCOHOL DEHYDROGENASE. 602124644F1 NIH_MGC_56 Hamo septens CDNA clone IMAGE:4281635 57 **095162 PEROXISOMAL SHORT-CHAIN ALCOHOL DEHYDROGENASE.** Homo sepiens cep250 centroeome associated protein mRNA, complete cds Homo saplens cep250 centrosome associated protein mRNA, complete cds 600943771F1 NIH_MGC_8 Hamo sepiens cDNA clone IMAGE:2966585 5 600843771F1 NIH_MGC_8 Homo sepiens cDNA clone IMAGE:2986585 5 Homo sepiens T-cell lymphome invesion and metastasis 1 (TIAM1) mRNA Human muscle glycogen phosphorylase (PYGM) gene, excus 6 through 17 Homo sapiena glutemate receptor, tonotropic, kainate 1 (GRIK1) mRNA Homo sepiens hypothetical protein FLJ10300 (FLJ10300), mRNA Top Hit Descriptor Homo sepiens leucine-rich, glioma inactivated 1 (LGI1), mRNA Human fibronectin gene extra type III repeat (EDII), excn x+1 AV645633 GLC Homo septems cDNA dane GLCACE04 3" AV645633 GLC Homo sepiens cDNA clane GLCACE04 3 AV711263 Cu Homo septens aDNA alone CuAADF07 5 Homo sapiens ribosomal protein L5 (RPL5) mRNA Homo sapiens gene for B120, excn 11 M.musculus mRNA for hours gene Single Exon Probes Expressed in Brain EST_HUMAN **EST HUMAN** EST_HUMAN EST HUMAN EST_HUMAN **EST HUMAN** EST_HUMAN EST HUMAN EST HUMAN EST HUMAN **EST HUMAN** HUMAN EST_HUMAN **EST HUMAN EST HUMAN** Database Source 上の光 EST 눋 눋 11420654 NT 눋 4504116 NT 8922337 NT 4506654 NT 4507500 NT 4506786 NT Ż Top Hit Acession 11432087 1.0E-124 AW612106.1 1.0E-124 BE271295.1 1.0E-124 AA630331.1 1.0E-124 AB024069.1 1.0E-124 BF696135.1 1.0E-124 AV711263.1 1.0E-124 BE271285.1 1.0E-124 AW612106.1 1.0E-124 AW985883.1 .0E-124 AV645633.1 1.0E-124 AV645633.1 .0E-124 AF022655.1 1.0E-124 AW503755. Ś 1.0E-124 AI799864.1 AI799864.1 1.0E-124 AF022855. 1.0E-124 AI767133.1 I.0E-124 AI767133,1 1.0E-124 S78684.1 M18178.1 1.0E-124 Y11717.1 1.0E-124 U94778.1 1.0E-124|X13794.1 1.0E-124 1.0E-124 1.0E-124 1.0E-124 1.0E-124 1.0E-124 1.0E-124 (Top) Hit BLASTE 1.0E-124 1.0E-124 Vette 6.94 12.12 2 2 2 3 9 8 \$ \$ 0.92 8 0.62 9. 8.07 8 231 0.52 3.51 9.0 9.0 231 7.57 7.57 1.57 1.61 Expression Signer 28895 29033 29260 29432 30061 32786 34105 33220 ORF SEQ 30647 31293 31514 32787 33982 34908 35223 35309 35310 35342 35343 31823 32895 34007 35630 36905 37265 35224 ÖΝΩ 16230 18023 SEQ ID 16239 16383 16801 17430 17608 18588 19709 19729 21055 22052 16630 18383 19640 19729 20128 21740 18856 27855 22130 22052 ង្គ 22161 22161 23852 23964 <u>0</u> 2000 2422 Ö 3482 3840 3880 899 6216 5586 5797 4696 6339 SEQ ID 3482 4881 8912 8362 8362 8 8 8156 8906 9390 9508 8090 10076 11305 8 47 10804 977

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Single exon Probes expressed in Brain	Top Hit Descriptor	#19e03.x1 NCI_CGAP_Ges4 Homo sapiens cDNA clone IMAGE:2141980 3' similar to TR:031662 031662 YKRS PROTEIN.;	#19e03.x1 NCI_CGAP_Gas4 Homo septens cDNA done IMAGE:2141980 3' similar to TR:031962 031662 YKRS PROTEIN.;	281b04.rl Strategene schizo brain S11 Homo sapiens cDNA clore IMAGE:728719 6 stmilar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT) ;	281b04.rf Strategere achtzo brain S11 Homo agolens CNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL-REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT)	Homo septens mRNA for KIAA1083 protein, partial cds	Homo sepiens calcineurin binding protein 1 (KIAA0330), mRNA	Homo sepiens celcineurin binding protein 1 (KIAA0330), mRNA	hv9ex08x1 NCI_CGAP_Lu24 Hamp septems cDNA done IMAGE:3177886 3' similier to TR:Q25058 Q25058 FIBROPELLIN IA;	hw89e08.xf NCL CGAP_Lu24 Homo septens cDNA clone IMAGE:3177698 3' stmiter to TR:Q25058 Q25058 FIBROPELLIN IA	Homo septens mRNA for KIAA1172 protein, pertial cds	601577081F1 NIH MGC 9 Hamo eaplens aDNA dane IMAGE:3928886 6	HA0086 Human fetal liver cDNA illorary Homo sapiens cDNA	HA0086 Hizmen felai liver cDNA library Homo sapiens cDNA	Homo sapiens ALR-like protein mRNA, pertial cde	2633-07.s1 30eres_pregnent_uterus_Nid-IPU Homo septens cDNA clone IMAGE:486540 3' similar to section (HUMAN):	Homo saplens chromosome 21 segment HS21C010	Homo sepiens KIAA0744 gene product; histone descetylese 7 (KIAA0744); mRNA	Homo sepiens KiAA0022 gene product (KIAA0022), mRNA	Homo sapiens Bruton's tyrosine khase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete ods	Hamo sapians Usurpin-alpha mRNA, complete cds	Homo sepiens Usurpin-alphe mRNA, complete cds	201g09.rt Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA otone IMAGE:429568 5	263307.s1 Soares, pregnent, uterus, NbHPU Homo sapiens cDNA clone IMAGE:496540 3' similar to gb:X65857, ods1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMPOTE (HIMAN).	Homo sepiens Inhibin, alpha (INHA) mRNA	Homo septens trhibth, alpha (INHA) mRNA
gie exon Prop	Top Hit Detabese Source	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	Ę	Z	Ę	EST_HUMAN	EST HIMAN	5	EST HUMAN	Г	EST_HUMAN		EST_HUMAN	Г				Ę	Ę	EST HUMAN	EST HUMAN		
ZIIO	Top Hit Acession No.	1.0E-124 Al446455.1	1.0E-124 AI446455.1	1.0E-124 AA397551.1	AA397551.1	1.9	11417862 NT	11417862 NT	1.0E-125 BE219510.1	10.1	28.4		1.0E-125 AI110656.1	1.0E-125 Ai110666.1	1.0E-125 AF284750.1	3.1	0.2	T062279 NT	7661867 NT	+	1.0E-125 AF015450.1	1.0E-125 AF015450.1		3.1	4504606	4504688 NT
	Most Similar (Top) Hit BLASTE Value	1.0E-124	1.0E-124	1.0E-124	1.0E-124 AA3978	1.0E-124	1.0E-124	1.0E-124	1.0E-125	1.0E-125 BE2185	1.0E-125	1.0E-126	1.0E-125	1.0E-125	1.0E-125	1.0E-125 AA0428	1.0E-125 AL1632	1.0E-125	1.0E-125	1.0E-126 U78027.	1.0E-125	1.0E-125	1.0E-125	1.0E-125 AA0428	1.0E-126	1.0E-126
	Expression Signal	3	8	4.1	4.1	1.61	1.44	1.44	1.74	1.74	5.40	5.47	1.18	1.18	1.56	2.29	1.22	1.78	68.0	10.0	1.59	1.59	1.68	0.99	1.3	13
	ORF SEQ ID NO:	36452	36453	28082	28083	31026	30729	30730	25603	25804		25441	26043	26044		26280	26405	28545	27105	27242	27258	27259	27816	27967	28057	28058
	Exon SEQ ID NO:	23219	23219	13450	13450			25279	12961	12981	13115	12828	13408	13408	13485	13610	13743	13887	15575	14533	14544	14544	15080	15225	15317	15317
	Probe SEQ ID NO:	11452	11462	12029	12029	12454	12706	12708	146	146	311	417	6239	629	711	840	978	1131	1968	1703	1804	1804	2358	2508	2804	2804

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Fig. 2017 Cop. 1850 Expression Cop. 18				_				_		_	_	_	Τ-	_	_	_	_	_	_	Т		Ť	7	1	Ť	Ŧ		П	T	Ť			٦	
Caperage Caperage		Top Hit Descriptor	11 serviews murein heavy bothogotide 1, skoletal muscle, adult (MYH1), mRNA	Harris series rolf A) binding protein II (PABP2) gene, complete ods	DCC ST0186-250200-018-c11 ST0186 Homo saplens cDNA	0.02-870569-020200-075-g09-BT0569-Homo septens cDNA	QV3-8T0569-020200-075-g09 BT0669 Homo saplens cONA	Homo servers CDC-life kinese (CLK) mRNA	H seciens gene for alpha1-antichymotrypsin, expn 3	Homo septens hypothetical protein FLJ20048 (FLJ20048), mRNA	Homo sections hypothetical protein FLJ20048 (FLJ20048), mrthA	Homo eaplens RAN binding protein 2 (RANBP2), mRNA	Homo sepiens glutamate receptor, ionotropic, keinete 1 (GRIK1) mKNA	2072c03.r1 Stratagene penoreee (#837208) Homo sapiens cONA clone IMAGE BEANAN F	m72cc3.r1 Strategene pencrees (#637208) Homo saplens cDNA clone IMAGE: 382m20 3	H septens DNA for liver cytochrome b5 pseudogene	Homo sapiens death receptor 6 (DR6), mRNA	NATROB 11 Sources melanocyte 2NbHM Homo eaplens cDNA clone IMAGE 20/500 5	801577981F1 NIH MGC 9 Homo sepiens cDNA done IMAGE:3928885 5	Sources folds liver spleen 1NFLS Home explents CDNA Gons IMACEL COLD.	266803.71 Source total fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:790444 b sanital to	TR:G1145880 G1146880 TITIN;	Homo saprems marky for nary local property of the control of the c	Home separate in the transport of DNAH9) mRNA, complete cds	Home septents come y dynam heavy chain 9 (DNAH9) mRNA, complete ods	AL 1138463 PLACE I Homo eaplens oDNA clone PLACE1004325 5	W/08/01 x1 Sources NPL T GBC S1 Homo suplens cDNA clone IMAGE: 2350006 3 Smilled to	SWIMPP2_HUMAN Q14108 MAGUK P65 SUBFAMILY MEMBER 21	Hamo septents intrivation Non-1224 protein, pertiel cds	Transpersion in New York (Verlant 2.1)			T	
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Single Exon Probes Expressed in Brain	Top Hit Descriptor	Human macrophage marnose receptor (MRC1) gene, exon 5	602139138F1 NIH MGC 46 Homo septens CDNA clone IMAGF-4208240 51	801149404F1 NIH MGC 19 Homo septems cDNA clone IMAGE:3502129 5	601577981F1 NIH_MGC 9 Hamo suplens cDNA clane IMAGE:3926685 5	Homo sapiens mRNA for casein kinase I epsilon, complete cds	Homo expiens mRNA for casein kinase I epation, complete cos	Homo sapiens mRNA for casein kinase I epsilon, complete cds	Homo saplens mRNA for casein kinase I epsilon, complete cds	Hamo sapiens DNA for emyloid precursor protein, complete cds	Homo saplens DNA for emykold precursor protein, complete cds	Homo sapiens intersectin short isoform (ITSN) mRNA, complete ods	Homo sapiens fost on transformedon LOT1 mRNA, complete ods	Homo sapiens ubiquitin specific protesse 8 (USP8) mRNA	Homo sepiens leukocyte Immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA	Homo sepiens ieukocyte Immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LLRA1), mRNA	Home seniors althoursel participal 28 (DDI 28) mDNIA	Homo saniona milita menulata ode	Hunan mRNA for cytokerufin 18	242802.r1 Sogres total fetus Nb2HF8 9w Home seniens cDNA close IMACE-780008 K	Z42802.11 Sogree, total fetus Nb2HF8 9w Homo sapiens cDNA clone IMAGE:789098 5	au80e08.y1 Schneider felul brein 00004 Homo sepiens cDNA clone IMAGE:2782594 6 similar to TR:015170 015170 TRANSCRIPTION FACTOR S-IRRELATED PROTEIN ;contains element MER22	repeditive element;	notice supports delayed recurrer potassium channel subunit isk mYNA, complete eds	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA	Homo sapiens neuroblescome-emplified protein (LOC51564), mRNA	Homo septens cytochrome P450 retinoid metabolizing protein P450RAI-2 mRNA, complete cds	Homo septens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products	Hama sepiens chramosome 21 segment HS210068	Homo septions Ring1 and YY1 binding protein (RYBP), mRNA
gle Exon Prob	Top Hit Database Source	N	EST HUMAN	Г	Γ	IN	N	Ę		N.										T HUMAN	Г		EST HUMAN							
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	Expression Signal	127	2.36	5.47	7.17	4.63	4.63	4.71	4.71	3.54	3.54	2.03	1.37	1.08	2.44	244	6.02	2.73	3.04	1.1	1.1	2	2 6	72.82	23.74	1,33	3.0	4.35	1.92	138
	ORF SEQ ID NO:	38624	39992		30413	25622	25623	25622	25623	25718	25717	28301	26330	27128	27515	27516	27661	27801	28068	28081	28062	8	20165	20200	78087	2000	22024	220020	1	COMPACT
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om68h08.s1 NCI_CGAP_GC4 Homo saplens cDNA clone IMAGE:1652383 3' similer to gb:X54941 CYCLIN ns04a11.r1 NCI_CGAP_Ew1 Homo saplens cDNA clone IMAGE:1182820 eimilar to TR:0951338 G951338 CHROMOSOME SEGREGATION GENE HOMOLOG CAS.; CAYYA5 Human cardiac muscle expression library Homo sepiens cDNA clone 4151835 elmilar to CMYA5 CAYYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYA5 Homo sapiens gutathlone S-transferace theta 2 (GSTT2) and glutathlone S-transferace theta 1 (GSTT1) Homo sepiens giutathione S-transferese theta 2 (GSTT2) and gluiathione S-transferase theta 1 (GSTT1) insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4]. Novel human mRNA containing Zinc finger C2H2 type domains. insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4] Homo sepiers glutamate receptor, tonotropic, N-methyl D-aspartate 2D (GRIN2D), mRNA Hamo seplens phosphodiestersse 1C, celmodulin-dependent (70kD) (PDE1C), mRNA 601277828F1 NIH_MGC_20 Hamo sepiens cDNA clans IMAGE:3618750 5 601503846F1 NIH_MGC_71 Homo sepiens cDNA clone IMAGE:3905784 5' Homo sepiene putetive ABC transporter (WHITE2), mRNA Homo saplens Zinc finger probeh 76 (expressed in testis) (ZNF76), mRNA 601590469F1 NIH_MGC_9 Hamo sapiens cDNA clane IMAGE:3929057 5 601580488F1 NIH_MGC_9 Hamo sapiens cDNA clane IMAGE:3829057 6 H.sapiens gene for trian-alpha-trypsin inhibitor heavy chain H1, exon 12 7q86b10,x1 NCI_CGAP_Lu24 Homo septens dDNA clone IMAGE: DEPENDENT KINASES REGULATORY SUBUNIT 1 (HUMAN); EST367360 MAGE resequences, MAGC Homo saplens cDNA Top 14 Descriptor Homo saplens prospero-related homedoox 1 (PROX1), mRNA Homo septens mRNA for TRABID protein (TRABID gene) Homo sepiene mRNA for KIAA1459 protein, pertial cds Homo sapiens mRNA for KIAA0454 protein, pertial cds Horno sapiens mRNA for KIAA0454 protein, pertial ods Cardiomyopathy associated gene 5 Cardiomyopathy associated gene 5 ZINC FINGER PROTEIN HZF10 ZINC FINGER PROTEIN HZF10 ZINC FINGER PROTEIN HZF10 Single Exon Probes Expressed in Brain genes, complete cds genes, complete ods EST HUMAN EST_HUMAN SWISSPROT EST_HUMAN EST HUMAN EST HUMAN SWISSPROT SWISSPROT EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN 불용 Database Source 눌 눋 눋 È 눋 Ę 눋 F 눌 눋 ż 11426873 NT 11645923 11425254 Top Hit Acession 1.0E-129 AW 755254.1 1.0E-129 AW756254.1 1.0E-129 AF240786.1 1.0E-129 AF240786.1 1.0E-129 AB040892.1 1.0E-128 AA926959.1 1.0E-128 BE384475.1 1.0E-128 AW955290. 1.0E-128 AB007923.1 1.0E-128 AACC9198.1 BF224345.1 AB007923.1 .0E-128 A.1252050.1 AL096880. 1.0E-128 BE747981.1 BE747081.1 BE614105.1 8377221 014585 1.0E-129 Q14585 5377221 1.0E-129 Q14585 1.0E-128 X69539.1 1,06-120 1.0E-129 1.0E-129 1.0E-129 **621-90.** 1.05-128 1.0E-128 .0E-128 1.00-128 1.0E-128 1.0E-128 1.0E-128 .OE-128 至(金) Aost Simila BLASTE 228 2.28 2,3 <u>1</u>3 5 1.57 79 7 ğ 0.62 सू हु 7.02 0.73 <u>8</u> 3.52 0.67 6.1 0.65 0.65 0.7 2.58 6.9 Expression 28532 28533 29516 28612 27158 27159 28631 28611 25839 26830 31614 35903 36550 36628 39689 32082 32516 31013 33089 33471 36541 34276 20086 3427 ORF SEQ ÖΝΩ 10988 15890 16068 23445 15890 16885 23390 13180 13189 14456 **2 2 8 2 8** 14578 15890 2302 24610 1468 19493 20010 21138 233 19094 18257 20356 18672 SEO D 17351 18672 Š ö 4247 3125 4247 3125 4143 1713 1717 1717 1838 3125 10618 10680 1217 \$ 7692 10037 10608 4616 5888 6831 8448 10761 5458 9889 6324 7327 SEO ID ö

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SP-B48150 B48150 HP-26-HIBERNATION-RELATED PROTEIN - TAMIAS ASIATIOUS-ASIAN yq8c05.r1 Socree fetal fiver spicen 1NFLS Homo septens cDNA clone IMAGE:199112 6' similar to Hamo saplens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA ass21c01.s1 Strategene soluto brain S11 Homo sapiens cDNA done IMAGE:1020288 3 Homo sapiens mRNA for KIAA0634 protein, pertial cds Homo sapiens solute cerrier family 21 (organic enion transporter), member 9 (SLC21A9), mRNA UI-HF-BNO-ety-g-08-0-UI.r1 NIH_MGC_50 Homo septems cDNA done IMAGE:3078731 5 DKFZp762K171_r1 762 (synonym: hmsl2) Homo sepiens cDNA done DKFZp762K171 5 Homo septems retinal dehydrogenses homolog tedform-1 (RDH) mRNA, complete ads 801343016F1 NIH_MGC_53 Hamo septems cDNA clane IMAGE:3685486 67 801343016F1 NIH_MGC_53 Hamo septems cDNA clane IMAGE:3685406 57 Human gene for catalase (EC 1.11.1.8) exon 9 mapping to chromosome 11, band p13 Human T-cell receptor (V alpha 22.1, J alpha RPMI4265-variant, C alpha 1) mRNA Homo sepiens similar to ribosomal protein S26 (H. sepiens) (LOC63694), mRNA ef72f07.r1 Soures_NIHIMPu_S1 Homo septens cDNA clone IMAGE:1047589 \$ Homo sepiens similar to ribosomal protein S26 (H. sepiens) (LOC63684), mRNA 801121995F1 NIH_MGC_20 Homo septens cONA clone IMAGE:3346396 57 901121996F1 NIH_MGC_20 Homo septens cDNA clone IMAGE:3346396 57 Homo sapiens RET finger protein-like 1 antisense transcript, partial e01343016F1 NIH_MGC_S3 Homo sapiens oDNA clone IMAGE:3685496 5 801343016F1 NIH_MGC_83 Home septens cDNA clone MAGE:3685498 5 801449740F1 NIH MGC 05 Homo septens cDNA clone INAGE:3853688 5 601449740F1 NIH MGC 65 Homo sepiens CDNA clane IMAGE:3853688 5 AU143115 Y79AA1 Homo sepiens CONA clone Y79AA1001410 6 AU143115 Y79AA1 Homo sepiens CDNA clone Y79AA1001410 S CM4-CN0045-180200-511-f02 CN0045 Homo sepiens oDNA RC0-CT0318-201196-031-411 CT0318 Homo sepiens oDNA RC0-CT0318-201196-031-411 CT0318 Homo sepiens oDNA Top Hit Descriptor Homo seplens mRNA for KIAA1414 protein, partiel ods Homo seplens hypothetical protein (HSPC242), mRNA Homo sapiens WSCR4 gene, exons 3 and 4 Homo sepiens WSCR4 gene, excus 3 and 4 Homo sapiens KVLQT1 gene Homo sapiens KVLQT1 gene Single Exon Probes Expressed in Brain EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST_HUMAN EST_HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST HUMAN EST_HUMAN EST HUMAN HOMAN EST_HUMAN Top IIIt Detaberse Source 눋 눋 ż <u> ፰</u> Ę 7705530 11437282 11420850 11437282 11420850 Top Hit Acession 1.0E-130 AW363299.1 1.0E-130 AW 603580.1 1.0E-130 AW363299.1 1.0E-130 AW843993.1 .0E-130 BE564219.1 1.0E-130|BE564219.1 1.0E-130 BE584219.1 1.0E-130 AF240698.1 1.0E-130 BE564219.1 1.0E-129 AA682200.1 1.0E-129 AU143115.1 BE275192.1 DE-130 AJ010230.1 1.0E-129 AU143115.1 1.0E-130 BE275192.1 1.0E-129 AL120739.1 1.0E-130 AB037835.1 AA625526.1 1.0E-128 AF041058.1 1.0E-129 AF041056.1 1.0E-130|M97710.1 .0E-129 AB014534.1 BE869993.1 BE869893.1 1.0E-129 AJ006345.1 .0E-130 X04092.1 AJ006345.1 1.0E-129 H83155.1 £ 1.0E-129/ 1.0E-130 1.0E-129 S-18 1.0E-130 1.0E-129 1.0E-129 1.0E-129 1.0E-129 100-128 82-138 Most Similar H (doL) BLASTE Value 1.07 5.36 0.0 11.38 11.38 3.08 7 80. 5.36 <u>8</u> 5.37 2.66 5 249 3.94 1.38 4 15 0.97 6.57 3.93 0.57 0.56 0.97 0.58 Expression Signe 28305 29428 29869 30372 28290 28968 2820 30371 28584 27098 28291 25538 37137 37538 35835 36396 37637 33192 35836 32844 33191 32500 32776 ORF SEQ ÖNQ 16320 15648 15648 16798 15648 17757 16648 13902 14712 24001 24842 12901 <u>+</u> 15478 19770 24213 24213 23169 14407 19719 20105 8 20911 18781 19477 19477 19779 282 SEO ID <u>0</u> 5038 5038 3585 3750 3015 450± 3750 2773 12104 12483 1147 1661 1976 2881 <u>1</u> 11615 11615 11186 11269 7428 6266 9070 10523 6816 6816 7090 9000 7027 © S S S S S ÿ

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Probe SEO ID NO:		0629	8723	6723	6736	,	100	8778 8778	9114	8833	10463	10463	11242	11242	11703	47750	2017	4					18	8	28	33	38	8	18	188	8	88	29

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Chighe Later Tables Capressed in Digiri	Top Hit Descriptor		cr48e07.x1 Jis bone marrow stroma Homo saciens cDNA clone HBMSC cr48e07.31	G48e07.xt Jia bone marrow stroma Homo saciens cDNA clone HBMSC G48e07.3	Human von Willebrand factor pseudogene corresponding to exone 23 finauch 34	Human von Willebrand factor pseudogene corresponding to exons 23 finauch 34	Homo saplens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA	Homo supiers protein tyrosine phosphalasa, non-receptor type substrate 1 (PTPNS1) mRNA	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA	Hamo sepiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA	Homo septens amforide binding protein 1 (amine coddase (copper-containing)) (ABP1), nuclear gene encoding mitochondrial protein, mRNA	Homo sapiens heterogeneous nuclear ribonucleanotein A1 (HNRPA1) mRNA	Homo sacient beta (ACTB) mRNA	Human polyhomeotic 1 homolog (HPH1) mRNA, partial ods	HA1347 Human fetal liver cDNA library Home saciens cDNA	Homo sepiens mRNA for KIAA1363 protein, pertial cds	H. sepiens nact gene (exan 2)	1838b05.x1 NCI_CGAP_UM Homo septens cDNA clone IMAGE:2230833 3' similar to TR:099551 Q99551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR.;	1838b05.x1 NCI_CGAP_UM Homo espiens cDNA done IMAGE:2230833.3' similar to TR:Q99551 Q89551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECLESSOR	yothoe.rt Scares melanocyte 2NbHM Homo sepiens cDNA clone IMAGE:270017.5	yyO1h09_r1 Sogres melanocyte 2NbHM Homo septems cDNA clone IMAGE:270017 5	Homo expiens polymenses (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA	Homo sepiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA	ye83g04.r2 Strategene fetal spleen (#637205) Homo explens cDNA clone IMAGE:68310 5:	ye83g04.12 Stratagene fetal spleen (#637205) Homo sepiene cDNA clone INAGE:68310 5			Homo sepiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA	Homo sepiens serine paintitor transferages, subunit II gene, complete cds: and unknown genes			3E:345201 5' similar to	
01 1 1000 016	Top Hit Database Source		EST HUMAN	EST HUMAN	LZ.	LN LN	Ę	Ę	¥	LN	Ł	F	¥	Į,	EST HUMAN	LN.	LN	EST_HUMAN	EST HUMAN	EST_HUMAN	EST_HUMAN	7	4	EST_HUMAN	EST HUMAN	41	EST_HUMAN	5	Į,	EST HUMAN	EST_HUMAN	EST_HUMAN	
1	Top Hit Acession No.		AW069534.1	0.0E+00 AW069534.1			4758977 NT	4758977 NT	4758977 NT	4758977 NT	4601860 NT	450444 NT	5016088 NT	_	0.0E+00 AI114743.1	0.0E+00 AB037784.1	-	1.1	1.1		_	4505938 NT	4505938 NT	1	1	144	0.0E+00 BF036881.1	1	0.0E+00 AF111168.2		3.1	1	
	Most Stmiler (Top) Hit BLAST E	Væue	0.0E+00 AW069	0.0E+00	0.0E+00	0.0E+00 M60676.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 U89277.	0.0E+00	0.0E+00	0.0E+00 X91213.	0.0E+00 AI62370	0.0E+00 AI62370	0.0E+00 N30040.	0.0E+00 N36040.	0.0E+00	0.0E+00	0.0E+00 T56945.	0.0E+00 T58045.	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 BE29597	0.0E+00 BE29597	0.0E+00 W73973.	
	Expression Signal		12.55	12.55	1.5	0.91	10.36	10.36	10.18	10.18	0.78	15.25	17.68	23.28	3.51	1.72	1.33	0.89	1.47	1.48	1.48	4.38	4.38	1.29	1.29	8.88	2.1	25.83	+	1.15	0.88	5.4	
	ORF SEQ ID NO:			25520	25524					25537	25544			25556	25562	25563	25566	25572	25572	25573	26574	26586	25587	25593	25604		25609		25612	25613	25613	25614	
	Econ SEQ ID NO:		12888	12888	12801		- 1	1	12900	12800	12906	12907	12916	12919	12925	12926	12928	12935	12936	15513	15513	12843	12943	12850	12060	12864	12968	12070	12973	12975	12075	12976	
ſ	Probe SEQ ID NO:		20	59	63	85	2	23	76	2	80	81	06	88	88	100	105	113	114	115	115	28	8	<u>8</u>	38	<u>\$</u>	ا	155	28	18	- <u>1</u>	162	

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	QV3-HT0457-140200-088-d04 HT0457 Homo seniene cDNA	QV3-HT0457-140200-088-d04 HT0457 Horro seniens cDNA	Horno sapiens zinc fincer profein mRNA, complete cris	Homo sablens chromosome 21 segment HS210002	Homo septens chromosome 21 segment HS21C002	bb24e12.y1 NIH_MGC_14 Homo saplens cDNA clone IMAGE:2963854 5' strutter to WP:Y57A10A.Z GE22831:	bb24612.y1 NIH_MGC_14 Hamo sapiens cONA clone IMAGE:2963854 5' similar to WP:Y57A10A.Z CE22631;	Homo sapiens mRNA for KIAA0784 protein, pertiel ods	Homo septens mRNA for KIAA0784 protein, pertial ods	Human gamma-cytoplasmic actin (ACTGPS) pseudopene	Homo saplens CTCL tumor enfoen se14-3 mRNA, complete ods	Homo seplens CTCL tumor antigen se14-3 mRNA, complete ods	Homo seplens chromosome X MSL3-2 protein mRNA complete cris	Homo saplens chromosome X MSI 3-2 protein mRNA complete ode	tq04f08.xf NCI_CGAP_Ut3 Homo saplens cDNA done IMAGE:2207847 3' similar to gb:J03191 PROFILIN I (HUMAN);	tqQ4f08.x1 NCI_CGAP_Ut3 Homo septens cDNA clone IMAGE:2207847 3' similar to gb:J03191 PROFILIN I (HUMAN):	Homo septions DNA mismatch renair protein (AB H3) name complete puts	Homo septems abosomal protein 131 (RPI 31) mRNA	Homo sepiens TADA1 protein mRNA, complete cds	Homo septens mRNA for KIAA0721 protein, pertile cds	Homo sepiens mRNA for KIAA0721 protein, pertial cds	Mus musculus teetis-epecific protein, Y-encoded-like (Tsovi), mRNA			М			or (long form)		Homo septems T-cell tymphoma investon and metastasis 1 (TIAM1) mRNA
gie Exon Pro	Top Hit Detabese Source	EST HUMAN	EST HUMAN		뒫	K	EST HUMAN	EST HUMAN	NT	F	N	TN	Ę	IN	Z,	EST_HUMAN	EST HUMAN	L	Į	Ę	Ę	Į.	F	N	N.	Þ	Z.	Z	Z.	TN	누
OKI.	Top Hit Acession No.	0.0E+00 BE1628321	0.0E+00 BE1628321	0.0E+00 AF244088.1	0.0E+00 AL163202.2	0.0E+00 AL163202.2	0.0E+00 BE018970.1	0.0E+00 BE018970.1		0.0E+00 AB018327.1		0.0E+00 AF273045.1		0.0E+00 AF167174.1	0.0E+00 AF187174.1		0.0E+00 A[587308.1		9632	0.0E+00 AF132000.1	0.0E+00 AB018264.1	0.0E+00 AB018284.1	0878444 NT		0.0E+00 AB018301.1	5453805 NT	0.0E+00 AL163201.2	0.0E+00 AF231919.1		0.0E+00 AF231919.1	4507500 NT
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 D50859.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00/	0.0E+00	0.0E+00/	0.0E+00/	0.0E+00	0.0E+00/	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 X89772.1	0.0E+00	0.0E+00
	Expression Signal	0.81	0.81	1.42	29.73	29.73	5.95	5.85	3.05	3.05	77.79	3.74	3.74	4.81	4.81	9.26	976	3.08	23.37	4.72	9.19	8.34	3.5	1.23	1.23	3.97	6.94	3.85	1.71	9.14	1.68
	ORF SEQ ID NO:	25615	25616	25617	25620	25621	25627	25628	25631	25632	25843	25848	25849	25051	25852	25658	25659	25661			25664	25864	25865	25678	25879	26882		25688	25891	1	25710
	Exan SEQ ID NO:	12977	12821	12978	12981	12981	12988	12988	12903	12993	13002	13007	13007	13009	13009	15537	15537	13019	13021	13022	13026	13026	13027	13041	13041	13042	1304	13049	13051	13059	13071
	Probe SEQ ID NO:	163	183	184	167	167	178	176	181	181	189	Ţ	호	198	18	202	ä	202	209	210	77	215	218	ន្ត	8	ឆ	ន	2 8 0	242	S S	28

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	Homo saplens T-cell hymphoma invasion and metastasis 1 (TIAM1) mRNA	Homo septens hypothetical protein (LOC51250), mRNA	Homo sapiens DCRR1 mRNA, partial ods	Homo saptens DCRR1 mRNA, pertial cds	Homo saplens DCRR1 mRNA, pertial cds	IL2-CT0031-181199-020-B03 CT0031 Homo septiens cDNA	Homo saplens potassium inwardly-redifying channel, subfamily J, member 15 (KCNJ15) mRNA	Homo sapiens potassium inwardly-rectifying channel, subfamily J. member 15 (KCNU15) mRNA	Homo saplens mRNA for KIAA1019 protein, partial cds	Hamo sepiens mRNA for KIAA1019 protein, partial cds	Homo septens ribosomal protein S5 (RPS5) mRNA	ZY18008.r1 Somme NINHMPu, S1 Hamo emplens cDNA clare IMAGE:763994 5	Homo septens SON DNA binding profes (SON) mRNA	Hamo seplens SON DNA binding protein (SON) mRNA	Homo saciens intersectin short sociam (TSN) mRNA, complete ods	Homo explens hormonally upregulated neu tumor-associated kinase (HUNK) mRNA	Homo sepiens homonally upregulated neu fumor-essociated kinase (HUNK), mRNA	ndog); translocated to, 4	-box binding protein 1 (XBP1) mRNA	Human zinc finger protein zfp31 (zf31) mRNA, perfial cds	Homo sepiens chromosome 21 unknown mRNA	Homo sepiens chromosome 21 unknown mRNA	Homo septiens chromosome 21 unknown mRNA	Homo septens T-cell lymphome investon and metastasis 1 (TIAM1) mRNA	Homo septems GA-binding protein transcription factor, either subunit (60kD) (GABPA), mRNA	Human mRNA for KIAA0184 gene, partial cds		HRNA			one IMAGE:2018457 3' strutter to gb:X54199	RC2-CT0320-300100-016-e09 CT0320 Homo sembles chivia	Union allegations and the second
Je Exon Prof	Top Hit Detabase Source	N.	NT.	NT	TN	IN	EST_HUMAN	Ę	Ę	N	Į.	Ę	EST HUMAN	 	7	Ę	17	F	Ė	5	LN LN	TN	NT	LN LN	5	Ę	ĮŅ	닏		EST_HUMAN	Г	EST HUMAN	Т	1
Sing	Top Hit Acession No.	4507500 NT	TV08028 NT	_			83.1	4557029 NT	4557029 NT	21	(B028942.1	4506728 NT	2.1	4507152	4507152	F114488.1 NT	7857213 NT	7857213 NT	5174574 NT	4827057 NT		0.0E+00 AF231919.1	1.6	2.1	4507500 NT	4503854 NT			1507500	3.1	1.1]
	Most Similer (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00 D83327	0.0E+00 D83327.	0.0E+00 D83327.1	0.0E+00 AW8452	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AB02894	0.0E+00	0.0E+00 AA48000	0.0E+00	0.0E+00	0.0E+00 AF11448	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 U71600.1	0.0E+00	0.0E+00[AF23191	0.0E+00 AF231918	0.0E+00	0.0E+00	0.0E+00 D80006.1	0.0E+00 D80006.1	0.0E+00	0.0E+00 AU13496	0.0E+00 AB028042.1	0.0E+00 Al363014.1	0.0E+00 A	
	Expression Signal	1.68	3.07	1.19	3.28	3.28	0.78	6.65	6.65	4.97	4.63	4.23	3.76	18.93	16.53	2.33	4.97	6.23	2.66	1.71	1.45	2.42	2.42	3.84	2.33	0.94	4.1	1.9	1.89	1.07	8.31	1.54	1.83	
į	ORF SEQ ID NO:	25711			25726	25727		25734	25735		25745		-	25746	25746	25750	25759	25759	25771	25775		25784	25785	25786	25788	25782	25793	25783	25795	25806	25840	25850	25813	
	Exan SEQ ID NO:	13071	13073	13083	13084	13084	13085	13083	13093	13103	13104	15540	13105	13106	13106	13110	13122	13122	13136	13139	13142	13146	13146	15541	13148	13151	13152	13152	13154	13163	13203	13204	13170	
	Probe SEQ ID NO:	283	285	278	717	1112	278	282	287	282	887	882	300	301	302	306	319	320	335	338	341	346	88	347	8	327	333	354	388	367	378	379	383	

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ORF SEQ Expression (Top) Hit Top Hit Acession Database ID No: Signal Value	25816 1 58 0.0E+00 4503680 NT	1 4503680 NT	TN 088604 4503680 NT	25818 2.44 0.05.00 4503690 NT	26819 1.1/ 0.0E-100 4503680 NT	25820 1.39 0.0E-100 A502090 NT	25821 1.39 0.0E-100 4503680 NT	25822 2.11 U.S. V. V. V. V. V. V. V. V. V. V. V. V. V.	25823 0.84 0.02400 NT	25824 1.35 0.0E-00/10/10/10/10/10/10/10/10/10/10/10/10/1	25825 1.35 U.U.T. 100 A 101 U.U.	25824 1.07 0.0E+00/X/46/0.1	25825 1.07 0.0E+00 X748/0.1	28.13 0.0E+00 4508808IN	25435 1.5 0.0E+00 R17795.1 ESI_HUMAN	TN 4503014	25851 1.31 0.00.000 4506728 NT	TM + 0208000 A 20.20	25852 3.85 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0	25853 5.40 0.0E-700 4507452 NT	25854 3.40 U.UE-TOO A 5202407 4 NT	25855 4.02 U.UETUU A 193001.1	25865 1.99 0.0E+00 E-00 E-00 E-00 E-00 E-00 E-00 E-00	NAME TO THE PROPERTY OF THE PAR	0.0E+00 BE204447.3	3.15 0.0E+00 4504532 NI	3.15 0.0E+00 4504532 NT	1.23 0.0E+00 465/88/ NI	25889 1.23 0.0E+00 405/88/INI	25895 2.84 0.0E+00 AL163246.2 N	25896 9.28 0.0E+00 AL 163246.2 N	25897 9.28 0.0E+00/AL163246.2 NI	2590Z 3.46 0.0E+00 AB033035.1 N1	25904 1.97 0.0E+00 AU132898.1 ESI HUMAN	25910 2.68 0.0E+00 BE385144.1 EST FLUMAN
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SEQ ID	26.73	7/10	13175	33/33	13174	13175	13175	13178	13171	13178	13178	13178	13178	13182	12822		3205	1328	13207	13208	13208	13209				L.	<u></u>	<u> </u>	L	乚	Ļ	L	L	1 _	1_
Probe SEQ IO NO:		8	387	387	88	88	380	8	391	392	392	303	383	397	157		4	420	421	422	422	423	433	438	430	455	455	194	<u>\$</u>	471	472	472	<u></u>	\$	194

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	Top Hit Descriptor	PMO-DT0065-130400-002-c06 DT0065 Homo sepiens cDNA	Novel human gene mapping to chomosome 1	Homo sepiens PC326 protein (PC326), mRNA	11.2 FT0159-070800-120-F07 FT0159 Homo espiens cDNA	Homo eaplens chromosome 21 segment HS21C010	CV2-RTDR95-16040-142-H05 BT0635 Homo septens cDNA	CAST TARBEET NIN MIC ES Homo applients CDNA clone IMAGE:3896986 5	Down seniors mRNA for KIAA1476 protein, partial cds	Homo septems transcription elementary factor B (Sitt), polypeptide 1-like (TOEB1L) mRNA	TILLIN September and Confeder Incident problem (G Drobein), slipha 11 (Gq class) (GNA11) mRNA	Hamp Septients guerante investigation and a septient (Graphin, alpha 11 (Grades) (GNA11) mRNA	HOTO EXPRESS GLARITICS INCREASES IN THE STATE OF THE STAT	Horizo supperios aminim (LOCOTATA), minima de la company d	Hamo separate at mini (LOCOTTIO), minimal controlles a protein gene (EDA), exch 2 and flanking repeat	Horizo Sapisa is Availised as sections are sections and sections and sections are sections and sections are sections as sections are sections are sections as sections are sections as sections are sections as sections are sections as sections are sections as sections are sections as sections are sections are sections as sections are sections as sections are sections as sections are sections as sections are sections as sections are sections as sections are sections as sections are sections are sections as sections are sections are sections as sections are sections as sections are sections as sections are sections as sections are sections are sections as sections are sections as sections are sections are sections as sections are sections as sections are sections as sections are sections are sections are sections are sections are sections are sections are sections are sections are sectio	[ULH BIT ech 1-04-0-Ut at NCI_CGAP_Sub3 Homo saplens cDNA clone IMAGE 27 1350 I 3	Homo sepiens RGH1 dans, retrovins-like element	11	encoding mitochondria protein. MRNA	Human apolipopromin Art (Apolity) gene, over 1	8018ZZZZ/TI NIT MCC. CITATIO CHICAGO (FI 120701) TIRNA	HOTO SEPONDE INCOME TO THE POST OF THE POS	From Sapients hypothetical protection of the Carlot of the	Home explains exerging the properties of the finder protein mRNA, perties of the	From September 1 and Olf-Información zinc finger protein mRNA, partial cds	Home equies NOT1 moves (NOD1) gene exces 1, 2, and 3	Indian explain (CO) provide (CO) provide (CO) mRNA	Tromb separate for density throughout the property of LRP2), mRNA	Lower services for density thousands in religion protein 2 (LRP2), mRNA	Home seniors for density incorposity related protein 2 (LRP2), mRNA	Home services low density licondein-related protein 2 (LRP2), mRNA	HANGOT of Source beds NHT Homo septens obnA clone IMAGE:728732 5	Homo serviers RGH2 cene, retrovirus-like element	
e Exon Pio	Top Hit Deterbase Source	EST HUMAN	5	: 5	EST HIMAN	101	7 1.0 MANA	ESI HOMAN	EST HUMAN	Z	Z	Ę	¥	LN	5	5	POT ULIMAN	Land I Co	Z	F	¥	EST HOMAN	LZ.	LN	Z	E.	Į.	Z	z!	Į.	Z.	Z	A LOL	TOWAR TOWAR	Z
	Top Hit Acession No.	0 0F+00 AW838825.1	l	92396	0.000000	T	,		-	-	1N 0505009	4504036 NT	4504036 NT	8923831 NT	8923831 NT	O DELON AFORSES 1	7,70507.4	0.0E+00 AW136324.1	J10083.1	5174742 NT	JO4088.1	3F104898.1	8923631 NT	8923631 NT	4501854 NT	AF221712.1	AF221712.1		9806918 NT	6806918 N	0800818 N			AA399486.1	D11078.1
	Most Similar (Top) Hit T BLAST E Value	0 0F+00 A	0 0F±00 AI 447233		0.00	0.05+00	0.05+00	0.0E+00 BE0815Z	0.0E+00 B	0.0E+00 AB040908	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	7007300	0.01	0.0E+00.0	0.0E+00 D10083.1	0.0E+00	0.0E+00 JO4086.1	0.0E+00 BF10489	0.0E+00	0.0E+00	0.0E+00			0.0E+00 AF14977	. 0.0E+00	0.0E+00	0.0E+00	- [1	1	0.0E+00 D1107B
	Expression Signal	1	1	3 6	171	0.77	5.37	1.20	1.14	1.88	27.08	4.33	4.33	76.0	76.0		20.0	1.80	8	2.63	7	1.83	96.0	96.0	0.78	1.15	1.15	3.18	1.2	3,83			0.02		10.1
	ORF SEQ ID NO:	25044	11833	25913	25674			25628	25934		25944	L.	L					25958		25982		25008				26008	20000			28022		26024	28025		3 28038
	Exan SEQ ID NO:		3	. 1		_1	13200	15544	13302	13308	13311	L	1	L	L	<u>L</u>		13326	13336		1_	<u>l</u>	L	1_	1	4_	1	L		13391	13391	13392	13392	13399	4 13403
	Probe SEQ ID NO:	١	784	\$	1 05	400	909	513	518	624	527	528	623	530	530		535	543	553	j.	585	288	Ş	8 8	98	8	8	8	612	613	613	4	410	620	624

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	zh61b04.r1 Soares fetal liver spicen 1NFLS. S1 Homo sepiens cDNA clone IMAGE:41567 5' similer to gb:A21187 ALPHA-2-WACROGLOBULIN PRECURSOR (HUMAN).	zh51b04.r1 Soares_fetal Iliver_spieen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:415567 5' similar to ab-A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN).	Homo sapiens novel SH2-containing protein 3 (NSP3) mRNA	Homo sapiens glutamete receptor, lonotropic, N-methyl D-espertate 2B (GRIN2B) mRNA	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA	Human neutral amino acid transporter (ASCT1) gene, excn 8	Homo sapiens sodium/calcium exchanger ladform NaCs3 (NCX1) mRNA, complete cds	Homo espiens sodiumicaldum exchanger ladform NaCa3 (NCX1) mRNA, complete cds	Homo sapiens protein kinase, X-finked (PRKX) mRNA	Homo sapiens protein kinese, X-linked (PRKX) mRNA	Human endogenous retrovirus pHE 1 (ERV9)	Homo sapiens high-mobility group (nonhistone chromosomal) protein 1 (HMG1) mRNA	Homo sapiens mRNA for KIAA1089 protein, pertial cds	Homo sapiens similar to rat integral membrane giyooprotein POM121 (POM121L1), mRNA	np49d01.s1 NCI_CGAP_Br1.1 Homo sepiers cDNA done IMAGE:1129633 3' similar to gb:X57352 INTERFERON-INDUCIBLE PROTEIN 1-8U (HUMAN):	Human von Willebrand factor gene, exons 23 through 34	Human von Willebrand factor gene, exons 23 through 34	Homo saplens TNF receptor-essociated factor 1 (TRAF1) mRNA	Homo septens ALR-like protein mRNA, pertial cds	Homo sepiens ALR-like protein mRNA, partial cds	Homo seplens hypothetical protein FLJ21634 (FLJ21634), mRNA	TCAAP1D0779 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo	sepiens cDNA clone TCAAP0779	Homo sepiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds	Homo septens MHC class I entigen (HLA-G) mRNA, HLA-G1 allele, complete cds	Homo saptens chloride charnel CLC4 (CIC4) mRNA, complete ods	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9	Homo eaplens zinc finger protein 212 (ZNF212), mRNA	Homo sapiens mRNA for repressor protein, pertial cds	801445647F1 NIH_MGC_65 Homo sepiens CDNA clone IMAGE:3849803 5'
gie Exon Pro	Top Hit Defabase Source	EST_HUMAN	EST HUMAN	LN	IN	N.	N L	N.	LN	NT	Į.	Į.	Z	NT	L	EST HUMAN	N.	N	LN.	¥	TN	NT		EST HUMAN		IN	N-	NT				EST_HUMAN
OF I	Top Hit Acession Na	W78811.1	W78811.1		TN 6008008	5031624 NT	0.0E+00 U05235.1	0.0E+00 AF108389.1	0.0E+00 AF108389.1	4828947 NT	4826947 NT	X57147.1	4504424 NT	0.0E+00 AB029012.1	7657468 NT	0.0E+00 AA614537.1			5032192 NT	50.1	50.1	11545800 NT			30.2	20.2	92.1	1	1	912749		0.0E+00 BE860735.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00 W7881	0.0E+00 W7881	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00.0	0.0E+00	0.0E+00	0.0E+00	0.0E+00 M60675.1	0.0E+00	0.0E+00 AF2847	0.0E+00 AF2647	0.0E+00		0.0E+00	0.0E+00/	0.0E+00 AF2269	0.0E+00 AF1704	0.0E+00 J03764.	0.0E+00 J03784.	0.0E+00	0.0E+00 D306121	0.0E+00[E
	Expression Signal	0.76	0.76	4.89	2.88	1.17	2.53	1.07	1.07	4.98	4.98	1.15	10.4	4.49	2.43	9.24	4.34	4.34	1.71	4.95	4.95	12.29		2.12	1.07	1.07	2.41	1.07	1.07	1.38	1.86	3.01
	ORF SEQ ID NO:	28041	28042			i				26070	12002		20084	26088	28101	20115	26119	26120	20129	26135	26136	26139		28146	20170	28171	20172	20175	26176	26177	87.78 57.78	848
	Eeen SEQ ID NO:	13407	13407	13410	13417	13419	13422	13426	13428	13431	13431	16547	13443	13448	13456	13468	13471	13471	13481	13486	13486	13488		3463	13512	13512	13513	13516	13516	13519	13361	13521
	Probe SEQ ID NO:	628	829	631	638	640	643	647	647	83	653	820	687	672	681	983	969	989	ğ	712	712	714	- (18	900	8	6	₹ \$	743	248	748	740

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Table 4
Single Exon Probes Expressed in Brain

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	Uners and	Truit expens diranosame 21 segment HS21C003	CVV-510/WS-28040C-211-g11 BT0703 Homo septens cDNA	Live of the control o	Inditio septens dirempedine 21 segment HS21C003	Homo sepiens isminin receptor 1 (67kD, ribosomel protein SA) (LAMR1), mRNA	Home septents terminal receptor 1 (67/D), ribosomet protein SA) (LAMR1), mRNA	Home septents appears and only motry per precursor, mRNA, pertial cds	Hono equiens National (PM) gene, excess 1-4, complete cds	Homo earlies of cardiac alphaenthyceth negwy onen gene	Homo septems mRNA for KIAAndox meters and a september september and a september and a september and a september and a september and a september and a september and a september and a september a september and a september a	Homo seniens mena for Kila Andro a matein	Human nee inchitator mittar at 1	Se Not of the second se	Higher tee higher work of	London and the control of the contro	Homo entires discontinue of monographic according to the method	DEGRAMS AT NOT COME CONTROL MECTOR (TEFT) MICHA	COSCIONAL INC., CONT., GOA HOMO BESIGNS CLINA CIONE IMAGE: 1613404.3	descende in NC_CCAP_GCS Hamo septens a DNA clane IMAGE:1613404 3'	Homo sapiens KIAA0929 protein Mas2 interacting nuclear tenset (MINT) homolog (KIAA0020)	Homo septens mRNA for PSP24, complete cds	PM2-GN0014-060900-001-102 GN0014 Homo saplens cDNA	PM2-GN0014-050800-001-f02 GN0014 Homo sepiens cDNA	PMZ-GN0014-060900-001-f02 GN0014 Homo saplens cDNA	Homo sapiens partial ofgrigene, excus 2 and 3	Homo septens partial o-for gene, excus 2 and 3	House septens chromodomen protein, Y chromoeome-like (CDYL) mRNA	Trained Determined I UB4q) gene, complete ods	Human bake to the United States and the Complete Cds	Homo earliers 2073 4 miles 11 100 miles of 11 100 miles and 11 100 miles a	Homo services 8/22 1 region and 1 ff 20 (CBFA211) gene, partial cds	Homo sapiens 14d32 Jagded2 gene, complete cds and unique services
gle Exon Pro	Top Hit Database Source	Ę	TOT LEBESSE	EST HIMAN	TOWNER TOWNER				5	LN LN	Ę	F.	۲	Į					H IMAN	Т	NUMBER			HOMAN	7	HOMAN								
Sin	Top Hit Acession No.	203.2	700	2021	283	AKA AOKO	AKOAOSE NT	0.0E+00 AF089747 4			T	Ī	_				507430	4507430 NT				2,588	8.1		T	Ę,		4757000 NT			_	T	198490.1	П
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	Expression Signal	16.0	2.67	257	6.48	4.80	8.49	121	1.78	1.05	1.05	2.98	2.98	1.19	9.05	6.0	2.18	2.18	3.38	3.38		2 5	3.18		7	8	2	203	1.86	50.5	26.17	5.52	8.64	1.17
	ORF SEQ ID NO:	26311	26316	26317	26326			26332	26333	26338	26337	26356	26357	26362	26363	28364	26365	26366	26373	26374	1 82	20205	20000	26302	28393	26394	28395	28402	28410	28411	26411			26416
	SEQ ID NO:	13640	13847	13647	13657	13666	13666	13668	13669	13672	13672	13683	3863	388	388	13780	13701	13701	15558	15568	42700	43740	13727	13727	13727	13728	13728	13737	13748	13749	13749	13752	13752	13755
	Probe SEQ ID NO:	871	878	878	888	888	006	901	902	902	g	8	8	8	832	88	8	88	8	22	ş	8	8	88	296	288	1		984	985	_	\bot	_	8

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Top Hit Descriptor	Homo sepiers 14432 Jegged2 gene, complete cds, and unknown gene	Homo sapiers 14q32 Jagged2 gene, complete cos; and unknown gare	Homo septems 14q32 Jaggad2 gane, complete cds; and unknown gane	Homo sepiens DKFZP686N0122 protein (DKFZP586M0122), mHNA	Hamo saplens inner membrane protein, mitochandria (mitofilm) (IMM I), michano an almilar to	assesso? at Stratagene fetal retina 637202 Homo sapiens cDNA clone IMACC. 050220 5 on the	SW:PRSB_HUMAN P47210 26S PROTEASE REGULATORY SUBONIT 6.1.	Solution and Provide BLASTX or p) Solution and Provide BLASTX or p)	Calgment for and Pro with BLASTx or p) (calgment Ser and Pro with BLASTx or p)	Homo septerts have shock 70kD protein 98 (mortalin-2) (HSPA98) mRNA	Homo serviers cacherin 6, K-cacherin (fetal kidney) (CDH6) mRNA	Homo excherin 6, K-cacherin (fetal kidney) (CDH6) mRNA	Homo seciens hypothetical protein FLJ20695 (FLJ20695), mRNA	Homo saplens hypothetical protein FLJ20695 (FLJ20695), mRNA	Home sapiens mRNA for eights tubulin 8 (TUBA8 gene)	Hame seplens hypothetical protein FLJ20080 (FLJ20080), mRNA	Hamo sepiens elloylation repeir, alids hamolog (ABH), mRNA	Homo sepiens Death essocieted protein 3 (DAP3) mitthe	MR0-BN0115-200300-003-h08 BN0115 Homo sapters CUNA	Homo sapiens potaseium chennel, subrientily N. maniba a (NONK9) mRNA	Homo sapiens potassium channel, subjectify N. maniber a (Noving), III.	Homo saplens protein titnase, X-anica (Fritxy) misson	Homo septens protein kinase, X-linked (PRKX) missis	Homo septens ribosome protein S27a (RFS27A) michal	Homo seplens hypothetical protein FLuzusus (FLuzusus), nii sen	Home sepiens DNA for Human P2XM, complete cds	Homo sapiens DNA for Human P2XM, complete cds	Home septens similar to ret integral membrane phooprotein POM121 (POM121-1), Illican	Homo seplents exhilar to rat integral membrane glycoprotein POMIZI (POMIZILI), many	Homo septens Npw38-binding protein Npw8P (LOCS1728), mrdva	H. saplens ART4 gene	
Top Hit Detabase Source	5	1		_	_		EST HUMAN	EST_HUMAN	EST HUMAN	Ę		Z	Ž		1	N L	12	2	EST HUMAN	Ч.	Z	Į.	Ż	LZ.	Ę	Ιź	Ę	NI CON	NT.	FOO NT	12	Ē
Top Hit Acession				1111/03	TN 111000	1411shac				8922933 NT	4758569 NT	4820872 NI	4826672	8923624 NT	+70C7R0	0.0E+00 AJ245922.1 INI	1N /802308/	77E0447 NT	0.0E+00	7706134 NT	TN8134 NT	TACACAL	TN 749964	4506712	TNINGCACOO	A DONONEO 4	0.0E+00 AD002008.1	0.0E+00 AB00Z039.1	TN 8917397	3	7.70	XOSES, TO
\$ + 10	Value	0.0E+00 AF111170.3	0.0E+00/AF111/0.3	0.0E+00 AF111170.3	0.0E+00	0.0E+00	0.0E+00 AA458690.1	0.0E+00 N43182.1	0.0E+00 N43182.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.00	0.0E+00.	0.0E+00	0.0E-400	0.05-400	0.00	1		20100	0.00	1		1					
Expression Signal		1.83	23	3.76	3.06	2.5	1.43	1,9	6	3.55	240	1.89	1.89	3.63	3.63	119.02	1.10	3.52	2.3								7					1
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	z Z	ğ	885	8	88	1005	Ž	4007		200	35.5	\$25	105	1047	45	1048	2050 050	1052	1060	1074	1097	1097	1110	1110	1111	1113	1118	1118	1119	1110	1122	

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	Top Hit Descriptor	H.saplens ART4 gene	22410 xt Soares pregnant utents into in a local contro	Homo septens mRNA for KIAA0903 protein, partial cos	Homo sepiens chandraten suifete proteograem 2 (versican) (Cor G2) III/VA	Homo sapiens chondrottin sulfate proteoglycan 2 (versioan) (Correct) mixty	Homo saplens chromosome 12 open reading frame 3 (CIZORF3), mrstvA	Homo sepiens glutemate decerboxylase 1 (brain, 67kD) (GAD1), transcript variant CAD22, moust	Homo sapiens glutamate decarboxylase 1 (brain, 67kD1), transcript versal (500.00), in the	Homo sapiens mRNA for KIAA1414 protein, parter was	Homo sapiens keradin 18 (KK i 18) mknA	Homo sapiens amphiphysm I mrkny, artemative spinot leolonii, compress compression in mrkny, artemative spinot leolonii, compression in mrkny, artemative spinot leolonii, compression in mrkny, artemative spinot leolonii, compression in mrkny, artemative spinot leolonii, compression in mrkny, artemative spinot leolonii, compression in mrkny, artemative spinot leolonii, compression in mrkny, artemative spinot leolonii, compression in mrkny, artemative spinot leolonii, compression in mrkny, artemative spinot leolonii, compression in mrkny, artemative spinot leolonii, compression in mrkny, artemative spinot leolonii, compression in mrkny, artemative spinot leolonii, compression in mrkny, artemative spinot leolonii, compression in mrkny, artemative spinot leolonii, compression leolonii, compression in mrkny, artemative spinot leolonii, comp	Homo sapiens mult. (E. cdl) homolog 3 (MLH3), mirunh	Homo saplens hypothetical protein FLJ10897 (FLJ10847), minner	Homo saplens ALK-tike protein mitting, parties cus	Homo sepions ALR-tike protein mRNA, perteil cds	Homo sapiens ALR-like protein mRNA, perdal cos	Homo septens ALR-like protein mRNA, perdal ods	Homo servieras chromosome 3 subbelomento region	Homo sepiens chondrottin sulfate proteoglycan 4 (melanome-associated) (CSPG4), mRNA	Homo espidos NEO dens	Long envisor Hosping protein S2 (RPS2) mRNA	Homo serviens Williams Beuren syndrome deletion transcript 9 (WBSCR9) mRNA, complete cds	Homo seriens mRNA for KIAA1507 protein, partial cds	Homo services mRNA for KIAA1507 protein, pertiel cds	Amo series Wolfren sandrome (WFS) mRNA	HAIR September Workern swindrams (WFS) mRNA	Long enters Wolfren wording (WFS) mRNA	TUITO September 19 Marie (1997) September 24 PR remma suburil certa 6000 5	Home septens prouding makes and the property many	10THO SEQUENTS TREADED WITHOUT LONG TO A PROPERTY TO A PRO	Homo septens mendora turing defeating process I (1915);	Homo septens fing throat protein a (roves), minutes	Homo sapiens zno finger protein 173 (ZNF173) III was a	Homo eactions ring tinger protein 9 (1417.9), stands	
	Top Hit Database Source	Π	EST HUMAN 4												뉟			1														INT	INT	INT	INT	INI
5	Top Hit Acession No.	1	2	0.1	4758081 NT	TN 18081	1N:1418008	7305078 NT	T305076 NT	35.1	4557887 NT	I COL	7857336 NT	8922593 NT	50.1	50.1	A CORATEO 1	AE264750 1	7100710		Ni oansoot	0.0E+00 Y18000.1	4505718 N	AF084479.1	AB040940.1	XΙ	5174748 N	5174748INI		9	7657529 NT	7657529 NT	5803146 NT	4509004 NT		4508004 NI
	Most Similar (Top) Hit BLAST E Value	0.0E+00 X95826.	0.0E+00 A1147850	0.0E+00 AB0207	004-00	00+40	004	00+100	0.0E+00	0.0E+00 AB0378	0.0E+00	0.0E+00 AF0349	0 OE+00	0.0E+00	0 0E+00 AF2847	0.0E+00 AF2647	000	0.0E+00/AF2047	0.0	0.0E+00/AF109/	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AF084	0.0E+00 AB0408	0.0E+00 AB040	0.0E+00			0.0E+00 AF098	00+30.0	00+∃0:0	0.0E+00	0.0E+00		0.0E+00
1	Expression Signal	0.87	800	70.7	77.0	12.0	130		883	1 85	0.75	4 54	1 20	1.7	12	8		1.77			1.71	2.33							2.04	3.78						0.72
	ORF SEQ ID NO:	28539	36540	285.42	2000	2004	84C97	DCCCC.						28617	1						26647					26882	28895	2000			26709		28715			Ш
İ	Exam SEQ ID NO:	13870	3	13880	70051	3 3	Poor!	13890	13800	43003	13040	2000	1780	13838	1	13950	_[13074	13975	13992	14000	14007	14014	14014	14027	L	L	1	1.	1_		1.	1	11
	Probe SEQ ID NO:	1,13	3	1724	611	1133	1133	1134	1145	2	1140	3 6	/0[]	1867	3	120	1204	1205	1206	1224	1225	1243	1251	1258	1285	1285	1277	1277	122	1278	1388	4200	3 8	300	1298	1297

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	Homo sepiens mRNA for KIAA0577 protein, complete cds	Homo saplens KIAA0170 gene product (KIAA0170), mRNA	Homo sepiens KiAA0170 gens product (KIAA0170), mRNA	Homo septens period (Drosophila) homolog 3 (PER3), mRNA	Homo saplens period (Drosophilla) homolog 3 (PER3), mRNA	Human endogenous retrovirus HERV-K10	Homo sapiens mRNA for Familial Cylindromatosis cyld gene	Homo sapiens partial TTN gene for titlin	9938b08.x1 Soerse_bests_NHT Homo sapiens cDNA clone IMAGE:1837427 3' similar to WP:T27A1.5 CE14213;	RAN, member RAS orcodente familitationo seniens RAN, member RAS orcodente familitation minimitations member RAS orcodente familitation minimitations and management of the control of the	Homo earlens proprotein convertase subtilisin/kapin trae 2 (PCSK2) mRNA	Homo sepiens proprotein convertase subfilistrikesin hoe 2 (PCSK2) mRNA	Homo septens KIAA1114 protein (KIAA1114), mRNA	Homo sepiens KIAA1114 protein (KIAA1114), mRNA	Homo sepiens partial AF-4 gene, excris 2 to 7 and Alu repeat elements	Homo saplens alpha1-6fucosytransferase (alpha1-6FucT) gene, eron 7	Homo sepiens titin (TTN) mRNA	Homo saplens titin (TTN) mRNA	Human nebulin mRNA, partial cds	Human nebulin mRNA, pertial cds	Novel human gene on chromosome 20	Novel human gene mapping to chomosome 1	Human mRNA for KIAA0240 gene, partial cds	Homo septens calcineum binding protein 1 (KIAA0330), mRNA	Homo saplens KIAA0170 gene product (KIAA0170), mRNA	Homo septems KIAA0170 gene product (KIAA0170), mRNA	Human von Williebrand factor pseudogene corresponding to excre 23 through 34	Human von Willebrand factor peeudogene corresponding to excres 23 through 34	Homo saplems hHDC for homolog of Drosophila headcase (LOC51898), mRNA	EST371757 MAGE resequences, MAGF Homo sepiens cDNA	ea34ea3.r1 NCI_OGAP_GCB1 Homo sepiens cDNA clone IMAGE:815116 5'	Cercopithecus aethiope cyclophilin A mRNA, complete cds
gle Exon Pro	Top Hit Database Source	F	N.	IN	Έ	¥	<u>F</u>	۲	Ā	EST HUMAN	<u> </u>	Į.	Ę	N.	NT	L	NT	NT	TN	NT	TN	NT	TN	NT	IN	NT	NT	M				T_HUMAN	뉟
Sir	Top Hit Acessian No.	AB011149.1	7881985 NT	7681985 NT	B567387 NT	1N 28587387	M14123.1	AJ250014.1	0.0E+00 AJZ77892.1	0.0E+00 A(208756.1	8042208 NT	4605848 NT	4505646 NT	TV05585 NT	T/105686 NT	0.0E+00 AJ238099.1	4F038280.1	4507720 NT	4507720 NT	J35637.1	J35637.1	0.0E+00 AL132999.1	0.0E+00 AL137784.1	087077.1	6912457 NT	7861965 NT	7861965 NT	A80676.1		7706434 NT	0.0E+00 AW959887.1	A481172.1	0.0E+00 AF023860.1
	Moet Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 M14123	0.0E+00 AJ2500	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AF03828	0.0E+00	0.0E+00	0.0E+00 U35637	0.0E+00 U35637	0.0E+00/	0.0E+00/	0.0E+00 D87077.	0.0E+00	0.0E+00	0.0E+00	0.0E+00 M80676.	0.0E+00 M60676	0.0E+00	0.0E+00 /	0.0E+00 AA48117	0.0E+00/
	Expression Signal	4.71	2.04	5.88	3.01	3.01	1.82	1.38	3.39	1.50	13.21	٥	io.	4.08	4.08	4.59	3.02	5.39	5.39	17.93	17.93	259	1.82	1.73	4.63	1.55	1.55	0.97	0.97	1.37	121	1.70	40.82
	ORF SEQ ID NO:	28720	1202	28722	26723	28724	26737	50808	28817	20821	28822	26833	26834	28837	26838	28839	28852	28963	20804	26868	28889	20876	28877	28882	28885	28887	26888	28893	20894	28032	6 7 687	20850	28953
	Exan SEQ ID NO:	14048	14049	14050	14051	14051	14062	14134	14140	14143	14144	14153	14153	14155	14155	14157	14168	14178	14178	14183	14183	14188	14194	14198	1420	14203	14203	<u>-</u> 587	14207	14248	1 283	14284	14269
	Probe SEQ ID NO:	1299	1300	1301	1302	1302	1314	1387	1383	1396	1397	1406	1409	1408	1408	1410	1420	1431	1431	1436	1436	1 48	1447	1461	1454	1456	1456	1	1400	200	1518	1517	1522

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Oligie Exoli riodes Expressed in brain	Top Hit Descriptor	Cercopitiscus aethlops exclopitin A mRNA complain ode	EST388206 MAGE resequences, MAGN Homo serviens cDNA	EST388206 MAGE reseguences, MAGN Homo seniens, cDNA	Bowne mRNA for neurocation	Homo saplens Bruton's tyrosine kinase (BTK), alpha-D-galactosidese A (GLA), L44-like ribosomal protein (1.44) and ETB3 (ETB3 name committee of	Hamo sepiens transmembrane olyconomin (GDNIMR) mRNA	Homo saplens transmembrane divocación (GPNAR) mRNA	Homo eaplens KIAA0957 protein (KIAA0957, mRNA	Homo sepiens TNF-inducible protein CG12-1 (CG12-1) mRNA	Human bansglutaminasa mRNA, complete cds	Homo saplens titn (TTN) mRNA	Homo sapiens titin (TTN) mRNA	Homo saplens ribosomal protein L5 (RPL5) mRNA	Human laminin receptor (2H6 exitose) mRNA. 6 end	Homo sepiens tith (TTN) mRNA	Homo septens tith (TTN) mRNA	Homo septens chandrottin sulfate proteophoan 4 (melanome-essociated) (CSPCA) mRNA	human cyes-2 gene	H. seplens hH28/e gene	Homo saplens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA	Homo sepiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA	AV690831 GKC Hamo saplens cDNA clane GKCBOF02 5'	AV690831 GKC Hamo sepiens cDNA clane GKCBOF02 5'	Homo sepiens mRNA for KIAA1472 protein, pertial cds	Homo sepiens DNA polymerase zete catalytic suburit (REV3) mRNA, complete cats	Homo sepiens KIAA0569 gene product (KIAA0569), mRNA	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA	Homo sepiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA	Homo septens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA	Human sodium channel mRNA	yo76c05.s1 Sogres adult brain N254HB55Y Homo sapiens cDNA clone IMAGE:183848.3*	Homo saplens mRNA for KIAA1609 protein, partial cds	Homo sapiens mRNA for KIAA1609 protein, pertial cds
GIO EXVII FIG	Top Hill Databese Source	L _N	EST HUMAN	EST HUMAN	Ę	<u> </u>	Į.	N.	Ę	Į.	N	Z	Ę	Z	F	N-	۲	Z	NT	뒫	TA		EST_HUMAN	EST_HUMAN	LΝ	N N	Þ	5	F	F	Z	EST_HUMAN	건	М
5	Top Hit Acession No.	AF023860.1	0.0E+00 AW978097.1	0.0E+00 AW978097.1	0.0E+00 D10884.1	U78027.1	4505404 NT	4505404 NT	7662405 NT	7656972/NT	1.7	4507720 NT	4507720 NT	j	-	4507720 NT	4507720 NT	4503098 NT			5921460 NT	5921460 NT				0.0E+00 AF157476.1	7662183 NT	7662183 NT	5729876 NT	5729876 NT	Ţ	1	29.1	29.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00 AF023	0.05+00	0.0E+00	0.0E+00	0.0E+00 U7802	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 M9847	0.0E+00	0.0E+00	0.0E+00	0.0E+00 M14199	0.0E+00	0.0E+00	0.0E+00	0.0E+00 D00333	0.0E+00 Z83738.1	0.0E+00	0.0E+00	0.0E+00/	0.0E+00/	0.0E+00/	0.0E+00/	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 M91803	0.0E+00 H28973.	0.0E+00 AB0468	0.0E+00 AB0468
	Expression	49.82	1.24	1.24	5.49	207	2.1	2.1	3.3	7.29	1.84	3.72	3.72	11.72	11.72	2.86	2.86	11.7	1.21	1.05	1.59	38.	11.18	11.18	9.82	1.83	9.78	9.78	42,76	42.75	7.94	5.85	2	2
	ORF SEQ ID NO:	26954	Ш		28959				20065		20071	26973	26974		26975	26088	20089	28990		27007	27008	27009	27010	27011	27014	27015	27018	27019	27020	27021	27023	27039	27051	27052
	Econ SEQ ID NO:	14269		14271	14272	14274	14275	14275	14277	14278	14284	14287	14287	15572	14288	14300	4300	14302	14310	14321	14322	14322	14323	14323	15573	4328	14331	14331	4333	14333	14335	14350	14381	14361
Г	Probe SEQ ID NO:	1522	1524	1524	1525	1527	1528	1528	1530	<u>8</u>	1 33	割	2	ξ	1542	1553	<u>8</u>	\$	<u>8</u>	1 2	1575	2/2	15/6	1576	1579	1583	1585	1585	1587	1587	288	\$	<u></u>	1614

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1		Т	T	1_	Ŧ	Т	Т	T	Т	Т	15	7	T	т	T^-	Ť	一	T	7	7	Ť	Ť	$\overline{}$	T	T	_	1	7	-	T -
olingie Excit Probes Expressed in Brain	Top Hit Descriptor	MR0-HT0168-191189-004-b11 HT0168 Homo serviens cDNA	MR0-HT0166-191199-004-b11 HT0109 Hamp septens cDNA	wg81b07.x1 Soarse_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371477 3' similar to TR:Q62788 Q62788 CYS2/HS2 ZINC FINGER PROTEIN.	Homo sapiens hematopoletic-derived zinc finger protein (HD-ZNF1) mRNA	Homo saplens T-cell receptor garrima V1 gene region	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds	Homo saplens keratin 18 (KRT18) mRNA	Homo sapiens webs evien erythroblestoels wrus E26 oncogene related (ERG) mRNA	hu11d05x1 NCI_CGAP_Lu24 Homo septens cDNA clone IMAGE:31862813' similar to TR:095147 095147 MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE:	hu11d05x1 NCI_CGAP_Lu24 Home expiens cDNA clone IMAGE:31662813' similar to TR:095147 095147 MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE:	Homo septens gamme-eminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA	yo59e08.rf Soures breest 3NbHBst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64099 GAMMA-GLUTAMYLTRANSPEPTIDASE 5 PRECURSOR (HUMAN):	vo59e08.rf Soeres breest 3NbHBst Homo septens cDNA clone IMAGE:182246 5' similar to gb:M64099 GAMMA-GLUTAMYLTRANSPEPTIDASF 5 PRECTRESOR (HIMAN)	H.saplens H2B/h gene	H.saplens H2B/h gene	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA	Homo saplens WNT16 protein (WNT16) mRNA, complete ods	Homo saplens FOXJ2 forthead factor (LOC55810), mRNA	Homo saplens RNA binding motif protein, Y chromosome, family 1, member A1 (RBMY1A1) mRNA	Homo eaplens WAVE2 mRNA for WASP-family protein, complete cds	TCR zota [human, Genomic/mRNA, 365 nt, segment 1 of 8]	Homo saplens NOD2 protein (NOD2), mRNA	Homo sapiens SMCY (SMCY) gene, complete cds	Homo saplens ribosomal protein S2 (RPS2) mRNA	Homo sapiens E1A binding protein p300 (EP300) mRNA	Homo saptens E1A binding protein p300 (EP300) mRNA	Human CSF-1 receptor (FMS) gene, complete ods, and (SMF) gene, partial ods	2d88g09.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:345684 51
JIB EXON PIO	Top Hit Database Source	EST HUMAN	EST_HUMAN	EST HUMAN	Į.	Σ	١	Ę	F	5	EST_HUMAN	EST HUMAN	 	EST_HUMAN	EST HUMAN	N F	IN		TN	Ę	Ę	NT	F	ίΤ	NŢ	IT	П.			EST_HUMAN
	Top Hit Acession No.	2 .	0.0E+00 BE144364.1	2.	4758513	AF05717	7.	1.1	4557887 NT	7857065 NT	0.0E+00 BE222374.1	0.0E+00 BE222374.1	57610	-	0.0E+00 H30132.1	L	1	5031748 NT	0.0E+00 AF169963.1	8923841 NT	52053	42.1	S94400.1	11545911 NT	41.1	4506718 NT	4557556 NT	4557556	1	+
	Most Similar (Top) Hit BLAST E Velue	0.0E+00 BE144	0.0E+00	0.0E+00 AI7681	0.0E+00	0.0E+00 AF057	0.0E+00 M2958C	0.0E+00 M2958C	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 H30132	0.0E+00	0.0E+00 Z80780	0.0E+00 Z80780.	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 S94400	0.0E+00	0.0E+00 AF2738	0.0E+00	0.0E+00	0.0E+00	0.0E+00 U63963	0.0E+00 W78571
	Expression Signal	1.25	1,25	1.68	12	261	1.76	1.78	1.35	1.6	1.12	1.12	3.24	3.18	3.18	1.32	1.32	13.71	1.11	3.53	1.11	4.08	2.19	1.16	1.88	98.	3.37	3.37	1.42	12
	ORF SEQ ID NO:	27095	27096			27102	27108	27107	27109	27110	27113	27114	27116	27119	27120	27122	27123		27133	27138	27145	27162		27167	27181	+	27228	27220	27232	
	Exen SEQ ID NO:	14405	14405	14409	14410	14411	1414	14414	14416	14417	14420	14420	14421	14424	14424	14426	14426	14429	14437	1	3	14461	1 53	15577	1483	15578	14523	14523	14525	14528
	Probe SEQ ID NO:	1659	1659	1683	1664	1665	1669	1669	1671	1672	1675	1675	1677	1680	1680	1682	1682	1685	1693	98	7/02	R0/1	17.0	22/	1/30	1778	1782	1782	78	1787

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	Top Hit Descriptor	Homo saniens nuclear autoentigenic sperm protein (histone-binding) (NASP) mRNA	Homes december or make Complete cds	Chursh manua for KIAA0333 cene, partial cds		Homo sepiens activeting transcription factor 4 (tex-responsive enhancer element B67) (ATF4) mRNA	Homo sepiens activating transcription factor 4 (tex-responsive enhancer element B67) (ATF4) mRNA	Homo septens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA	Homo sapiens protein tyrosine phosphatase, receptor-type, zew polyceptor	Homo sepiens Retine derived Pour contain factor 1 (RPF-1), mRNA	Home series REINA for KIAA1152 protein, partial ods	Linear earliene mRNA for KIAA1152 protein, partial cds		Homo sepiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mrove.	Homo seplens potassium voltage-gated charnel, Shab-related subfamily, member 1 (KCNB1) mRNA	Human retinal degeneration alow (RDS) gene, exch 1	Human retinal degeneration slow (RDS) gene, each 1	UI-H-BI1-efn-f-07-0-UI-s1 NCI_CGAP_Sub3 Homo septents CONA CICIE MACAP-7727223 3	ULT-BIT-eff-f-07-0-ULS-1 NCI_CGAP_Subs. Home separate cover core investigation of the contract	601178164F1 NIH MCC_20 Hallo services CDNA done IMAGE:3547239 5	0011/81041 1111 mcc	Home emigra RAD1 (S. bombe) homolog (RAD1) mRNA, and translated products	Homo serviers RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products	Homo saciens DNA polymentase zeta cetalytic subunit (REV3) mRNA, complete ods	Human franschlaminese mRNA, complete ods	Human transclutaminase mRNA, complete cds	Home sapiens transforming growth factor, beta 3 (TGFB3), mRNA	Home services transforming growth factor, beta 3 (TGFB3), mRNA	Homo saciens death receptor 6 (DR6), mRNA	
	Top Hit Database Source			Į.	Z	7	ΤΛ	<u> </u>	NT	Z	٤		IN.	ΤN	Ę	Ę	칟	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	FSI HOMAN	Z	Z	Z	ž į	2	Z	124	2
	Top Hit Acession No.	1000000	7252004			4502284 NT	4502284 NT	4502284 NT	4506328 NT	9005855 NT	6005855	9	81	4828783 NT	4826783 NT	J07147.1	107147.1	AW 207280.1	0,0E+00 AW 207280.1	0.0E+00 BE277465.1	0.0E+00 BEZ77465.1	BE006292.1	4506384 NI	4506384 N	0.0E+00 AF157476.1	0.0E+00 M98478.1	0.0E+00 M98478.1	4507464 N	450/464 IN	7657038 N
-	Most Similar (Top) Hit BLAST E		0.0E+00	0.0E+00 U14967.1	0.0E+00 AB00233	0.05+00	0.0E+00	00 1400	8	0.0E+00	0.0E+00	0.0E+00 AB03297	0.0E+00 AB03297	0.0E+00	005+00	0.0E+00 U07147.	0.05+001107147	0 0F+00 AW 2072	0.0E+00/	0.0E+00	0.0E+00	0.0E+00	0.0E+00			0.0E+00	0.0E+00	0.0E+00	١	0.0F+00
	Expression Signal		2.74	5.68	2.79	4.07	4.07	4.07	183	582	5.82	1.12	1.12	4.35	135	5.47		4.48	1.00	3.40	3.49	0.93	2.16	2.16						1.42
	ORF SEQ EID NO:		27238	27251	27254	77256	27258	E CEC	16217				27288	27290		77700			777077			27334		27363			2 27373	3 27380	3 27381	9 27383
	Exam SEQ ID NO:		15579	<u>. </u>	1	l _		1	35	1_		<u> </u>	L	14578	1.	L		┙	14582	1	1_	7 14624	L	14653	L	5 15582	1_	1_	14666	3 14668
	Probe SEQ ID NO:		1788	98	1802	768	200	3	1803	1812	1828	1836	1836	1840		1840	1841	<u>\$</u>	48	1868	1868	1887	1916	1916	1924	1925	1925	1930	1930	1933

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Single Explication Lypidesect in District	Top Hit Descriptor	Homo sepiens glutatrione S-transferase frieta 2 (GSTT2) and glutatrione S-transferase treta 1 (GSTT1) genes, complete cds	Human topolsomerase I pseudogene 1	Homo septens histófine anmonia-lyase (HAL) mKNA	Homo sepiens histidine errmonta-lyese (HAL) mirun	Hamo sepiens chramosome 21 segment HSZ10352	Homo sapiens nebulin (NEB), mitava	Homo sapiens neoulin (NEB), many	Homo sapiens sourm, apina + (ACTIN4) in u.e.	Homo sapiens action, entries 4 (ACTIVE) minutes	Home septens mirdry for Nirval for protein, person and	Hand septens minute (or nine) process,	Human I FEB protein mickey, per use cos	Human Their probin mixer, per use cos	X08DOLXO NO. COAP THE TOTAL SECTION COME IMAGE 26799133	XOSECUL XI NO. COST. Part notice estate Cost. Co	HOME SECTION IN THE PROPERTY OF THE PROPERTY O	Homo septens determent protein (Navasco), in the septens determined by the septens of the septen	Homo seprens ruizzanzo gane produk (ruizzanzo), militaria	Hamp septens mixthe for hundred of process of the p	H. sapiente genes for sementigem I i sin a sementigui i i	H. septems genes for extremogram 1 and extremogram in	HOMO SECOND LINEAR TO MANA COUNTY PARTY.	Thomas and the state of the sta	TOTIO SECURIO (CITO) COMO COMO COMO COMO COMO COMO COMO CO	ACTION SECURIS 11 WILLIAM SECTION CONTRACTOR PLACE 4000321 5	CONTROL KIRA 1114 Peritain (KIRA 1114) IIIRNA	THE SECTION OF A STATE OF THE SECTION OF THE SECTIO	Tronzen Character 7 East Right Child I Bran Home sapiens cDNA clone 7822E10	Transfer Officers 7 Earl Brain O'NA Prany Home sections CONA clone 7822E10	1622E-10 Citronicative to not interest membrane abcountein POM121 (POM121L1), mRNA	Home annians characterises 64, cOMP-specific, rod, siche (PDESA), mRNA	HSCAICASA normalizad infant brain cDNA Homo saplens cDNA clone c-0ic02	
	Top Hit Detabase Source	7	۲	Ϋ́	NT.	NT	¥	Ę	L	L L	LN		Z	NT	EST HUMAN	EST HOMAN	LN	Į	닐	Ę	Ę	¥	Į.	ž!	Z	- (ı	EST HOMAIN	z	LN L	ESI HUMAN	EST HUMAN	Z .	INI TOT	ESI TOWN
Buis	Top Hit Acession No.	0.0E+00 AF240786.1		4809282 NT	4809282 NT	0.0E+00 AL163252.2	8400716 NT	8400716 NT	4828638 NT	4826638	33.1	\B018333.1	JB3782.1	VI33782.1	4W193024.1		8912457 NT	6012457 NT	7662096 NT	AB011149.1	247556.1	Z47558.1	0.0E+00 AB040946.1	0.0E+00 AF273841.1	0.0E+00 AF273841.1	7706742 NT	0.0E+00 AU140831.1	7705585 N I	7706585 NT	0.0E+00 AA077589.1	0.0E+00 AA077589.1			242399.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00.A	0.0E+00 M55632	0.0E+00	0.0E+00	0.0E+00/	0.0E+00	0.0E+00	0.0€+00	0.0E+00	0.0E+00 AB0183	0.0E+00 AB0183	0.0E+00 M33782.1	0.0E+00 M33782.1	0.0E+00 AW1930	0.0E+00 AW193(0.0E+00	0.0E+00	0.0E+00	0.0E+00 AB0111	0.0E+00 Z47556	0.0E+00 Z47558.	0.0E+00	0.0E+00	0.0E+00	0.05+00		١				0.0E+00	0.0E+00	0.0E+00 Z4Z399
	Expression Signal	427	135	2	4	1.15	1.09	1.09	2.49	249	1.36	1.36	1.80	1.89	1.57	1.57	96.3	5.96	2	1.19	1.58	1.58	3.75		1.02	1.64	4.13	1.55				2.41		0.97
	ORF SEQ ID NO:		+	27396	79577		27410	27411	27412	27413	27427	27428	L.			27436			L				27451		27477			26837						27517
	Exen SEQ ID NO:	14870	14875	14884	14684	14605	14697	14697	14698		1	1	1_	<u> </u>	L	14717	14718	_	L	Ì_	L		1.	14749	14749	14779	14785	14166	14155	14787	14787	14789	ll	14792
	Probe SEQ ID NO:	ğ	200	2 0	96	1950	18	1981	1982	1962	1973	1973	1979	1979	188	1981	1982	1982	1984	1985	1986	1986	1993	2014	2014	2046	2052	2053	2053	2055	2025	2057	2059	2080

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Top Hit Detaberse Top Hit Descriptor	qv80f08.xf NCL_CGAP_Ut2 Homo sepiens cDNA cione IMAGE:1988871.3° similar to contains Alu repetitive element.	801485148F1 NIH MGC 69 Home septems cDNA clone IMAGE-3887747 K	601902604F1 NIH MGC 19 Hamo sepiens oDNA clone IMAGE:4135320 5'	601902604F1 NIH MGC 19 Hamo septems cDNA clone IMAGE:4135320 5	RC3-CT0413-270700-022-d10 CT0413 Homo sepiens cDNA	RC3-CT0413-270700-022-d10 CT0413 Hamp septens cDNA	Human plasma membrane caldum ATP ase (soform 2 (APT2B2) mRNA, comiete cds	Human plasma membrane calcium ATPase Isoform 2 (APT2B2) mRNA comiete cds	Homo sapiens GTP binding protein 1 (GTPBP1) mRNA	QV1-GN0085-140800-318-c10 GN0085 Homo saplens cDNA	Homo septens X-linked juvenile retinoschists protein (XLRS1) gene, each 6 and complete cds	601672086F1 NIH_MGC 20 Homo septens cDNA clone IMAGE:3964785 6	PMO-BT0547-210300-004-F04 BT0547 Homo sepiens cDNA	Homo septems glutathione S-transferase theta 2 (GST12) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds.	I.3-CT0219-271099-022-G10 CT0219 Homo serviens cDNA	Homo sepiens metabotropic glutamate receptor 1 stoha (mGLA? sloha) mRNA complete cds	QV-BT065-020399-092 BT065 Home serviers GDNA	QV-BT066-020399-092 BT066 Homo septens cDNA	Homo septiens potassium large conductance calcium-activated channel, subfamily M, beta member 3-like (KCNMB3L), mRNA	Human DNA-binding protein mRNA, 3'end	601122338F1 NIH_MGC_20 Homo sepiens cDNA clone IMAGE:3346888 51	AV735288 CB Hamo septens cDNA clane CBNBDE08 5'	AV738288 CB Homo septens cDNA clane CBNBDE08 5'	0032e01.s1 NCI_CGAP_Lu5 Homo sepiens cDNA clone IMAGE:1587898 3'	602014829F1 NCL_CGAP_Bm64 Home sapiens cDNA clone IMAGE-4150734 5	601572188T1 NIH_MGC_55 Hamo sapiens cDNA clone IMAGE:3839012.3	CM1-TN0141-250900-439-b08 TN0141 Homo sablens cDNA	CM1-TN0141-250800-439-b08 TN0141 Hamo septens cDNA	601900261F1 NIH_MGC_19 Homo sepiens cDNA clone IMAGE:4129622 5	bb84e02.y1 NIH_MGC_10 Hamo sepiens cDNA clone IMAGE:3049082 5' similar to TR:Q15170 Q15170 TRANSCRIPTION FACTOR S-II-RELATED PROTEIN;
Top Hit Detabese Source	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	N	LN PA	NT	EST_HUMAN	LN	EST_HUMAN	EST HUMAN	Į.	EST HUMAN	NT	EST HUMAN	EST_HUMAN	LV.	NT	EST_HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN	EST HUMAN	Г	EST_HUMAN	EST_HUMAN
Top Hit Acession No.	A 244247.1	0.0E+00 BE877225.1	0.0E+00 BF316325.1	0.0E+00 BF315325.1	0.0E+00 BE697125.1	0.0E+00 BE697125.1	.00620.1		4758489 NT	0.0E+00 BE767964.1	\F018963.1	0.0E+00 BF027562.1	0.0E+00 BE072624.1	0.0E+00 AF240786.1	W752708.1		0.0E+00 AI904640.1	0.0E+00 Al904640.1	7857252 NT			<u></u>	<u></u>	-		2	7	1.		+-
Moet Similar (Top) Hit BLAST E Value	0.0E+00 AI244247	0.05+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 L00620.1	0.0E+00 L00820.1	0.0E+00	0.0E+00	0.0E+00 AF01896	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AW75270	0.0E+00 L78627.1	0.0E+00/	0.0E+00/	0.0E+00	0.0E+00 L14787.1	0.0E+00 BE274690	0.0E+00 AV738288	0.0E+00 AV738288	0.0E+00 AA93169	0.0E+00 BF34443	0.0E+00 BE748800	0.0E+00 BF377897	0.0E+00 BF377897	0.0E+00 BF313617	0.0E+00 BE018750
Expression Signal	1.78	3.48	1.48	1.48	3.07	3.07	3.71	3.71	1.36	2.06	1.59	3.76	1.03	1.06	1.3	1.47	6.39	6:38	1.05	1.22	1.05	7.59	7.59	1.4	5.68	1214	3.55	3.55	2.04	1.83
ORF SEQ ID NO:		27526	27528	27529		Z7533	27544	27545	27540			27672	27573	27574	27576	27577	27579	27580			27644	27647	27648	27850	27654	27855	27859	27660	27865	27668
Exen SEQ ID NO:	14794	14799	14801	14801		14804	14812	14812		14838	14839	14841	14842	14844	14847	14848	14850	14850	14883	14908	14912	14914	14014	14916	14920	14921	14925	14925	15588	14931
Probe SEQ ID NO:	2002	2087	2069	2069	2072	2072	2080	2080	2085	2107	2108	2110	2111	2113	2116	2117	2119	2119	2163	2179	788 788	2185	2185	2187	2191	2192	2196	2188	8	2203

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Onigio Exoli riodos Explessod III Dialli	Top Hit Descriptor	Homo sepiens KIAA0218 gans product (KIAA0218), mRNA	Homo septens signal regulatory protein, beta. 1 (SIRP-BETA-1) mRNA	AU131142 NT2RP3 Homo septens cDNA clone NT2RP3002064 5	601586843F1 NIH MGC 7 Hamp septens cDNA clone IMAGE 3941003 5	WR1-SN0033-120400-002-e04 SN0033 Homo sepiens cDNA	Homo sepiens KIAA0244 protein (KIAA0244), mRNA	Homo septens hacese-C-phosphate dehydrogenase (dlucose 1-dehydrogenase) (H6PD) mRNA	Homo sapiens herose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA	Homo septens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450	polypeptide 5 (CTP3A5) gene, partial cds	AUTIBUSZ HEMBAT Homo septens obyva done HEMBA1002839 51	AU118082 HEMBA1 Hamo sepiens cDNA clone HEMBA1002839 5'	AU118082 HEMBA1 Hamo sepiens cDNA clone HEMBA1002839 5'	Homo sepiens hypothetical protein FLJ20081 (FLJ20081), mRNA	MR0-BN0070-090600-029-d12 BN0070 Homo septens cDNA	AU119582 HEMBA1 Homo septens cDNA done HEMBA1006155 5	0x00b02x1 Soaree_NhHMPu_S1 Homo septens cDNA clone IMAGE:1660683 3' similar to TR:008662 008662 230KDA PHOSPHATIDYLINOSITOL 4KINASE	Homo septens hypothetical protein FLI20893 (FLI20893), mRNA	601432808F1 NIH MGC 72 Homo expiens cDNA clone IMAGE:3918168 61	MR1-TN0021-280800-001-h06 TN0021 Homo septems cDNA	AB005622 HeLa cDNA (T. Norna) Homo sepiens cDNA straiter to adenylate kinase isozyme 2	Homo sapiens glutamate receptor, lonotropic, N-methyl D-aspertate 2A (GRIN2A) mRNA	Homo sapiens gane for cholecystokinin type-A receptor, complete cds	Homo sepiens gene for cholecystokinin type-A receptor, complete cds	Homo saplens immunoglobulin-like transcript to variant 4 (ILT10) gene, econ 6	802018068F1 NCL CGAP Bm67 Home septems cDNA clone IMAGE:4153670 5	Homo sapiens collegen, type XII, alpha 1 (COL12A1), mRNA	CM0-MT0033-150600-428-h11 MT0033 Homo saplens cDNA	CM0-MT0033-150800-428-h11 MT0033 Homo septens cDNA	Human G protein-coupled receptor (GPR1) gene, complete cds	Human G protein-coupled receptor (GPR1) gene, complets cds	802/84558T1 NIH_MGC_42 Homo septerts cDNA clone IMAGE:4300383 3'
אום דעמוו גווי	Top Hit Databese Source	Z	Z	EST HUMAN	EST HUMAN	EST HUMAN		Z.	TN	_	IN TOU	ES I HOMAN	EST HUMAN	EST HUMAN	Į,	EST_HUMAN	EST_HUMAN	EST HUMAN	Ę	EST_HUMAN	EST_HUMAN	EST_HUMAN	TA.	닐	M	NT.	EST_HUMAN	F	EST_HUMAN	EST_HUMAN	NT	LN.	EST HUMAN
5	Top Hit Acession No.	7882007 NT	5174678 NT	14	3E794026.1	1W867076.1	7862017	4758497 NT	4758497 NT		2.7	01100021	W118082.1	0.0E+00 AU118082.1	8923089 NT	0.0E+00 BE814424.1	0.0E+00 AU119582.1	0.0E+00 Al042035.1	23620		12.1	2.1	6006002 NT	_	1	5.1	4.1	5729777 NT]	13
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00 AU1311	0.0E+00 BE7940	0.0E+00 AW8670	0.0E+00	0.0E+00	0.0E+00	i i	0.0E+00 AFZ801(30.0	0.0E+00 AU1180	0.00+000	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AB00562	0.0E+00	0.0E+00 D85606.	0.0E+00[D86806.	0.0E+00 AF10627	0.0E+00 BP34527	0.0E+00	0.0E+00 B	0.0E+00 BE831003.1	0.0E+00 U13666.1	0.0E+00 U13688.1	0.0E+00 BF569144
	Expression Signal	1.24	3.2	2.39	4.31	1.51	2.99	2.03	2.03	4	2,23	8 8	8 2	88.	88.0	0.91	1.08	3.74	96'0	4.44	F	0.98	4.5	2.09	200	1.81	1.22	4.45	1.24	124	880	0.83	2.08
	ORF SEQ ID NO:	27794	27807	27811		27812			27815		27847	10,0	27818	819/7	27820		27872		27873		27878		27892	27896	27897	27906	27911	27919	27822	27023	27927	27928	27920
	_ თ	15058		15074	15075		ı	_	15078	4.5070	_			1	19082		15130	15137	15138	15141	15145	15154	15157	16180	15160	15168	15172	15179	15183	15183	15188	15188	15180
	Probe SEQ ID NO:	2334	2348	2352	2353	2354	2355	2356	2356	7347	2359	2050	22.50	803	7300	2377	2415	2416	2417	2420	2424	2433	2437	2441	2441	2449	7 2	2461	200	2465	2 7 1 9	242	2471

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7qZ7h12x1 NGL CGAP_GC8 Homo septiens CDNA clone INAGE: 3' similar to TR:000248 000246 UI-H-BW1-emp-f-12-0-UI,s1 NCI_CGAP_Sub7 Homo sepiens cDNA clone IMAGE:3070631 3 UI-H-BI4-802-b-08-0-UI.s1 NCI_CGAP_Sub8 Homo sepiens cDNA olone IMAGE:3086535 3" UHF-BP0p-ets-c-07-0-ULA NIH MGC_61 Homo septens cDNA clone IMAGE:3072780 5 Homo sepiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA Homo sepiens hypothetical protein FLJ20368 (FLJ20368), mRNA Homo sepiens protein kinase, AMP-ectivated, sipha 2 catalytic subunit (PRKAA2) mRNA RC3-ST0197-300300-016-c04 ST0197 Homo sepiens cDNA Homo sapiens protein knase, AMP-activated, alpha 2 catalytic suburit (PRKAA2) mRNA 601869073F1 NIH_MGC_17 Homo saplens cDNA clone IMAGE:4111411 5 601869073F1 NIH_MGC_17 Homo saplens cDNA clone IMAGE:4111411 5 602152653F1 NIH_MGC_81 Homo septens cDNA clone IMAGE:4293612 6 601173631F1 NIH_MGC_17 Homo septens cDNA clone IMAGE:3525159 5 601105312F1 NIH MGC 15 Homo septens cDNA done IMAGE:2987955 5 ha04h04.x1 NCI_CGAP_Kid12 Hamo sepiens aDNA clane IMAGE:2872759 3 601106312F1 NIH MGC 15 Homo seplens cDNA clone INAGE 2387955 5 601489241F1 NIH_MGC_89 Hamp septens aDNA clane IMAGE:3891371 67 601489241F1 NIH_MGC_89 Hamp septens aDNA clane IMAGE:3891371 57 601064738F1 NIH MGC 10 Homo sepiens cDNA clone IMAGE:3451161 5 601508211F1 NIH MGC_71 Hamp septens cDNA clare IMAGE:3909696 5 601503356F1 NIH_MGC_70 Homo septens cDNA done MAGE:3805148 5 801562530F1 NIH_MGC_7 Homo septens cDNA clane IMAGE:3946518 5 Homo sepiens platislet-derived growth factor receptor-like (PDGFRL) mRNA AU143277 Y79AA1 Homo sepiens cDNA done Y79AA1001673 5 AU143277 Y79AA1 Homo seplens cDNA clone Y79AA1001673 5 Homo saplens mRNA for membrane transport protein (XK gene) Top Hit Descriptor Homo sepiens mRNA for KIAA1415 protein, pertial cds Homo sepiens mRNA for KIAA1415 protein, partial ods Homo sapiens death receptor 6 (DR6), mRNA Homo sepiens adlicen mRNA, complete cds Human Sectiz (Sectiz) mRNA, complete cds Homo sapiens adicen mRNA, complete cds HYPOTHETICAL 9.3 KD PROTEIN; Single Exon Probes Expressed in Brain EST HUMAN EST HUMAN EST_HUMAN EST HUMAN EST_HUMAN EST HUMAN EST HUMAN EST_HUMAN EST HUMAN EST HUMAN EST_HUMAN EST HUMAN EST_HUMAN EST_HUMAN EST HUMAN EST HUMAN EST HUMAN EST_HUMAN EST HUMAN Top Hit Database Source 눋 7657468 NT 8923340 NT 7657038 NT 5453965|N 5453871 5453965 Top Hit Acession 0.0E+00|BF204131.1 BF204131.1 0.0E+00 AB037836.1 BF672818.1 0.0E+00|BF223041.1 0.0E+00 BE296613.1 0.0E+00|BF513835.1 0.0E+00 BE292896.1 0.0E+00 AB037836.1 BE292898.1 0.0E+00 AF245505.1 0.0E+00 AW813853.1 0.0E+00 BE910378.1 0.0E+00 BE886490.1 0.0E+00 BE875511.1 0.0E+00|BE875511.1 0.0E+00 BE536921.1 0.0E+00|AU143277.1 0.0E+00 AW 486922.1 0.0E+00 AW 501010.1 0.0E+00 AF245505.1 0.0E+00 BF509482.1 0.0E+00 AU143277. 0.0E+00 BE795542.1 2 193239.1 0.0E+00|Z32684.2 0.0E+00.0 0.05+00 0.0E+00 0.0E+00 0.0E+00 0.0E+00 0.0E+00 0.0E+00 0.06+00 0.0E+00 (Top) Hit BLAST E Most Similar 1.83 7.94 213 2.13 1.38 5.18 1.19 70. 5.16 297 297 1.86. 201 1.83 3.28 3.34 0.91 1.06 0.91 Expression 28085 28018 28070 28039 28061 28002 27984 27989 27990 27963 28013 27980 27978 27940 27058 27859 27383 27972 27941 27971 27974 ORF SEQ Ö S S 15323 15326 <u> 왕</u>19 15275 15278 15277 15280 15303 15531 15531 15269 15249 15276 15276 15248 15249 15238 15240 15251 15239 15241 15215 16228 15234 15200 15202 15215 14008 15232 15230 SEQ ID 15231 Ö 2815 2808 2615 2607 2011 2566 2563 882 2661 2662 2562 2518 2520 2523 2524 2526 2530 2634 2554 2498 2509 2515 2516 2484 SEQ ID

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Top Hit Descriptor	th19608.x1 NCI_CGAP_Bm25 Homo sapiens cDNA done IMAGE:x108033 3 stimes to general CALCIUM-TRANSPORTING ATPASE PLASMA MEMBRANE, BRAIN ISOFORM 2 (HUMAN); CALCIUM-TRANSPORTING ATPASE PLASMA MEMBRANE, BRAIN ISOFORM 2 (HUMAN);	mRNA mentals in the second sec	Homo septiate introvious processing the MAGE 3944304 6	BOLDSOLIOSET NITH MIGG 7 Homo septems CDNA clone INAGE:3944304 5	601143722F1 NIH MGC 15 Homo septens cDNA done IMAGE:3051389 5	SATSSAGGOFT NIH MGC 7 Hamo septens cDNA clane IMAGE:3938222 6	Homo sepiens IMP (inosine monophosphate) dehydrogenese 1 (iMPDH1) mRNA	Homo serients Bruton's tyrosine khasse (BTK), alphe-D-galactosidese A (GLA), L44-like ribosomal protein	(L4L) and FIP3 (FIP3) genes, complete cds	Home saprens guaryrane cycles and the NT2PA001984 5	AUTSSESS NI ZAT 4 TAUTO SEPTEMBER (RPAG1) mRNA, complete ods	Human burious paripulayora angles (Co. 1)	AUTSCHUS NITZERS Home sapiens cDNA clone NT2RP3000779 5	DOT OTTORIS 220200-011-407 OT0086 Hano sepiens aDNA	TAMENDS A NO. COAP CO16 Homo septens cDNA done IMAGE;3316089 3'	PAY TAKE NIH MGC 18 Hamo septens of NA clone IMA GE:3828923 5	00 1250 151 171 170 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	EST188414 HCC cell line (metastasis to liver in mouse) il Homo sapiens cDNA 5' end similar to ribosome	probabil L29	University (RAM22) dens. excm 5	Human Court, M. Carrier (C. M. Carrier C. M.	Turno explane ekaletel musche LIM-problem 1 (FHL1) gene, complete ods	Trollo access second fire GTP-binding protein like 1, complete cds	Trotto septeta 11023/11 til 1200 7 Hamo embens cDNA clone IMAGE:3945963 51	AN 1335 ABRETA NIEL MAC 39 Homo septems aDNA clane IMAGE:3689564 5	AV 754427 HTB Home seriens dDNA clone HTBBYE09 5'	Lower sections enormationaries associated PD1 (KIAA0757) mRNA	Trollic separates exemplates associated PD1 (KJA40757) mRNA	Homo septents throughout protein FLJ20477 (FLJ20477), mRNA	Total organical statements and the statement of the state
Top Hit Detabese Source	EST HUMAN	5	Т	EST HUMAN	EST HUMAN	TOT LE MAN	TA CENT IN THE PARTY OF THE PAR		, LN		EST HUMAN	LN.	EST HUMAN	ESI MUMAN	ESI HUMAN	TOLL TOWN	EST HUMAN	EST TICIMAN	EST HUMAN	EST HUMAN	5	z!	Z	LN L	ESI HUMAN	ESI HUMAN	ESI HUMAN	N.	Ę.	N.
Top Hit Acession No.		032150	-	1	١	0.0E+00 BE283328.1	35.792472.1	DON-NOW		5	1.	W69225.1	0.0E+00 AU130403.1	0.0E+00 AU130403.1		BF000018.1	0.0E+00 BE383165.1	0.0E+00 BE531263.1	0.0E+00 AA316723.1	0.0E+00 BE794884.1	0.0E+00 U36253.1	7000517 NT	0.0E+00 AF110783.1	0.0E+00 AB051828.1	0.0E+00 BE796376.1	0.0E+00 BE563433.1	A7724			8023441 N
Most Similar (Top) Hit BLAST E Value	0.0E+00 AI571737.1	0.0E+00	0.0E+00 AB037859	0.0E+00 E	0.0E+00 E	0.0E+001	0.0E+00 BE/924/2	0.01	0.0E+00 U78027.1	0.0E+00 AF1732ZI	0.0E+00	0.0E+00 M69225.1	0.0E+00	0.00+00				0.0E+00	0.0E+00	0.0E+00										0.0E+00
Expression Signal	2.08	2.19	4.95	1.02	1.02	2.55	4.92	1.51	121	6.55	1.22	1.08	2.22	222		1.25		2.57	4.21	5.57	3.83	1.33	1.78	1.27		3.48	1.18	2.25		121
ORF SEQ ID NO:	28072	28073	28077	28078	28079	28080		28096		28103	L	28107		28110		28115	28118			28169	28177	28178	28179	3 28181		4 28191	=	3 28194		4 28196
SEQ ID	15329	<u> </u>	I_	<u> </u>		15337		15352	15361	L	L	L	<u>l</u>	16371	L	15376	1 15377	3 15378	15432	3 15433	1	_	1_	l	15448	15604	15451	<u>L</u>	Ι'	15454
Probe SEQ ID NO:	2618	2619	2821	2822	2622	2625	2632	2841	2851	2652	2858	2639	2861	2661	2063	2688	2687	2868	2725	2726	2732	2733	2734	2736	2742	2745	2746	2748	274	2749

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Single Exon Probes Expressed in Brain	Top H# Descriptor	Homo septens hypothetical protein FLJ20477 (FLJ20477), mRNA	Homo sations hypertension-related calcium-requised gene mRNA complete cuts	AV651086 GLC Homo septens cDNA clone GLCC D073'	CM1-TN0141-260900-439-b08 TN0141 Homo sepiens cDNA	CM1-TN0141-250900-439-b08 TN0141 Homo sepiens cDNA	Homo saplens cerebellar dedensesson-related protein (3440) (CDR1) mRNA	Homo sepiens cerebeller degeneration-related protein (34kD) (CDR1) mRNA	801580803F1 NIH MGC 9 Homo septens cDNA clone IMAGE:3026472 5:	Homo saciens chromosome 21 segment HS210001	UI-H-BW1-enw-607-0-UI.st NCI CGAP Sub7 Homo sablens cDNA close IMAGE: 2071940 2'	Homo sapiens chardrollin suffate protectivem 4 (melanome-associated) (CSPQ4) mRNA	Homo septems and ordering (ANC) menu	Homo seciens and cocietin-3 (ANG-3) mRNA	602085579F1 NIH MGC 83 Hmm seniens cDNA chare IMAGE 4240005 F1	Homo sepiens protein troothe phosphatase recent have I (PTPRT) mena	AV725534 HTC Home series and Adona HTCCCAR.	AV725534 HTC Home sections con A close HTC Country 6"	au55604.y1 Sohneider febal brain 00004 Homo septems cDNA clone IMAGE-2518883 57 similar to	SW:R13A_HUMAN P40429 60S RIBOSCMAL PROTEIN L13A;	602071957F1 NCI_CGAP_Bm67 Hamo sepiens cDNA clane IMAGE:4214879 5	601450812F1 NIH_MGC_65 Homo septens cDNA clone IMAGE:3854642 5	AU131494 NT2RP3 Homo sepiens cDNA clone NT2RP3002672 5'	AU131494 NTZRP3 Homo sepiens cDNA done NTZRP3002672 5	600944794F1 NIH_MGC_17 Hamp saplens cONA clane IMAGE:2900806 5	600944794F1 NIH_MGC_17 Hamp septens cDNA clane IMAGE:2960906 5	glycoprotein D=Duffy group antigen (human, blood, Genomic DNA, 3068 nt)	Homo explans BTRCP2 mRNA for F-box and WD-repeats protein Isoform C. complete cds.	Homo sepiens ALR-like protein mRNA, perties cds	Homo sepiens ALR-like protein mRNA, partial cds	Homo seplens cytochrone P450, subfamily I (diodn-Inducible), potypoptide 1 (glaucome 3, primary Infantile) (CYP1B1) mRNA	Homo septens cytochrome P450, subfamily I (diodn-inducible), potypeptide 1 (glaucoma 3, primary infamile) (CYP181) mRNA	H. sepiens serine hydroxymethyltransferase pseudogene
gle Exon Pro	Top Hit Detebase Source	N F	Ž	EST HUMAN	EST HUMAN	EST_HUMAN	닏	F	EST HUMAN	2	EST HUMAN	Ę	L	LZ	EST HUMAN		FST HIMAN	EST HUMAN		EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST_HUMAN	EST HUMAN	EST_HUMAN	뉟	Z	N _T	Ā	5	5	Ę
Sin	Top Hit Acession No.	8923441 NT	I⇔	AV651098.1	BF377897.1	0.0E+00 BF377897.1	4757963 NT	ı	BE747183.1		BF514110.1	4503098 NT	7705275 NT	7706275 NT	10	7427522	0.0E+00 AV725534 1	0.0E+00 AV725534.1		0.0E+00 AI879163.1	0.0E+00 BF530661.1	3E872788.1		0.0E+00 AU131494.1	0.0E+00 BE300344.1	3E300344.1		81.1	50.1	50.1	4503202 NT	4503202 NT	
	Most Similar (Top) Hit BLAST E Velue	0.0E+00	0.0E+00 AF290	0.0E+00 AV651	0.0E+00 BF377	0.0E+00	0.0E+00	0.0E+00	0.0E+00 BE747	0.0E+00 AL 1632	0.0E+00 BF514	0.0E+00	0.0E+00	0.0E+00	0.0E+00 BF6776	0.0E+00	0.0E+00	0.0E+00		0.0E+00	0.0E+00	0.0E+00 BE8727	0.0E+00	0.0E+00	0.0E+00	0.0E+00 BE3003	0.0E+00 S76830	0.0E+00/	0.0E+00 AF2847	0.0E+00 AF2647	0.0E+00	0.0E+00	0.0E+00 X85980.
	Expression Signal	1.21	25	13.80	3.13	3.13	33.8	33.8	258	1.15	3.36	0.99	. 2.1	2.1	4.67	1.75	13.56	13.56		7.61	5.41	5.55	1.6	1.6	20.25	20.25	4.22	4.35	8.39	8:38	3.52	3.52	3.52
	ORF SEQ ID NO:	28197	28198		28199	28200	28203	28204	28209		28219		28227	28228	28229	28237	28239	28240			28245	28246	28247	28248	28240	28250	25634		26144	20145	26436	26437	28258
	Econ SEQ ID NO:	15454			15457				15465				15489	15489	15490	15496	15499			15501	15504	15505	15507	15507	15508	15508	12995	15515	13401	13491	13776	13776	15608
	Probe SEQ ID NO:	2749	2750	2751	2752	2752	2756	2756	2700	277.1	2772	2778	2784	2784	2785	2791	2794	2794		2798	2789	2800	2802	2802	2803	88	2808	2812	2818	2818	2822	2822	2840

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le Exon Probes Expressed in Brain	Top Hit Descriptor Source	VT Homo sepiens 5-eminolevulinate synthese 2 (ALAS2) gene, complete cds				VT Human AHNAK nucleoprotein mRNA, 5 end					T Homo sapiens zinc finger protein 221 (ZNF221), m-RNA	(T Homo sepiens zinc finger protein 221 (ZNF221), mRNA	IT Homo sepiens zinc finger protein 221 (ZNF221), mRNA	IT Homo septiens germme-cytoplasmic actin (ACTGP3) pseudogene	IT Homo septens germme-cytopleamic actin (ACTGP3) pseudogene			if Homo sepiers protocedherh sipha Ct (PCDH-sipha-Ct) mRNA, complete ods				T_HUMAN				HUMAN	T_HUMAN			Homo septens hHb5 gene for hair feerefin, exons 1 to 9		T Homo septens eukeryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA	In18407.x1 NCI_CGAP_Bm26 Homo saplens cDNA clone IMAGE:2167981 3' similar to TR;O16247
Single Exon Probes Expressed in Brain		NT Homo sapiens 5-eminolevulinate synt	NT Homo sepiens mRNA for KIAA1527 p	NT Homo saplens chromosome 21 segm	NT Human sodium channel mRNA	NT Human AHINAK nucleoprobath mRNA									INT Homo agolens germme-cytoplesmic	NT Novel human mRNA from chromosom	NT H.sapiens mRNA for nuclear DNA he	NT Homo sepiens protocedherin alpha C				T_HUMAN				١,	T_HUMAN	NT Homo aspiens chromosome 21 aegmi	INT Homo saplens chromosome 21 segme	NT Homo sapiens hHb5 gene for hair kern			
JIS	Top Htt Acessian No.	AF068624.1	AB040980.1	0.0E+00 AL163201.2	0.0E+00 M91803.1	M80902.1	BE154504.1	BE154504.1	X73428.1	AL16326		7019584 NT	7019584 NT	D50657.1	D50857.1	0.0E+00 AL096857.1	Y10658.1	AF152303.1	TN 0745034	4503470 NT	4507280 NT	0.0E+00 ALO47599.1	7661883 NT	7861883 NT	4503098 NT	BE081896.1	BE081896.1	0.0E+00 AL163206.2	0.0E+00 AL163206.2	0.0E+00 Y19210.1	4768279 NT	4503470 NT	
	Moet Similar (Top) Hit BLAST E Value	0.0E+00 AF068	0.0E+00 AB040			0.0E+00 M8090						0.0E+00																	0.0E+00		0.0E+00	0.0E+00	
	Expression Signal	1.34	1.22	281	2.63	1.94	1.29	1.29	1.18	2.59	1.03	1.03	1.03	18.48	18.48	1.69	7.2	1.42	47.87	47.87	2.36	1.06	0.97	0.97	2.96	5.48	5.46	2.09	2.09	4.18	1.33	20.94	707
	ORF SEQ ID NO:			28263	28266			28270		•	28272	28273	28274	28277	28278	28281			28282	28283	28282	28296	28297	28298		28300	28304	28312	28313		28321	28322	8000
	Bean SEQ ID NO:	15609				15622	15625	15625	15627	15628	15629	15629	15629	15833	15833	15636	15637	- 1	- 1	ı	15649	15652	15853	15853	15654	15857	15857	15864	15004	15671	15673	15674	1076
ſ	Probe SEQ ID NO:	2841	2843	2840	2862	7882	2857	2857	828	28 28 28 28 28 28 28 28 28 28 28 28 28 2	88	289	<u>§</u>	888 7888	888	8	28 28 29	287	2872	2872	88	8	2886	88	2887		88	2807	2897	8	<u>2</u>	88	8

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		1247									located to, 4	located to, 4	¥	Ę													Ţ	
Single Exon Probes Expressed in Brain	Top Hit Descriptor	ht18d07x1 NCI_CGAP_BIn25 Homo sapiens cDNA clone IMAGE:2167981 3' similar to TR:O16247 O16347 F44F7 2 PROTFIN	ZINC FINGER PROTEIN 132	Homo saplens protocatherin cemma CA (PCDH-cremma, CA) mBNA	Homo saplens mRNA for KIAA1287 protein partial cris	Homo sepiens mRNA for KIAA1287 protein, pertial cds	Homo saplens mRNA for KIAA 1508 protein pertial cds	Homo sepiens mRNA for KIAA1508 protein, pential cals	Homo sepiens KIAA0100 gene product (KIAA0100), mRNA	Homo septens KIAA0100 gene product (KIAA0100), mRNA	Homo septiens myeloid/fymphold or mbod-Inneage leukemie (#tithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA	Homo septiens myeloid/lymphold or mbœd-lineage leukemie (#rithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA	7n40d03.x1 NCI_CGAP_Lu24 Homo eapiens cDNA clone IMAGE:3567028.3' similar to TR:Q9VLN1 Q9VLN1 CG17283 PROTEIN :	7n40d03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3567028 3' similar to TR:Q9VLN1 Q9VLN1 CG17283 PROTEIN -	Homo sepiens melanoma entition family if 4 (44 ACCD4)DNA	Homo saciens melanoma anticen family R. 4 (MAGERA) TRNA	Homo saplens neurodn (NRXN3) mRNA	H. sepiens mRNA for M phase phosphoprotein 10	Homo sepiens mRNA for KIAA1208 protein, partial cds	H.saplens NF-H gene, exon 4	H.sapiens NF-H gene, excn 4	Homo seplens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6	4143109.X1 Source, testre_NHT Homo seplens cDNA clone IMAGE:1752809.3*	Home sections to Date & DATE & DATE & CONTRACT (PROAT) INCINA	Homo explains KIA A 0737 game annul at 7KVA A 0737	Homo sapiens calcium channel without demonstrate actions as to the 2000 contract	Homo sapiens celcium channel, voltace-dependent, cemme subsett (CACNES), micha	Home sentence DNA 4. MA 4. 464
JIS EXOII PIODS	Top Hit Detablesse Source	EST HUMAN O	Т	T				E IN					EST HUMAN Q										HOMAN					
JIIO I	Top Hit Acession No.	21		38.1			Γ	Γ	£ 83	T881903 NT	5174574 NT	5174574 NT	2.1	2.1	4505084	4505084 NT	4758827 NT		4.1			5.1	4508118	0.0F+00 ABOOABA 4	3	5729755 NT	5729766 NT	BO37852 4 NT
	Most Similer (Top) Hit BLAST E Value	0.0E+00 AI56100	0.0E+00 P52740	0.0E+00	0.0E+00,	0.0E+00	0.0E+00,	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 BF11070	0.0E+00 BF11070	0.0E+00	0.0E+00	0.0E+00	0.0E+00 XD8494.	0.0E+00	0.0E+00 X15309.1	0.0E+00 X15309.1	0.0E+00 AF10627	0.00-100 7414888	A DOF TOO	0.0E+00	0.0€+00	0.0E+00	0.0E+00 AB03785
	Expression	19:	1.63	201	1.92	1.02	4.56	4.58	3.58	3.58	3.21	3.21	1.16	1.16	2.15	2.15	1.00	96.0	2.38	5.56	90.58	\$ 5	12 5	2.85	1.52	3.75	3.76	1.1
	ORF SEQ ID NO:	28324	28326	28327	28339	28340	28341	28342	28345	28346	28347	28348	28352	28353	28364	28365	28370		28373	28374	0/297	0/007	28394	28395	28404	28406	28407	28412
	Exan SEQ ID NO:	15675	15677		15594	15894	15695	15695	15698	15698	15699	15699	15703	15703	15712	15712	15719	15720	15723	15724	42/01	45730	15746	15747	15757	15759	15750	15763
	Probe SEQ ID NO:	2909	2011	2912	2928	2028	2929	2828	2032	2882	2933	2833	2038	2838	2948	2946	2953	38	2967	80 S	8 28	200	2882	2081	2884	2983	2003	2887

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Moet Similar (Top Hit Acession Databese BLASTE No. Source	0.0E+00 4508882 NT Homo sacients semenogelin I (SEMG1) mRNA 0.0E+00 4508882 NT Homo sacients semenogelin I (SEMG1) mRNA	AF195953.1 NT	0.0E+00 5579469 NT Hamp sepiens heat shock 70kU prosent 1 (HSPA1A), IIINON	5579469 NT	AL359403.1 NT	0.0E+00 AF017433.1 NT Homo sapiens putative transcription recent characters 1M4 protein, JM5 protein, T54 protein,	ΓN	2.1 NT	TA	5.1	Z	18.1 N	0.0E+00 AF149773.1 NT	0.0E+00 7862139NT	0.0E+00/AF042076.1 N.I	0.0E+00 4826783	0.0E+00[L20941.1 NT	0.0E+00 AB011121.1	0.0E+00 AB011121.1	0.0E+00 T94870.1 EST HUMAN	0.0E+00 BF243336.1 EST_HUMAN	0.0E+00 X98022.1 NT	0.0E+00 X98922.1 NT	0.0E+00 4758627 N1	0.0E+00 4758827/N1	0.0E+00 4504658 N I	0.0E+00 MZ8698.1	0.0E+00 4502098 NT	0.0E+00 4758055 NT
	0.0E+00	0.0E+00 AF	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AF	O OF+00 AF	0.0E+00 AF	0.0E+00 X	0.0E+00 AF	0.0E+00 AF	0.0E+00 A	0.0E+00 AI	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 A	0.0E+00.A	0.0E+00 T	0.0E+00 B	0.0E+00 X	0.0E+00 X	0.0E+00	0.0E+00		0.0E+00.0	}	
Expression Signal	0.71	4 62	3.74	3.74	5.88	1.8	8	140	28	25.	1.72	3.2	7.83	3.42	121	3.74	26.91	1.32	1.32	8.83		4.39	4.39	1.31	1.31		3.25	1.96	
ORF SEQ ID NO:	28445		28454	28455	2	28460		20475	28483		28490					28547			28560	28567			28592		28802		1 28626	28628	
Exan SEQ ID NO:	45700		15808	18	15000	15815	3	01001	10002	15845	15840	1_	1.	L	L	<u> </u>	1.		15914	15921	١.	L	1	L	L	<u> </u>	15974	15977	t
Probe SEQ ID NO:	333		3 2	3 6	3 8	8 8				2000	3 8	310	3105	3110	3111	38	3148	3151	3161	3158	3172	3178	3478	3187	3187	3195	뛇	3214	322

PCT/US01/00667

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	Top Hit Descriptor	VIO-CORDINATION CONTRACTOR OF THE CONTRACTOR OF	Homo sapiens CREB binding protein (Rubinstein-Tayla syndrome) (CREBOT) IIINNA	ae67b11.s1 Stratagene schtzo brain S11 Homo septens cDNA done invast.str 1.55 5	Home seniors and california protein 1 mRNA, complete cds	Lance services envisability binding trobein 1 mRNA, complete cds	Homo services (fibrillin 1 (Martier syndrome) (FBN1) mRNA	William Market	HOTTO SECRETA LEGIC (1117) THE CO.	(Tutination in the control of the co	Homo sapiens HLA dates in region contenting to meaning. Indicately, RD, complement factor B hydroxylase (CYP21B), complement factor B hydroxylase (CYP21B), complement factor B hydroxylase (CYP21B), complement factor B	(Bf), and complement control and C2 (C2, garren).	THO SECURIS VALVE AND AND AND AND AND AND AND AND AND AND	HOTIO SERVEIS CLAND TO THE PROPERTY OF THE PRO	Homo septens NiANV44V (Novem (NiANV4))	HOMO SEPRETS A MINESO (1144) STATES PROTECTION (1444PA) THRNA	Homo septens A kingsol (1705) Fixed Common 270 mRNA, partial cds	Homo septens on Ford Company FI PAGES (FL 20895), mRNA	HOMO BADION IN TOWN OF THE WAY IN	Hamp septents update to the control of the control	Consequence of Indian Property 24 (GPR24), mRNA	Homo septents of process control country of the septents of the IMAGE: 2222535 3' striller to SW:RL11_RAT	P25121 60S RIBOSOMAL PROTEIN L11. ;contains Alu repetitive element;	Homo sapiens retornerase retrained transcripture (TERT) cene, exche 1-8	Homo septems taken are reversed transfer than the september of the septemb	HOMO Septens Inclined and Applications of the Company of the Company (HUNK), mRNA	Homo saprens municipally type of the process (CASP8) mRNA	Trans secreta carpeas & anotherisareleted crateine protesse (CASP8) mRNA	HOMO Sapidais deliptado U, apopuesto montro de la completa del completa de la completa de la completa del completa de la completa del la completa del la completa de la completa de la completa de la completa de la completa de la completa de la completa de la completa de la completa de la com	Figure Saperis Lynn (min. 17) yours, company perfect class.	Home saplens mind to the first promise CDNA clone IMAGE:3868246 5	COLHAMA AT NOT COAP GCS Hamp saciens CDNA clone IMAGE 2305279 3' similar to TR:Q91929 Q91929	ZINC FINGER PROTEIN. : ALI 123664 NTZRMZ Horro sepiens cDNA clone NTZRMZ000735 5	
	Top Hit Database	Source		H LI MAN	TOMO!																HOMAN		EST HUMAN F	_							丁	EST HUMAN		EST HOWAN
	Top Hit Acession	oj Z	TN 9208574	ļ	2	1	0.0E+00 AF286598.1	4557590 NI	4507720	1		13.1	oo i	7862125 NT	7662125 NT	4502014 NT	4502014	98.1	8023624 NT	7657038 NT	0.0E+00 AA994842.1	4885312 NT	0.0E+00 AI589294.1	93.1	I SQL	ı			4502582 NT	AF111163.1	AB040940.1	0.0E+00 BE779039.1	0.0E+00 AI632650.1	0.0E+00 AU123664.1
+		Value	00+100	3	0.0E+00 AA//4/	0.0E+00	0.0E+00.0	0.0E+00	0.0E+00	0.0E+00 M65189		0.0E+00 AF0194	0.0E+00 AF0550	0.0E+00	0.0E+00	0.0€+00	0.0E+00	0.0E+00 AF2652	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AF1288	0.0E+00 AF128					0.0E+00 AF111	0.0E+00 AB040	0.0E+00		0.0E+00
	 8	Signal	900	200	3.07	5.43	5.43	1.36	1	5.8		1.28	3.96	1.11	1.11	2.08	2.00	225	1.17	122	1.00	1.18	1.89	2.33	233	1.22	1.22	127	1.27	9.77	1.28	0.84		4.44
+	a	Ö Q	-	7803/	28638	28646	28647	28653	28661			28008		28672			L		L		28710		86786										28767	Ц
}	E CO	Ş Ş Ş Ş		15983	15985	15993	15993	16004	19010	1	`]	16018	.	1	16073	1.	L	L	L	١	1	1 .	1 an 7 a		1.	1	L	1_	L	L	1	1	2 10112	Ш
	Probe			3220	3222	3230	3230	3242	3248	3265		3258	3258	33	S S	2260	3200	3285	3288	3297	3300	3308		32.10	3 8	3377	3327	33.20	32.00	i E	388	3342	3352	3391

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<i>y</i> (1/3/2/3	_	7-	-	, -	_	_	_	_	_	- -	_			1.5		_ =			7-	-	_	r	Ų I	/ <u>L</u>	20	1//	nÃ	06/
olingie Exuli Probes Expressed in Brain	Top Hit Descriptor	Homo saplens offschory receptor, family 10, subfamily C, member 1 (OR10C1), mRNA	Homo sapiens offactory receptor, family 10, subfamily C, member 1 (OR10C1), mRNA	Homo sapiens neuroblestorne-emptified protein (LOC5/594), mRNA	Homo sapiens T-type calclum channel alpha f subunit Alphari Le isoform (CACNA1) mRNA commisse exe	MR1-SN0033-100400-001-c08 SN0033 Hamo sapiens cDNA	Homo sapiens KIAA0952 protein (KIAA0952), mRNA	Homo sepiens KIAA0952 protein (KIAA0952), mRNA	Homo saplens beaded filament structural protein 1, filensin (BFSP1) mRNA	Homo sepiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2 (LiLRA2), mRNA	Homo saplens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds	Homo septens death receptor 6 (DR6), mRNA	Becteriophage P1 replication region including repA, perA, and perB genes and incA, incB, and incC incommentally determinants	Homo saplens protein tyrosine phosphatase, recenter type T (PTPRT) mRNA	wp14d10.x1 NCI_COAP_LL(19 Homo sapients cDNA clone IMAGE:2464819.3' similar to TR:073634 073634 NEURAL CELL ADHESION MOLECULE:	Wp14410.x1 NCI_CGAP_Lu19 Homo septens cDNA clone IMAGE:2464819 3' similar to TR:073634 073634 NEURAL CELL ADHESION MOLECULE:	Homo saplens mRNA for putative envolun-evest containing protein (ORF1)	Hamo sapiens w/os FBJ murtne osteosercome virel ancogene homotog (FOS) mRNA	Homo sepiens v-fos FBJ murine ostecearcoms viral choogene homolog (FOS), mRNA	Human endogenous retrovirus HERV-K10	Human MDS1A (AML1MDS1 fusion) mRNA, pertial cds	Homo expiens hypothetical protein (AF038169), mRNA	Homo sapiens hypothetical protein (AF038169), mRNA	Homo sepiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds	Homo saplene cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds	Hamo sepiens chramosome 21 unknown mRNA	601143853F1 NIH_MGC_15 Hamo septens aDNA clone IMAGE:3051373 5	801143853F1 NIH_MGC_15 Hamo explens cDNA clans IMAGE:3051373 57	Homo sapiens potassium voltage-gated channel, isk-related family, member 2 (KCNE2) mRNA
JIB EXOLI PIOL	Top Hit Database Source	K	Į.	LN LN	NŢ	EST HUMAN	1	NT.	LN	¥	LZ.	N	Į	L	T HUMAN		Т			TN						NT	EST_HUMAN	T_HUMAN	
	Top Hit Acession No.	7363436 NT	7363436 NT	T706239 NT	0.0E+00 AF211189.1	0.0E+00 AW867015.1	7662401 NT	7862401 NT	4502398 NT	5803067 NT		7857038	•	7427522	0.0E+00 Al835158.1	0.0E+00 Al835156.1	0.0E+00 AJ278120.1	6562332 NT	6552332 NT	1	.1	9558718 NT	9558718 NT					0.0E+00 BE304791.1	4828795 NT
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AF11076	0.0E+00	0.0E+00.K02380	0.0E+00	0.05+00	0.05+00	0.0E+00/	0.0E+00	0.0E+00	0.0E+00 M14123	0.0E+00 U43293	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00/	0.0E+00	0.0E+00	0.011+00
	Expression Signal	96.0	98'0	1.36	1.42	00.0	1.68	1.66	1.34	5.37	1.75	24	5.47	£.	3.54	3.54	2.48	1.82	1.82	1.31	5.4	1.18	1.18	1.84	1.84	1.12	221	224	0.92
	ORF SEQ ID NO:				28811			28825	28826	28827	28179	28840	28844	28846	28853	28854	28859	28868	28869	28874	28880	28884	28885	28890	28861	28898	28805	28008	28606
	Exem SEQ ID NO:	16156		16159	16150	16164		16175	16178	16178	15441	16191	16194	16196	16204	16204	16208	16215	16215	16220	16226	<u>\$</u>	16231	16235	16235	16241	16252	16252	16255
	Probe SEQ ID NO:	3398	3398	3401	3402	3408	3418	3418	3419	3421	3430	3435	3438	3440	3448	3448	3452	3459	3459	8 20 20	34.70	3476	3475	878	3479	88	8 8 8	800	3498

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Single Exon Probes Expressed in Brain	Exam ORF SEQ Expression (Top) Hit Top Hit Acession No. Signal Value Source	16280 28914 0.89 0.0E+00 A1384007.1 EST_HUMAN CO0468 MYASTHENIA GRAVIS AUTOANTIGEN GRAVIN:	N	28940 1.29 0.0E+00 AV701969.1 EST HUMAN	28941 0.85 0.0E+00 4506884 NT	1.74 0.0E+00 AF078888.1 NT	28945 1.49 0.0E+00 AL133204.1 NT	28948 1.21 0.0E+00[AB040909.1 NT	28963 1.37 0.0E+00 6997248 NT	1.37 0.0E+00 6997248 NT	0.0E+00 A1081907.1 EST HUMAN CE13742:	0.0E+00 6325463 NT	T HUMAN	0.78 0.0E+00 AF118848.1 NT	28976 6.46 0.0E+00 BF678383.1 EST HUMAN	28988 0.9 0.0E+00 AW937977.1 EST HUMAN	28996 0.74 0.0E+00 BF672054.1 EST_HUMAN	28007 0.74 0.0E+00 BF672054.1 EST_HUMAN	0.95 0.0E+00 4828867 NT	28999 1.08 0.0E+00 AW664693.1 EST_HUMAN	20000 1.08 0.0E+00/AW664693.1 EST_HUMAN	29004 1.42 0.0E+00 4828763 NT	28007 0.83 0.0E+00 7662319 NT	29015 0.82 0.0E+00 4557752 NT	29016 0.82 0.0E+00 4557752 NT	29030 2.67 0.0E+00[D87327.1 NT	33.2 0.0E+00 7889491 NT	29049 2.6 0.0E+00 AB028542.1 NT	29051 3.38 0.0E+00 AF124250.1 NT	29052 3.38 0.0E+00(AF124250.1 INT	29061 1.85 0.0E+00 AL163204.2 NT	29062 1.86 0.0E+00/AL.163204.2 NT	29085 1.62 0.0E+00 AW851714.1 EST_HUMAN	
											7		+	1																				
														6 16331	Ш							_	┙	_	1		_1			[1 16424	
	Prabe SEQ ID NO:	3504	3507	3529	3530	3531	3539	3542	3561	3661	3562	3564	3569	3576	3577	3589	3603	3603	388	88	3808	808	3611	3624	882	3638	3642	3668	88	3000	3668	3968	3671	

Page 496 of 536 Table 4 Single Exon Probes Expressed in Brain

					·																						•	8							
	Top Hit Descriptor	metallox observable (Membrane inserted) (MMP24), mRNA	HOUTO Septembria for KIAA0706 protein, partial cds	Trong services mRNA for KIAA0910 protein, partial cds	Train services mRNA for KIAA0910 protein, partial ods	Lines entene KIAA0670 protein/achus (KIAA0670), mRNA	TAIN SECTION IN THE PROPERTY OF THE PRINCE O	Harro septions N. Control Can Subs Hano septions CDNA done IMAGE:2733022 3	UH-BW0-als-6-12-0-UI-s1 NCI CGAP Sub6 Homo sapiens cDNA clone IMAGE:2733022 3	Particular of Spares Nin-HMPu S1 Homo sepiens cDNA clone IMAGE:812495 6' similar to	SW.KRB4 SHEEP P02445 KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIIB4. [1];	Home septens minute for influence promoting discouration POM121 (POM121L1), mRNA	HOMO SAIDIBLE TO LAKA 4444 Protein Partial CAS	Homo explens mixing to the promit, parties and the promiting many and the promiting to the	Homo septems Kirkhubos yang product (Karanga) mana	Homo septers moderne process of the September of the Page of Care of the many many in the september of the s	Homo sepietrs viols awai in ya conserved with FOR concerns related (ERG), mRNA	Hono sepiens viets awar erymonastices with Let any any complete cels	Homo saplens DNA memeron repert process (mic. 15) gard.	Pan inglocytes dilatura i received (in the party of power (POM121 (POM121L1), mRNA	Hamo septiens strate to ter integral membrane discoprotein POM121 (POM121L1), mRNA	Home services RABS member RAS choosene family (RABS) mRNA	Mis mecalus (unctophilin 1 (Jp1-pending), mRNA	1e62f10_x1 Source NFL_T_GBC_S1 Homo explens cDNA clone IMAGE:20913073	Home seniens protocadinarin beta 3 (PCDH-beta3) mRNA, complete cds	Homo sections desmonletin (DPI, DPII) (DSP) mRNA		Homo sepiens ATP-senetive invertily rectifying K-channel subunit (KCNJ6/BIR1) gene, compress cus	Homo sepiens methy CPG binding process 2 (MLC) 2), im co.	Homo sepiens KIAA0569 gene product (KIAA0569), miraya	Homo sepiens myosin light chain kinase isoform 2 (MLCX) mixing, compress one	Homo eaplens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds	Hamo sapiens gene for TMEM1 and PWP2, complete and partial ods	Hamo saplens gene for TMEM1 and PWP2, complete and partial cds	
	Top Hit Database Source								Т	ESI HOMAIN	EST HUMAN	NT NT	Z	NT NT	Ę	K	Z	Į,	N	۲	Σ	EN!	Z	COT LIMAN	10 10 E	Į.	- 2	ź	INE	IN S	LN	į	2 5	F N	
	Top Hit Acession No.		729028	Z.	-		7662237 NT	8		0.0E+00 AW 298134.1	0.1	0.1	7657468 NT	0.0E+00 AB037835.1	7862183 NT	4506718 NT	TN 5807287	TN 2867065	NF195658.1			7857488 NT	4759011 N	1018113801	AI3//088.1	0.0E+00 AF152496.1	1/081897A	S78685.1	7710148 NT	TM82/83/NT	15	ALVOSOULA	0.0E+00 AF-00001.4	0.0E+00 AB001523.1	ADV 10km.1
-	<u> </u>	A seuce	0.0E+00	0.0E+00 AB018339	0.0E+00 AB020717	0.0E+00 AB02071	0.0E+00	0.0E+00	0.0E+00	0.0E+00 A	0.0E+00	0.0E+00 AB02071	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AF1956	0.0E+00 AF1797	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AI3//08	0.0E+00	0.0E+00	0.0E+00 S78685		1	1		1	١	
	Expression Signal		1.53	1.81	1.1	1.1	22.21	22.21	4.35	4.35	9.1	1.14	3.31	0.82	6.4	4.20	1 08	108	0.71	2.88	2.3	2.3	1.24	1.01	1.01	1.97	1.14	10.39					1.23		0.97
	ORF SEQ ID NO:	-	29067	29069	23071	23072	23074	28075		29085	20105									20185			29193	29194	1 29197	100	3 29198	COCCE	1						0 29214
	SEQ ID	į	16426	1	L	16430	1_	L	1_	\mathbf{l}_{-}	18487		L	1	1	L		┙	10000	┸	上				16584	3 16565	16568	<u> </u>	_L			4 16576	16576	!	39 16580
	Probe SEQ ID	į	25.73	3875	3877	3677	25,70	3670	3882	3692	2744	2748	37.10	3/2	37.50	3/4/2		200	3/91		3904	3804	3808	3808	3812	3813	3814		3818	3819	3820	3824	3824	3820	3829

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	Homo septens transferrit receptor potential channel 5 (TRPC5), mRNA	Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA	Homo saplens chromosome X open reading frame 5 (CXORF5) mRNA	Human zinc finger protein ZNF134 mRNA, complete cds	Homo sepiens intersectin short Isoform (ITSN) mRNA, complete cds	Homo septions potessium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA	Homo saplens familial mental retardation protein 2 (FMR2) gene, expn 11	Homo saplens SC35-Interacting protein 1 (SRRP129), mRNA	Homo sapiens emphiphysin gene, pertiel ods	W601f01.X1 NCI_CGAP_Lym12 Homo septems cDNA cione IMAGE:2411065.3' similar to TR:O43340 O43340 R29830. 2 : contains element PTR7 requiring element.	Homo eaciers ribosomal protein S8 (RPS8), mRNA	DKFZp434N0413_11 434 (synonym: htes3) Homo septens cDNA clone DKFZp434N0413 5'	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA	Homo sepiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA	Homo sepiens glutamate receptor, metabotropic 3 (GRMS) mRNA	Homo saplens melanome entigen, family B, 1 (MAGEB1) mRNA	Homo septens HBP17 heparin-binding and FGF-binding protein gene, complete ods	Homo septens ryanodine receptor 3 (RYR3) mRNA	Homo septens zinc finger protein (KIAA0412) mRNA	RC3-HT0880-170800-011-412 HT0880 Homo sepiens oDNA	WXRA5 Human matrix tissue expression library Homo sapiens cDNA clone incyle 1996725 similar to MXRA5 Matrix remodeling associated gene 5	MXRA5 Human matrix tissue expression library Homo septens oDNA clone tnoyte 1996723 similar to MXRA5 Metrix remodeling associated case 5.	Homo eaplens F-box protein Fb3b (FBI.3B) mRNA, bertiel pds	UI-H-BI3-alth-g-07-0-UI.st NCI CGAP Sub5 Homo sepiens cDNA clone INAGE 2736949 3	601236068F1 NIH_MGC_44 Hamo septens cDNA clane IMAGE:3808800 5	PMS-LT0031-100100-003-h09 LT0031 Homo sapiens cDNA	Homo sepiens Iduronate 2-sulfatese (Hunter syndrome) (IDS), transcript variant 1, mRNA	601193827F1 NIH_MGC_7 Hamo sepiens cDNA clone IMAGE:3537774 5	601193827F1 NIH_MGC_7 Hamo saplens cDNA clone IMAGE:3537774 5	Human G2 protein mRNA, partial cds
gle Exon Prol	Top Hit Dakabase Source	Z	N.	N-1	LN TN	IN	Ę	IN	Ę	Į.	EST HIMAN	.1	EST_HUMAN	Z	F	FZ	Ę	NT	NT	TN	EST HUMAN	EST HUMAN	EST HUMAN	Z	EST HUMAN	EST HUMAN	EST_HUMAN	Ę	EST_HUMAN	EST_HUMAN	5
Sin	Top Hit Acesston No.	6912735 NT	4503178 NT	4503178 NT	J09412.1	0.0E+00 AF114488.1	4826783 NT	AF012615.1	4759171 NT	17.1	7.4	4506742	38.1	6005887	6005887 NT	4504138 NT	4505078 NT	↽	4506758 NT	4585642 NT	0.0E+00 BF355295.1	0.0E+00 AW888221.1					740.1	5360215	98.1	98.1	-
	Most Similer (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00 U09412.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AF0991	0.0E+00 AI8647	0.0E+00	0.0E+00 AL0403	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AF1494	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.05+000	0.0E+00	0.0E+00/	0.0E+00	0.0E+00 AW580	0.0E+00	0.0E+00	0.0E+00 BE2649	0.0E+00 U10991
	Expression Signal	1.12	6.16	6.18	4.04	0.69	2.96	1.05	1.43	0.74	2.16	424	1.35	1.28	1.28	3.22	1.82	1.18	1.2	1.47	1.18	1.05	1.05	1.82	+	281	0.92	2.40	96.0	96.0	1.42
	ORF SEQ ID NO:	28216	ZZZ8Z	82282	28226	12282	28220	28232		29235	20244	29248	29251	20256	29257	29259		29263	28273	29277	29286	29288	29289	29295	20208	28303	28311	20312	28313	29314	20330
	<u>w</u> _			16586	L	16589	16692			16598	16606	16809	16612	16617	16617	16619	16621	16825	1883	19838	18846	16648	10048	18654	16657	16862	16670	16672	16673	16673	18702
	Probe SEQ ID NO:	3831	3835	3835	3837	3838	3841	3844	3845	3847	3856	3829	3862	3867	3867	3869	3871	3875	388	3888	3898	3898	3898	3904	3907	3912	3920	3922	3923	3923	3952

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	Top Hit Descriptor		Human G2 protein mRNA, partial cds	Human Gz protein mRNA, partiel cos	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds	Homo aacients cancer-testis antigen CT10 (CT10) gene, complete cds	Human MHC class II lymphocyte artigen DPw4-beta-2 pseudogene, excn 2	Lorns earliese chermosome 21 sections HS21C103	Now Termen days mencha to chambe 20	Lower change change of segment HS210084	Comparation of the Comparation o	Library envisors envisoration translation elongation factor 1 alpha 1 (EEF1A1) mRNA	TAIN CALLAND COR LAND Serviews CONA Clone IMAGE: 2244734 3' similar to TR: 060309 060309	KIAA0563 PROTEIN:	Homo saplens KIAA0569 gene product (KIAA0569), mrvva	Human zinc finger protein Zur 133	x201e10.x1 NC_CGAP_Luz4 Homo septents duty due introduced cos	Chicrocebus sections mixing for increase this associated antidento protein (IRNA48 gene)	Home explens mixiva to Olda suppliessor in the Company of the Comp	Homo sapiens mRNA for KIAA0316 protein, per tale cus	Homo sapients criticities in a service of the complete ods	Homo septents myetin versiculpuoli sector ilinin (ilinin omisee mRNA for mee-2 (repe dene)	Homo services mRNA for rape-2 (rape gene)	Home servious retirnoblestome-binding protein 4 (RBBP4) mRNA	Home serieus retinoblestorne binding protein 4 (RBBP4) mRNA	Home saviens G probain-coupled receptor 21 (GPR21), mRNA	Homo seniens mRNA for KIAA0287 gene, pertial cds	Home septens res GTP are activating protein-like (NGAP) mRNA	Home series IMP (mosine monophosphate) dehydrogenese 1 (IMPDH1), mRNA	No. 1 kinner mRNA from chromosome 1, which has eimiterties to BAT2 genes	Home series DGCR8 (DGCR8) mRNA, complete ods	Home earliest profess. X-tirked (PRKX) mRNA	Home series protein kinese, X-Inked (PRKX) mRNA	Homo saciens butyrophilin, subfemily 3, member A2 (BTN3A2), mRNA	Home sepiens GA-binding protein transcription factor, eighe subunit (80kD) (GABPA), mRNA	
-	Top Hit Database	Source	TN.	Ę								i i	Z	EST_HUMAN	7662183 NT	NT	EST HUMAN	F	LN.	Ļ.	Ę	뒫	Į,	I L	2	I. I.	T.	L L	121	2	2	Z	N.	121	17/2	I NI
	Top Hit Acession	ď Z	-	Į	- 1	T	Ę,					0.0E+00 AL163288.2	4503470 NT	1057076.1	7662183	109366.1	0.0E+00 AW339490.1	0.0E+00 AB015610.1	0 0E+00 AJ238617.1	0.0E+00 AB002314.2	0.0E+00 AL163203.2	0.0E+00 AF036943.1	0.0E+00 AJZ77Z76.1	0.0E+00 AJZ//2/6.1	5032020IN	5032020 IN	4883300 IN	AB006625.1	100014	1141929/ N	0.0E+00 AL096857.1	0.0E+00 AF165527.1	482894/IN	N /80797	IN COURTORS	
-	_	BLAST E Value	0 OF +00 U10991.	14004	0.05.00	0.05+001	0.0=+00	0.0E+00 MZ381U.	0.0E+00 AL16330	0.0E+00	0.05+00	0.0E+00/	0.0E+00	0.0E+00.A(85707	0.0E+00	0 OE+00 U08366	0.0E+00	0.0E+00	00F+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00			0.0E+00					١		0.0E+00
- - - -	8	Signal	C# 1		74.	80.4	66.4	4.30	5.74	1.35	3.22	1.71	27.98	, 7.	297	2.85	0.95	6.33	22	- R	8	1.18	2.65	2.65		•					1.94					1.08
	ORF SEQ	Ö Ö Ö	9	2000	28341	28344	28345			29359	28361	28369			20082				1	20418		L		29422		29430				3 29445	20446	3 29453				2 29469
	0 t	NO.	70000	10/02	16702	16706	16706	16715	16717	18724	<u> </u>	16735		1	16750	L	10/02			10//0	L		1_	16793	16799	L	16813	16814	16817	L	16819	L		13867		16842
				3952	3952	3967	3957	3968	3968	3975	3979	3987	000		4003	3	400	1007	224	4033	404	4047	4048	4048	4054	4054	200	4070	4073	4074	4075	4082	9	4091	409	4080

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17012 4.32 0.0E+00 U14520.1 NT 17024 20850 1.35 0.0E+00 G450846 NT 17030 20867 0.76 0.0E+00 G58384 NT 17030 20868 0.78 0.0E+00 G50384 NT 17030 20868 0.78 0.0E+00 G50384 NT 17034 17036 0.0E+00 G50394 NT		SEC 1D 1D NO: NO: 10842 29476 10855 29483 10855 29483 10857 29486 10857 29486 10857 29486 10857 29486 10857 29486 10857 29486 10857 29486 10857 29486 10857 29486 10857 29486 10857 29514 10896 29537 10896 29537 10906 29538 177002 29638 177002 29638 177002 29638 177004 29638 1770	Signal 1.08		4503854 4503854 177.1 177.1 177.1 177.1 1778.1 8922466 8922466 8922466 8922466 8922466 8922466 8922466 8922466 8922466 8922466 8922466	SOURCE THUMAN THUMAN ST HUMAN ST HUMAN ST HUMAN ST HUMAN ST HUMAN ST HUMAN ST HUMAN	Homo sapiens GA-binding proben trenscription factor, alpha subunit (60kD) (GABPA), mRNA Homo sapiens mRNA for KIAA0835 proben, partial cds wudddo4x1 NQT CGAP_GCB Homo sapiens cDNA clone IMAGE:2515975 3' wudddo4x1 NQT CGAP_GCB Homo sapiens cDNA clone IMAGE:2515975 3' Wudddo4x1 NQT CGAP_GCB Homo sapiens cDNA clone IMAGE:2615975 3' WUDddo4x1 NQT CGAP_GCB Homo sapiens cDNA clone IMAGE:2615975 3' WRT-HT0707-100500-001-402 HT0707 Homo sapiens cDNA WRT-HT0707-100500-001-402 HT0707 Homo sapiens cDNA WRT-HT0707-100500-001-402 HT0707 Homo sapiens cDNA WRT-HT0707-100500-001-402 HT0707 Homo sapiens cDNA WRT-HT0707-100500-001-402 HT0707 Homo sapiens cDNA WRT-HT0707-100500-001-402 HT0707 Homo sapiens cDNA WRT-HT0707-100500-001-402 HT0707 Homo sapiens cDNA WRT-HT0707-100500-001-402 HT0707 Homo sapiens cDNA WRT-HT0707-100500-001-402 HT0707 Homo sapiens cDNA WRT-HT0707-100500-001-402 HT0707 Homo sapiens cDNA WRT-HT0707-100500-001-402 HT0707 HT0408 (FLJ10498), mRNA Homo sapiens nycotherical probein FLJ10498 (FLJ10498), mRNA Homo sapiens hypotherical probein FLJ10498 (FLJ10498), mRNA Homo sapiens hypotherical probein FLJ10498 (FLJ10498), mRNA Homo sapiens hypotherical probein FLJ10498 (FLJ10498), mRNA Homo sapiens hypotherical probein FLJ10498 (FLJ10498), mRNA Homo sapiens probein B-100 mRNA, complete cds WRZ-DT0002-080300-004-408 DT0023 Homo sapiens cDNA Homo sapiens repolitorycein B-100 mRNA, complete cds PNZ-DT0002-080300-004-408 DT0023 Homo sapiens cDNA Homo sapiens repolitorycein B-100 mRNA, complete cds PNZ-DT0002-080300-004-408 DT0002 MRDS) mRNA Homo sapiens F-box probein FB-4 (FBL4) mRNA Homo sapiens F-box probein FB-4 (FBL4) mRNA Homo sapiens repolitorycein B-100 mRNA, complete cds putz-2010-072-080300-004-408 DT002-090490-40-2010-40-40-40-40-40-40-40-40-40-40-40-40-40
17024 20650 1.35 0.0E+00 4505846 IN I 17030 22667 0.76 0.0E+00 6563384 INT 17030 22658 0.78 0.0E+00 6563384 INT 47030 22668 0.78 0.0E+00 6563384 INT 47030 22668 0.78 0.0E+00 INT		915 912	4.32]]	U14520.1	<u> </u>	Human CBFA3 (Cbfa3) gene, parties ods Huma sacions procedula convertase subditish/kedn type 2 (PCSK2) mRNA
17030 29057 0.76 0.0E+00 6563394 N1 17030 28058 0.76 0.0E+00 6563394 NT 4.7703 0.0E+00 U10991.1 NT	1_	<u> </u>			4505846	LN.	Home septens propriet carveriage substant report by a company and an ambient profession (PRKCN), mRNA
17030 23058 0.78 0.0E+00 6563364[NT 47728 200544 1.58 0.0E+00 U10991.1 NT	1_					NT	Home septens protein reness of nu (Franch), mind of
477020 20084 1.58 0.0E+00[U10991.1 NT	Ŧ				6563384	NT	Homo eaplens protein kinase C, nu (mrncha), manan
	1				U10001.1	N.T	Human G2 protein mKNA, paruar cos

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Table 4

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	Homo septens ATP-sensitive inverdiy rectifying K-channel subunit (KCNJ&BIR1) gene, each	Homo sepiens pyrh (MEFV) gene, complete cds	Homo sepiens pyrin (MEFV) gene, complete ods	Homo septems zinc finger protein 195 (ZNF195), mRNA	Homo sepiens syncytin precursor, mRNA, complete cds	Homo sepiens protoceditierin genume C3 (PCDH-genime-C3) mRNA, complete cds	Homo septens zinc finger protein 211 (ZNF211), mRNA	Homo sepiens eukenyotic transletion ekongation factor 1 alpha 1 (EEF) 41) mRNA	Homo septens (ow density licoprotein recentor-related protein 6 (LRP6) mRNA and translated numbers	Homo sapiens chandratin sulfate profesolivaen 4 (melanama-associated) (CSPC4) mRNA	Homo explens calclumical modulin-decembent profesh (cheese IV (CAMKA) mRNA	Homo sepiens idurante sulphate sulphatese (IDS) gene, complete cds	Homo saplens KIAA0390 gene product (KIAA0390), mRNA	Homo septems KIAA0390 gene product (KIAA0390), mRNA	Homo septens PTEN (PTEN) gene, excris 3 finough 5	Homo sepiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)	Homo septens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)	2018008.81 Strategione fetal retire 037202 Homo sentene cDNA Adme IMACE encosts 2	Homo seplens odz (odd Ozfen-m, Droscohila) homolog 1 (ODZ1), mRNA	Homo sepiens cirromosome 21 segment HS21C084	y92b01.s1 Source, pined, gland, N3HPG Homo suplens cDNA clone (MAGE:231721.3)	y92b01.s1 Sceres_pined_gland_NSHPG Hamo septens aDNA done IMAGE:231721.31	Homo sepiens cyclophilin-related protein (NKTR) gene, complete cds	Homo saplens chromosome 21 segment HS21C100	Homo sapiens gene for netrituretic protein, pertial cds	Homo sepiens learatin 18 (KRT18) mRNA	Homo sepiens leradin 18 (KRT18) mRNA	Homo sepiens inwardly-recitiving potessium channel Kir2.1 (KCNJ2) gene, excn 2 and complete cds.	Homo sapiens inwardiy-rectifying potassium channel Kir2.1 (KCNJ2) gene, excn 2 and complete cds
le Exon Prob	Top Fitt Database Source	ŢN	IN	Į.	F	Į.	Ę										Ę	<u> </u>	T HUMAN	ı		EST_HUMAN	EST HUMAN	F	12				<u>-</u> -	TN TA
Siiv	Top Hit Acesston No.	0.0E+00 S78684.1	83.1	83.1	FN 5265000	61.1	37.1	5454175 NT	4503470 NT	4505016 NT	4503098 NT	4502656 NT	-	7862091 NT	7862091 NT	1	8.1	18.1	72.1	7657410		1			0.0E+00 AL163300.2		4557887 NT	4557887 NT	19.1	10.1
	Most Similar (Top) Hit BLASTE Value	0.0E+00	0.0E+00 AF1111	0.0E+00 AF1111	0.0E+00	0.0E+00 AF2081	0.0E+00 AF1523	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 1.35485	0.0E+00	0.0E+00	0.0E+00 AF1433	0.0E+00 AJ2454	0.0E+00 A.12454	0.0E+00 AA1740	0.0E+00	0.0E+00 AL16328	0.0E+00 H92741.	0.0E+00 H92741.	0.0E+00/	0.0E+00	0.0E+00 AB0375	0.0E+00	0.0E+00	0.0E+00 AF1538	0.0E+00 AF15381
	Expression	1.28	1.06	1.06	2.50	6.16	4.31	1.32	15.47	0.79	1.61	203	238	12.72	12.72	96.0	10.33	10.33	1.68	1.46	3.16	1.04	1.04	2.8	4.94	1.66	1.53	1.53	1.52	1.52
	ORF SEQ ID NO:	22858		29860	29870	29875	29882	29886	29894	29900	29903	29908		29910	29911	28925	29028	28829	 			20947	28948	29949	28950		29958	29959	29960	29961
	SEQ ID	17229	17230	17230	17882	17242	17247	17250	17260	17267	17271	17275	17279	17281	17281	17298	17301	17301	17316	17318	17320	17321	17321	17322	17323	17324	133	17331	17332	17332
	Probe SEQ ID NO:	4483	4494	4494	4502	4507	4512	4515	4525	4532	4536	4540	4544	4546	4548	4563	4586	4586	4581	4583	4585	888	889	4587	4588	4689	4596	25.00 200 200 200 200 200 200 200 200 200	4597	4507

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Top Hit Descriptor	Name and the Encember of harding problem E7 mRNA, complete cds	West Incoming a Communication of the Communication	DOING SERVICE THE CANADAT Avenue restill refer	Homo saplens mitthe tot Night Light protection and any denses	Human endogenous retroits type N (TIETY TV) 1949, Portion of the property of the Property of t		Γ	neglon	Homo eaplens chromosome 21 aegment h3210070	Homo septems of another in the control of the contr	Homo septens mixing to Nukanose protein, peruel vos	Homo septens mixiva to Nukhi see promit per use con	Humen displacement protein (CCAA I) mixtha	Homo sepiens butyrophilin, subfamily 2, member A2 (5 IN 2A2), minuth	Homo sapiens butyrophilin, subfamily 2, member A2 (B INZAZ), minuck		Г	Т	Т	Himmen AHNAK nucleoproblem MRNA, 6' end	Linear harborithin and harborithin-related protein (HP and HPR) genes, complete ods	Human handschip and harbotichkin-related protein (HP and HPR) genes, complete cds	Linner impegerent in the complete of the compl	Trust and the Angels are the Angels	Tions expenses the contract of	Human proto-oncogene tyrosine-protein kinasa (ABL) gene, expn 1a and expna 2-10, complete cds	SONTA Exert type I sodium charmet appre-subum (III to transmental la region y (Indiana), pre-subum (III to transmental la region y (Indian	1556 ntj	עלאואים ואספון אספותיין מופוונים פוליום אספותיין (יייסי יייסי אייסי אספותיין אספון אספותיין אייניין אספותיין אספותיין אספותיין אספותיין אספותיין אספותיין אספותיין אספותיין אספותיין אספותיין אספותיין אספותיין אספותיין אספותיין אספותיין אייניין אספותיין איינייין אייניין אייניין אייניין אייניין אייניין איינ	1.000 mg	Human CYP. 277 AP pseudogane in Cyronicine 1 100 200 (BAZ28), mRNA	Homo septems bromocomism superceit at the september 20 (BA729) mRNA	Homo sapiens bromodomen edjacent to zinc tinger dulines, 25 (unitato) in a constant to the con	Homo sapiens alpha-3 type IX collegen (COLLANA) gens, promoter region, and consider the same sapients and consider the same same sapients and same same sapients and same same sapients and same same sapients and same sapients and same sapients and same same same same same same same same	Hamo sepiens prosenzature (ALCLS), minura	
Top Hit Detabase Source		Z	Į.	M	IN	EST HUMAN		F	MT	۲	Z	L _N	N	N	LN	EST HUMAN	FST HUMAN	EST HIMAN		2 2	z!	Z	Ž!	Z	<u> </u>	Z	_	노		Ž	N N	2 NT	2 NT	Ł	LNO	
Top Hit Acession No.		-	0.1	0.1	718890.1	A418248.1		VF086641.1	AL163278.2	1L163278.2	0.0E+00 AB037820.1	0.0E+00 AB037820.1	M74099.1	6453812 NT	6453812 NT	T56945.1	TEROAK 1	1 30873.1	BE2/8/30.1	U58851.1			M80197.1	0.0E+00 AF184110.1	7682181 NT	0.0E+00 U07563.1		S71446.1		571446.1	X58467.	7304022 NT	7304922 NT	IRI	7019320 NT	
Most Similar (Top) Hit BLAST E		0.0E+00 AF16744	0.0E+00 AB02897	0.0E+00	0.0E+00 Y18890.1	0 0F+00 AA41824		0.0E+00 AF0868	0.0E+00 AL16327	0.0E+00 AL16327	0.0E+00	0.0E+00/	0 0F+00 M74099	0.0E+00	00+40	0.0E+00 T56945.	200	0.00=+00 308+5	0.0E+00 BE2/8/	0.0E+00 U58651	0.0E+00	0.0E+00 MB0197	0.0E+00 MB9197	0.0E+00	0.0E+00	0.05+00		0.0E+00 S71446		0.0E+00 S7144¢	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AF028	00+30	
Expression Signal		1.5	1.22	122	5,25	8	1	22	1.00	1.06	272	272	1280	187	18	28.0	18	0.82	1.34				2.23	4.9	2.02	0.95		76.0		0.97	1.45				0.84	
ORF SEQ ID NO:		29862	29970	20071	07007	2000	10000		20008	20000					1			25594			30033	30036	30037	30040	30042	aruus.		30050		30051		30065				
SEQ ID		17333	17340	73.40	410.00	2101	1302	47750	17864	17861		L	L	1.	L	1/3/0	_		17373	17394	17399	17402	17402	17405		4777	1	17415	1_	17415	1_		1	.		J
Probe SEQ ID NO:	_	4508	4805	300	3 4	1 1	4617	1001	1870	76.00	1830	١		138	6204	4633	4030	4636	4639	4000	4065	4668	4668	4871	4673		300	4884		1884	4807	Ě	10,4	4709		4/12

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ORF SEQ Expression (Top) Hit Accession (Top) H		30077 0.84 0.0E+00 7019320 NT	30103 1.88 0.0E+00 AW444637.1 EST HUMAN	1.82 0.0E+00 AF083242.1 NT	2.28 0.0E+00 M65189.1 N i	2 79 0.0E+00 AF240786.1 NT	90147 202 0.0E+00 X87205.1 NT	30149 1.11 0.0E+00 AF084479.1 INT	30150 1.96 0.0E+00 AF097416.1 N1	30151 3.01 0.0E+00 4603786 N.I	30153 13.57 0.0E+00 4885048 N1	30154 1.04 0.0E+00 P52740 SWISSPROI	30159 5.7 0.0E+00 8923080 NT	30163 0.97 0.0E+00 7661979 NT	TN 1.1804081.1	30184	30165 1.84 0.0E+00 M94081.1 NT	30167 1.44 0.0E+00 X94628.1 NI	30168 1.44 0.0E+00 X94628.1 NT	30171 2.98 0.0E+00 AL163280.2 NI	6032150 NT	301/0 1.13 0.0E 4.00 NG2841.1 NT	30163 1 04 0 0E+00 4585642 NT	30188 1.81 0.0E+00 AB014633.1 NT	30187 2.24 0.0E+00 6677848 NT	30188 0.95 0.0E+00 5174560 NT	20120 119 0.0E+00 4758199 NT	30191 1.81 0.0E+00 7705548 NT	30196 12.62 0.0E+00 AF055066.1 NT	3.47 0.0E+00 4505508(N	30199 2.39 0.0E+00 AF091711.1 NI	30210 1.07 0.0E+00 U63502.1
		30077	30103	_			30147	30149	30150	30151	30153											1	1				1					
SEQ ID	<u> </u>	17444	L		L		L	1_		١.		┸	L	L	1	17541	17541	L	L				17501	-L	L	L	L	4830 1750 4838 47560	L	L		4858 17587
Probe SEQ ID	<u> </u>	47.42	4735	4740	4750		367	4796	4797	4798	4800	\$ E	4805	ABOO		4810	4840	48/2	4812	4815		4823	4830	4832	3	455	\$ 1	\$ 6	4	1 4	4	4

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oligio Lacin Flores Expressed III Digiti	Top Hit Descriptor	Homo septens farnesyl diphosphete synthese (farnesyl pyrophosphete synthetese, dimethylellytranstransferase, geranytransferase) (FDPS) mRNA	Homo septens statytrensferase 8 (alpha-N-acetylneuraminate: alpha-2,8-siatytransferase, GD3 synthase) (SIAT8) mRNA	Homo sepiens mRNA for KIAA0287 gene, pertial cds	Homo sepiens mRNA for KIAA0287 gene, pertial cds	Homo septions DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete ods)	Homo saplene chromosome 21 segment HS21C084	UHH-BI3-etvf-02-0-UI.s1 NCI_CGAP_Sub5 Hamo sepiens cDNA clone IMAGE:3068691 3*	Homo septions hypothetical protein FLJ11190 (FLJ11190), mRNA	Homo septens beaded filament structural protein 1, filensin (BFSP1) mRNA	Human ribosomal protein L21 mRNA, complete cds	801303729F1 NIH_MGC_21 Hamo sepiens oDNA clone IMAGE:3638118 5	Homo septiens desmoplatin (DPI, DPII) (DSP) mRNA	Homo sepiens KIAA0852 protein (KIAA0852), mRNA	Homo septiens mRNA for KIAA1043 protein, pertial cds	Homo saciens hypothetical protein FLJ20477 (FLJ20477), mRNA	Homo septens hypothetical protein FLJ20477 (FLJ20477), mRNA	no14g08.s1 NCI_CGAP_Phot Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E239140 E239140 SPALT PROTEIN;	no14g08.s1 NCI_CGAP_Phot Homo saplens cDNA clone IMAGE:1100704.3' similar to TR:E239140 = E239140 SPALT PROTEIN;	no14g08.s.1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704.5' similar to TR:E239140	Home serious HCDC44 mDNA complete col-	Total Separate History, Collision College	Home series DNA mismatch render meters (MI LS) and according of	H. september 2017 i institution of self protein (MLTA) gene, conjudes cos. H. september mRNA similar to D29763 mouse mRNA for selzure-related one product 6. Shares domains with	BMPs, Talloid, Sushi repeat proteins	Homo sepiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 3	Mus musculus mRNA for aczonin, short spiloed variant (acz gene)	Mus musculus mRNA for aczonin, short spliced verlant (acz gene)	Homo seplens chramosome 21 segment HS21C009
חום ריסוו גווחד	Top Hit Detabase Source	TN	k	NT.	NT	¥		EST_HUMAN				EST_HUMAN			IN			EST_HUMAN	EST_HUMAN	NOT IN TOU	T		LA		TA.				LN
5	Top Hit Acession No.	4503684 NT	4506952 NT	0.0E+00 AB008625.1		0.0E+00 AB026898.1		0.0E+00 AW452728.1	TN 9222388	4502398 NT	U14067.1	0.0E+00 BE408863.1	4758199 NT	7882401 NT	0.0E+00 AB028968.1	8923441 NT	8923441 NT	0.0E+00 AA601246.1	0.0E+00 AA601246.1	0 0F+00 AA@0124# 1	T	T	I		0.0E+00 AL050253.1	05.1	1	_	0.0E+00 AL163209.2
	Most Similar (Top) Hit BLASTE Veitue	0.0E+00	0.0E+00	0.0E+00	0.0E+00			0.0E+00	0.0E+00	0.0E+00	0.0E+00 U14967	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.05+00	004300	200	100 C		0.0E+00/	0.0E+00 AF0167	0.0E+00 Y19186.	0.0E+00 Y19186	0.0E+00
	Expression Signal	1.68	1.03	3.09	3.09	0.95	1.45	1.02	1.61	1.09	4.60	2.95	3.18	1.15	1.01	2.34	2.34	0.81	0.81	0.84	+++	-	0 77		0.84	1.63	1.5	1.5	178
	ORF SEQ ID NO:	30212		30224		30232	30243		30251	30255				30271	30274	30283	30284	30291	30282	30288	30208	30208	160%			30312	30313	30314	
	SEQ ID	17589	17224	17802	17802	17612	17626	17633	17637			17852	17656	17881	17686	17674	17874	17683	17883	17683	17686	17888	13010		17899	1708	47700	17709	17777
	Probe SEQ ID NO:	4850	4865	4875	4875	4885	4899	4906	4909	4912	4015	4924	4928	4033	4 638	4	4947	4958	4958	8504	488	88	4073		4976	408 5	4086	886	20

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	Top Hit Descriptor	Homo sapiens gammma-cytoplasmic actin (ACTGP3) pseudocene	Zn03g10.r1 Stratagerre hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:548402 51	ZR03g10.r1 Stratagene hNT neuron (#637233) Homo saniens cDNA clone (MAGE:548402 F)	Homo sepiers titin (TTN) mRNA	Homo sapiens (TTN) mRNA	Bacillus amyoliquefaciens sacB gene for levansucrase (EC 2.4.1.10)	Homo seplens vescular endothelial cedharin 2 mRNA, complete cds	Homo expiens vescular endothelial cacherin 2 mRNA, complete cds	Homo sapiens ecotropic viral integration site 24 (EVI2A), mRNA	Homo espiens ecotropic viral integration site 2A (EVI2A), mRNA	Homo sapiens chromosome 21 segment HS21C081	Homo sapiens HEF like Protein (HEFL), mRNA	Homo septens PR domein containing 1, with ZNF domein (PRDM1) mRNA	Homo sapiens putative GPR37 gene, excm 2	Homo sepiens putative GPR37 gene, exch 2	Human endogenous retrovirus-K, LTR U6 and gag gene	Homo septens potassium inwardit-rectifying channel subtarnity. J. member 16 (KCN-116). mRNA	Homo sapiens potassium Inwardiy-rectifying channel, subfamily J., member 16 (KCNJ16), mRNA		Homo sepiens 4F2 light chain (LOC51597), mRNA	Homo seplens deleted in bladder cancer chromosome region candidate 1 (DBCCR1), mRNA	Homo saplens mRNA for KIAA0559 protein, partial cds	Mus musculus mRNA for leucine-rich repeat protein, partial cds	Rettus norvegicus mutidornein presynaptic cytomatrix protein Piccoto mRNA, complete ods, long spilce verient	Ratus norvegicus multidornain presynaptic cytomatrix protein Piccolo mRNA, complete cds, long splice varient	Homo sapiens toll-like receptor 7 (TLR7) mRNA, complete cds	Homo sapiens microtubule-associated protein 2 (MAP2) mRNA	Homo seplens dutamete receptor, ionotropic, N-methyl D-estrantain 24 (GRIN2A) mRNA	Homo saplene glutamate receptor, ionotrocic, N-methyl D-asnartata 24 (GRIN2A) mRNA	EST367899 MAGE reaequences, MAGD Homo espiens cDNA	Homo sepiens mRNA for KIAA1513 protein, partiel cds	Hamo sapiens gababrit receptor gene, exan 6
מו ז ווסאם פועי	Top Hit Datebase Source	Z	EST HUMAN	EST HUMAN	1	Ę	Ę	F	F	뉟	5	Ę	F	F	Ę	Į,	LN	F	IN	님	Į.	NT	뒫	NT	뉟	<u> </u>	Þ	Ę	Į	¥	EST HUMAN		NT.
5 	Top Hit Acession No.	0.0E+00 D50857.1	0.0E+00 AA084272.1	0.0E+00 AA084272.1	4507720 NT	4507720 NT	Ì	0.0E+00 AF240835.1	0.0E+00 AF240635.1	7857074 NT	7857074 NT	0.0E+00 AL163281.2	11421001 NT	4557362 NT	112477.1	112477.1	r08032.1	B923822 NT	8923822	7706245	7706245 NT	7857008 NT	0.0E+00 AB011131.1)49802.1	0.0E+00 AF227534.1	0.0E+00 AF227534.1	Π	4505096	6006002	8008002 NT	0.0E+00 AW955819.1		0.0E+00 AJ010179.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 X52988.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 Y12477.1	0.0E+00 Y12477.1	0.0E+00 Y08032.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 D49802.1	0.0E+00	0.0E+00/	0.0E+00/	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00/
	Expression Signal	28.03	0.97	76.0	0.95	0.95	3	1.04	1.04	1.55	1.55	1.11	14.05	1.03	275	275	1.07	1.01	1.01	97.0	0.76	2.69	2.05	123	1.14		0.90	6.63	1.5	1,5	1.6	1.31	1.12
	ORF SEQ ID NO:		30320	30327	29553	29554		30375	30376	30380	30381	30387	30388	30389	30391	30392	30304	30414	30415	30417	30418	30423	30433	30444	30446	30446	30447	30449	30450	30451	30452		
	Exan SEQ ID NO:	17720	17724	17724	16924	16924	17747				17764	17768	17769	12221		17775	177771	17798	17798	17800	17800	17807	_	17827	17828	17829	17830	17833	17834	17834	17835	17837	17844
	Probe SEQ ID NO:	4997	5001	5001	5012	5012	5026	5042	5042	5045	5045	5049	5050	5052	5056	2056	9909	5079	5079	5081	5081	2088	6097	5100	5110	5111	5112	5115	5116	5116	5117	5119	5128

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	Top Hit Descriptor	Homo saciens mRNA for Nucleoscorne Assembly Protein 1.11ke 2. complete rule	Homo saciens mRNA for nermedn Leinha mintain complete Ade	Homo seciens mRNA for KIAA1117 brothen partiel cyle	Human socium channel mRNA	Homo saciens ring fines probin 15 (RNE45) mRNA	Homo septens aconitase (ACO2) gene, nuclear cene anocing mitrohondral professions 45	Homo saciens keratin 12 (KRT12) cene, comblete cds	Homo sapiens keratin 12 (KRT12) cene, complete cds	wp06g08.xt NCI CGAP Kid12 Home sepiens cDNA close IMAGE-2464no4 st	Homo seplens protocedherin sloke 13 (PCDHA13) mRNA	RC3-GN0078-310800-013-b03 GN0078 Homo septems cDNA	Homo estriens polycystic kidney dispesse the 2 protein (PKD) 2) mRNA consistence of	Homo septens polycystic kidney disease-like 2 gratein (PKDI 2) mRNA complete che	H. septens immunodobulin heery chain gene, verlable moinn	H. sepiens immunoglobulin heavy chain gene, variable region	7f10c06.xt NCI CGAP CLL1 Homo sepiens cDNA clone IMAGE-3294250.3	ht99a02.x1 NCI_CGAP_Lu24 Homo sapiens dDNA clone IMAGE:3165194 3' similar to SW:Y064_HUMAN P42894 HYPOTHETICAL PROTEN KIAA0064.	601589422F1 NIH MGC 7 Hamp saciens a DNA clane IMAGE 3047904 K	601589422F1 NIH MGC 7 Homo septeme cDNA clone IMA/CF-3023904 K1	qd04e04.x1 Sogree_plecenta_Sto0weeks_ZNDHP8to9W Home sepiens cDNA done IMAGE:1722702.3*	Homo september accelerability and ADD Ages Ages 7	Homo sablens So4 transcribition factor (SDA) mRNA	602118928F1 NIH MGC 56 Homo septems cDNA chows MAAGE 4278954 F	AU134408 OVARC1 Hamo sepiens cDNA clane OVARC1001804 5	AU134406 OVARC1 Hamo saplens aDNA clone OVARC1001894 5	801081489F1 NIH MGC 10 Hamp septens CDNA clane MAGE:3447830 F	601105891F1 NIH MGC 15 Homo septems cDNA come tNACE-Spagato F	72.5'			artial cds
BIG FAULT IG	Top Hit Defaberse Source	<u>LN</u>	¥	Z	I _N	Į.	NT	Ę	Į.	EST HUMAN	1.	EST HUMAN	N F	Ę	Ę	Ŋ	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HIMAN		Ŀ	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	EST HUMAN	TN.	Ę
5	Top Hit Acessian No.	0.0E+00 AB027013.1	0.0E+00 AB035358.1	0.0E+00 AB029040.1	0.0E+00 M91803.1	5454013 NT	0.0E+00 AF093083.1	0.0E+00 AF137286.1	0.0E+00 AF137286.1	0.0E+00 AI934964.1	9256579 NT	0.0E+00 BE831080.1	0.0E+00 AF182034.1	0.0E+00 AF182034.1	X56163.1	X56163.1	0.0E+00 BE675488.1	0.0E+00 BE220763.1	0.0E+00 BE794412.1	0.0E+00 BE794412.1	M180142 1	129008.1	11421038 NT	0.0E+00 BF665962.1	0.0E+00 AU134408.1	0.0E+00 AU134408.1	0.0E+00 BE538857.1	0.0E+00 BE292784.1	0.0E+00 BF528328.1	0.0E+00 BF528328.1	4557364 NT	0.0E+00 AB007p35.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 X56163.1	0.0E+00 X56163.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00.A1389142	0.0E+00 M29908.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00
	Expression Signal	5.57	1.19	1.18	1.08	1.37	3.44	2.52	2.52	1.29	1.77	3.81	3	3	1.66	1.86	6.56	1.75	1.83	1.83	18.0	6.17	4.88	7.18	0.73	0.73	1	1.07	1.60	1.69	1.82	10.0H
	ORF SEQ ID NO:	30473	30477	30481		30484		30495	30496	30623	30626	30639	30643	30644	30652	30653	30763	30764	30765	30766	30787	30770	30780		30791	30792	30799	30826	30831	30832	32513	30858
	Exan SEQ ID NO:	17857	17861	17868	17871	17872		17981		18000	18003	18017	18021	.	l	18027	18104	18105	18106	18106	18107	18111	25066	18132	18133	18133	18138	18147	18151	18161	<u>2</u>	18171
	Probe SEQ ID NO:	5139	5150	5151	5154	5155	5162	5172	5172	5192	5195	2208	5213	5213	5220	5220	6236	5300	5301	5301	5302	5306	5319	6329	2330	2330	5335	5344	5348	8348	2367	5370

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Top Hit Detablese Source	Homo saplens mRNA for KIAA0488 protein, pertiel ods	Homo septems citiary dynain heavy chain 9 (DNA)-19) mRNA, complete cds	Line continue cellus durant hours chap 9 (DNA-19) mRNA, complete cds	Trotto espetia outes by system respectively and second sec	Human gene in a ning augus and a ning an annual and a ning an annual and a ning a ning	Human gare for any analysis and the second s	Homo sapiens offectory receptor, remary 4, auditamy 1, months 1	H. septems mixty to impose	HUMA18005B Cantech numer real brain puly. HELLA (1800) Hours serient CNA close GEN 418005	HUM418D05B Clorifech human letal brain polyA+ m=NA (#0333) human 5 EST HUMAN 5	1UMAN 602042322F1 NC _CGAP_Brn87 Home sackers GJNA GGRE IMALCE: 11 1 8406 5	FET HUMAN (602042322F1 NGL CGAP_Bm67 Homo septems cDNA clothe IMAGE: 41 (1980) 5	7	Ī	FET IN INTAL SECTION MINIMAGE 19 Homo sapiens CDNA clone IMAGE:3502809 5	T	Т	7	EST HUMAN COLLEGE STREET (STATE STATE (STATE STA	Tright Sequence Charles (1997) 1997 (1997) mRNA (1997) mRNA	Home services ware long-chain son-CoA synthetise homolog 1 mRNA, complete ods	Home sequence very front-chain acyl-CoA swithelase homolog 1 mRNA, complete cds	Home services Surf-8 and Surf-8 denses	Home sendens Surf-5 and Surf-6 dense	Trains agreement amounts Stockwards 2NISHP8BGW Homo septems CDNA clone IMAGE:1757730 3'	EST HUMAN SIMILER TO SW.CADC_HUMAN PEG289 BRAIN-CADHERIN PRECURSOR;	T	Т	T	Т	T	Ţ	EST HUMAN Prince Lozova (2007) 1900 C. Comp. British (BAMZ2) gene, excm (3	
	Ę	1	z !	Z	뒫	Ż	19 NT	Ę	EST	EST	EST	EST	EST	:1.	100				֓֞֞֞֟֝֟֝֟֟֝֟֟֝֟֟֝֟֟֟֝֟֟֟֟֟֟֟֟֟ ֓֓֓֓֓֓֓֓֓֞֓֓֞֓֞֓֓֓֞֓֓֞֓֞֓֓֞	11420819INI	11420819 NI	z	z !			EST					S		EST	ž.
Top Hit Acession No.	0 0E+00 AB007035 1		0.0E+00 AF257/37.1	0.0E+00 AF257737.1	726535.1	728535.1	11420819 NT	238133.1	061564.1	D61564.1	0 0F+00 BF529931.1	BER20031 1	DE949490 4	4444400 NT		BE260777.1	AW86/316.1	0.0E+00 BE292889.1	0.0E+00 BE292889.1	11420	11420	0.0E+00 AF064254.1	AF084254.1	0.0E+00 AJZZ4639.1	0.0E+00 AJZ24639.1	0 0E±00 A1108515.1	M85740 4	WINDS I B. I	AW4034/2.1	0.0E+00 Z26269.1	0.0E+00 AW361877.1	AW361877.1	0.0E+00 AW361877.1	1036261.1
Most Similar (Top) Hit BLAST E Value	1001300	3	0.0E+00.	0.0E+00	0.0E+00 D28535.	0.0E+00 D26535.	0.0E+00	0.0E+00 Z38133.	0.0E+00 D61564.	0.0E+00 D61564	00+100	O OF TON BEROOD	0.0E-100 DI 02-04	0.00	O.VE.	0.0E+00 BE2607	İ	1	1		0.0E+00				0.0E+00	001300	1							
Expression Signal	180	(A)	4.85	4.85	1.06	1.06	1.88	0.81	0.78	67.0	2 65	1	7.30	7.87	4.37	1.15	3.51	233	233						2,95	4				1.25		1.04		2.55
ORF SEQ ID NO:	Circos	SCSOS	30863	30864	30878	30879	30906	30912	98908	20002	77000	1				31171			31197					31239	31240					31296	31306	31307		31315
Exan SEQ ID NO:		181/1	18174	18174	18187	18187	18201	18206	18225	9	270	2	18228	18233	18244	18276	18285	18298	18298	18319	18319	18326	18326	18333	18333				18374	18386	18396	18396		18401
Probe SEQ ID NO:		6370	5374	5374	6387	5387	250	2407	8428	3	8 8	828	<u>8</u>	\$ 3	3445	5477	5486	2500	5500	5521	5521	5628	6628	5535	5635		5586	5570	5577	9290	560	5801	5601	5605

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Probe SEQ ID S NO: NO: NO: NO: NO: NO: NO: NO: NO: NO:		ORF SEQ E 10 NO: 10 NO: 10 NO: 10 NO: 10 NO: 11446	Expression Signal 1.136 1.136 1.136 1.136 1.137	X X X X X X X X X X X X X X X X X X X	N N N N N N N N N N N N N N N N N N N	TOP LIK SOLICE SOLICE SOLICE SOLICE SOLICE HUMAN THUMAN ST HUMAN ST HUMAN ST HUMAN ST HUMAN	[[[[[[[[[[[[[[[[[[[
88 (8	5836 18625				0.0E+00 BF031742.1	EST HUMAN	_
8 8	5847 18634				0.0E+00 BF031742.1	EST HUMAN	_[_
8		1		0.58 0.0E+	0.0E+00 AW470846.1	EST HUMAN	
188	5872 18659	59 31599			0.0E+00 Br 1550/0.1		t

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Single Exon Probes Expressed in Brain	Top Hit Descriptor	QV4-HT0894-290600-399-e10 HT0894 Homo septens cDNA	2008h08.rl Soeres parathyroid fumor NbHPA Homo septens cDNA clone IMAGE:321755 5	2008h08.r1 Soeres parathyroid fumor NbHPA Homo eaplens cDNA clone IMAGE:321755 57	Homo sepiens familial mental retardation protein 2 (FMR2) gene, excn 14	801158515F1 NIH_MGC_21 Homo septens a DNA clane IMAGE:3505323 5	601512630F1 NIH_MGC_71 Homo sepiens cDNA clone IMAGE:3914238 5	IL3-CT0220-111199-028-E04 CT0220 Homo sepiens cDNA	Homo seplens KIAA0735 gene product, syneptic vesicle protein 28 homolog (KIAA0735), mRNA	Homo saplens KIAA0735 gene product synaptic vesicle protein 28 homolog (KIAA0735), mRNA	601677735F1 NIH_MGC_21 Homo sepiens oDNA clone IMAGE:3960200 5'	601677735F1 NIH_MGC_21 Homo sapiens CDNA clane IMAGE:3960200 5	601677735F1 NIH_MGC_21 Homo sapiens CDNA clone IMAGE:3960200 5'	Homo sepiens potassium voltage-gated charmel, Shel-related subfamily, member 2 (KCND2), mRNA	240h01.rt Soeres, NiHMPu, St Homo saplens, CDNA clone IMAGE: 895905 5' stimilar to SW:YY06, HUMAN P42904 HYPOTHETICAL MYELOID CELL LINE PROTEIN 6.:	ZAGINOLAT Socres, NIHIMPL ST Homo explens CDNA clone IMAGE:005005 0's similar to SW:YYD5, HUMAN P42094 HYPOTHETICAL MYELORI CELL LINE PROTEIN 5.	Human T cell surface glycoprotein CD-8 mRNA, complete cds	Human T cell surface glycoprotein CD-8 mRNA, complete cds	601114823F1 NIH_MGC_16 Hamp septens aDNA clane IMAGE:3355585 5'	QV0-HT0368-090200-099-e09 HT0368 Homo explens cDNA	Human neurofibromatosis type 1 (NF-1) mRNA, 3' and of ods	001236270F1 NIH_MGC_44 Homo septems cDNA clone IMAGE:3608490 5'	AU137772 PLACE1 Hamo sepiens cDNA clone PLACE1007201 5'	Human G protein-coupled receptor GPR-9-6 gene, complete cds	zq81d03.r1 Strategene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:648005 5' similar to TR:G854195 G854195 LEUKOCYTE SURFACE PROTEIN.	Homo sepiene xylosyltransferase [I (XT2), mRNA	Hamo sapiens xylosyltransferase II (XT2), mRNA	Homo sapiens carcinoambyonic antigen-related cell adhesion molecule 8 (CEACAMS), mRNA	601109632F1 NIH_MGC_16 Homo septens oDNA clone IMAGE:3350622 5	ttentron NC_CGAP_Pr28 Homo septens cDNA clone IMAGE:2248639 3' similar to TR:Q14839 Q14839 Mile PROTEIN:	
gie Exon Proc	Top Hit Databese Source	EST HUMAN	EST HUMAN	EST HUMAN	TN	EST_HUMAN	EST_HUMAN	EST_HUMAN	NT	Ę	EST_HUMAN	Γ	EST_HUMAN	 	EST HUMAN		П		EST_HUMAN	EST_HUMAN		HUMAN	HUMAN	TN	EST_HUMAN				EST_HUMAN	EST_HUMAN	
UIO .	Top Hit Acession No.	0.0E+00 BF155670.1	0.0E+00 W33069.1	0.0E+00 W33069.1	AF012818.1	BE280197.1	0.0E+00 BE880610.1	0.0E+00 AW752848.1	11433071 NT	11433071 NT	0.0E+00 BE901608.1	0.0E+00 BE901608.1	0.0E+00 BE901608.1	TN 09008/18	0.0E+00 AA193506.1	0.0E+00 AA183508.1						07.1	72.1		£0.1	11545913 NT	11545913 NT	11426367 NT	73.1	8.1	
	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00	0.0E+00	0.0E+00 AF0128	0.0E+00 BE2801	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.05+00	0.0E+00	0.0E+00	0.0E+00 U34625.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00 M38107	0.0E+00	0.0E+00 AU1377	0.0E+00 U45982.1	0.0E+00 AA2047	0.0E+00	0.0E+00	0.0E+00	0.0E+00 BE2571	0.0E+00 Al88604	
	Expression Signal	0.77	3.22	3.22	2.51	3.33	2.6	0.0	1.1	1.1	0.88	0.88	0.88	10.66	1.2	1.2	16.77	16.77	0.99	1.2	0.85	1.32	1.39	3.76	4.52	3.97	3.97	1.14	2.87	0.85	Í
	ORF SEQ ID NO:	31600	31604	31605		31609			31641	31642	31643	31644	31645	31001	31684	31885	31680	31660	31732	31740	31750	31781	31787	31809	31830	31840	31841	31875	31880		
	Exan SEQ ID NO:	18659	18664	18684	18965	18668	18675	1		18692	18693	18683	18603	25081	18710	18710	18730	18730	18768	18778	18788	18820	18828		18872	18873	18873	18907	18911	18924	
	Probe SEQ ID NO:	5872	5878	5878	5879	5882	2860	5905	2308	5908	6069	6069	2000	5923	5926	5926	6948	5948	5987	2009	2000	Q 00	9046	88	8094	9095	9095	6120	6133	6147	

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Single Exoli Pioles Expressed in Brain	Top Hit Descriptor	Human anion exchanger (AE1) gene, exons 1-20	601587971F1 NIH MGC 7 Homo seplens cDNA clone IMAGE:3942329 51	801587971F1 NIH_MGC_7 Hamo septens cDNA clane IMAGE:3942329 5	qE0b11.x1 NCI_CGAP_Bm25 Hamo septens cDNA clane IMAGE:1858901 3' similar to TR-Q12838 Q12838 TFIIIC ALPHA SUBUNIT:	q50b11.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1850801 3' similar to TR:Q12838 Q12838 TFIIIC ALPHA SUBUNIT:	MR0-HT0923-220800-102-b05 HT0923 Homo septens cDNA	Homo espiens peptide transporter 3 (LOC51296), mRNA	Human mRNA for alpha mannoeldase II laczyme, complete cds	IL3-HT0062-010999-014-A04 HT0062 Homo sepiens cDNA	7e02c12.x1 NG_CGAP_Lu24 Homo sepiens cDNA clone IMAGE:3281302.3' similar to SW:Y176_HUMAN Q14881 HYPOTHETICAL PROTEIN KIAA0178:	Homo septems KIAA0285 gene product (KIAA0285), mRNA	AV650020 GLC Homo serviers cDNA clone GLCCADop 3'	UI-HIF-BLO-acc-g-12-0-UI.s1 NIH MGC 37 Homo esciens cDNA clone IMAGE:30587513"	1/27b03.r1 Soares placenta Nb24P Homo espiens cDNA clone IMAGE:149833 57	Human gene for the light and heavy chains of myelopercoddase	aa14607.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:813252.67	1257408.x1 NCI_CGAP_OX35 Homo eachers cDNA done INAAGE.2282887.3' straier to SW.1NTCS_HUAAAN P85788 SODIUM-AND CHLORIDE-DEPENDENT CREATINE TRANSPORTER 2.	801305368F1 NIH MGC_39 Hamo septens cDNA clare IMAGE:3639616 5	601305368F1 NIH_MGC_39 Hamp septens aDNA clone IMAGE:3639616 5	MR0-BT0264-221199-002-111 BT0294 Homo sepiens cDNA	MR0-BT0264-221199-002-111 BT0264 Homo sepiens cDNA	Homo sepiens Acheste-Scute homologue 2 (ASCL2) gene, complete ods	AU119245 HEMBA1 Hamo saplens cDNA done HEMBA1005360 6	AU119245 HEMBA1 Hamo septens cDNA clone HEMBA1005360 5'	601468712F1 NIH_MGC_67 Hane septens cDNA dare IMAGE:3871899 5	H. aspiens germine immunoglobulin heavy chein, variable region, (13-2)	ws25c07.x1 NCI_CGAP_GC6 Homo expiens cDNA clone INAGE:2498220 3'	601105344F1 NIH_MGC_15 Homo septems cDNA clone IMAGE:2887963 67	601105344F1 NIH_MGC_15 Hamo septens cDNA clone IMAGE:2987963 5
nor Hora elf	Top Hit Deterberse Source	¥	EST HUMAN	EST_HUMAN	EST_HUMAN		Г			EST_HUMAN	EST HUMAN		T HUMAN	Т	EST_HUMAN	¥	EST_HUMAN	EST HUMAN	EST_HUMAN	EST HUMAN		EST_HUMAN	LN	EST HUMAN	Г	EST HUMAN	NT	HUMAN	П	EST_HUMAN
SIIO I	Top Hit Acession No.	L35830.1	0.0E+00 BE797385.1	0.0E+00 BE797385.1	0.0E+00 AI198025.1	4/198025.1	23.1	11435830 NT	55649.1	0.0E+00 AW178142.1	0.0E+00 BE674544.1	7862039 NT	0.0E+00 AV650020.1	0.0E+00 AW575598.1			0.0E+00 AA458375.1	11.1				1.1			0.0E+00 AU119245.1	53.1	1		83.1	33.1
	Most Similer (Top) Hit BLAST E Value	0.0E+00 L35830	0.0E+00	0.0E+00	0.0E+00	0.0E+00 Al1980	0.0E+00 BF357	0.0E+00	0.0E+00 D55849.1	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00 H01255.1	0.0E+00 X16377	0.0E+00	0.0E+00 AI61284	0.0E+00	0.0E+00	0.0E+00/	0.0E+00	0.0E+00 U77829.1	0.0E+00	0.0E+00	0.0E+00 BE7804	0.0E+00 XB2217.	0.0E+00 AI989483.1	0.0E+00 BE2831	0.0E+00 BE2831
	Expression Signal	1.53	1.22	1.22	0.57	0.57	0.85	1.08	0.85	1.03	0.88	1.33	8.59	3.13	6.26	1.6	0.65	1.3	4.71	4.71	0.86	0.86	9.0	15.59	15.59	0.8	1.12	1.52	6.91	6.91
	ORF SEQ ID NO:			31904	31919	31820	31921	31931	31939	31961	31078	31983		32003	32006	32019	32021	32022	32028	32029	32035	32036		32038	32039	32044	32045	32062	32072	32073
	Exan SEQ ID NO:	18928	18636	18936	18947	18947	18949	18957	18968	18982	19002	19006	19020	19028	19031	19042	1904	19045	19051	19061	19055	19055	19956	19058	19058	19062	19063	19076	19088	19088
	Probe SEQ ID NO:	6151	6159	6159	. 6170	6170	6172	6180	6189	9207	8228	6232	6246	6264	0257	6220	6271	6272	6278	8278	9282	6282	828	6285	6285	6280	828	83	8317	6817

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					5	Olingio Exciti i lobos	
Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Moet Similer (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Dertabese Source	Top Hit Descriptor
6355	19125	32119	0.58	0.05+00	0.0E+00 BF057438.1	EST_HUMAN	7k43h05.x1 NCI_CGAP_Ov18 Homo septens cDNA done IMAGE:3478496 3' similer to TR:O14553 O14553 R31240_1;
6388	19167	32157	1.89		0.0E+00 AW406348.1	EST_HUMAN	ULHF-BLO-eco-h-02-0-UL11 NIH MGC 37 Homo septens cDNA done IMAGE:3056631 5
6388	19157	32158	1.89	0.0E+00	0.0E+00 AW 406348.1	EST_HUMAN	UI-HF-BLO-eco-h-02-0-UI.r1 NIH_MGC_37 Hamo septens oDNA clane IMAGE:3059831 5
6418	19186	32184	62.0		AV719444.1	EST_HUMAN	AV719444 GLC Homo sapiens cDNA clone GLCEHC06 5"
6427	10195	32191	86'0		0.0E+00 BEB98340.1	EST_HUMAN	601681150F1 NIH_MGC_9 Homo seplens cDNA clone IMAGE:3951301 5'
6427	19195	32192	86'0		0.0E+00 BE898340.1	EST_HUMAN	601681150F1 NIH_MGC_9 Homo septens aDNA dane IMAGE:3951301 5
				1			Homo septens low voltage-ectivated T-type calctum channel alpha 1G splice varient CavT.1a (CACNA1G)
8430		32195		0.0E+00	0.0E+00 AF190860.1	노	mRNA, complete cds
6433	19201	32197	1.17	0.0E+00	11420658 NT	NT	Homo sapiens transformation/transcription domain-associated protein (TRRAP), mRNA
6440	19208	32204	7.5		0.0E+00 AW163640.1	EST_HUMAN	au.06/108.y1 Schneider fetel brain 00004 Homo sapiens cDNA clone IMAGE:2784159 5' similar to TR:O15390 015390 GT24. [3] TR:O43840 TR:O43206;
94	19208	32205	7.5		0.0E+00 AW 163640.1	EST HUMAN	80000000000000000000000000000000000000
1	1	32208		<u> </u>	W37163.1	EST HUMAN	2520e06.r1 Sceres Jebal Lang, NbHL19W Homo septens cDNA clone IMAGE:302026 5' similar to SW:2N45 HUMAN Q02389 ZNC FINGER PROTEIN 45:
8444	<u> </u>	\$2209	0.97	0 0F+00 W37483		EST HUMAN	2620e06.1 Sceres fetal Jung NbHL19W Homo septens cDNA clone IMAGE:302626 5' ehrilar to SW-2NA5 H1MAN 002286 ZNC FINGER PROTEIN 45:
25	L	32228	1.08	0.0E+00		EST HUMAN	601589371F1 NIIH MGC 7 Homo septens cDNA clone IMAGE:3943504 5'
9466	19233	32233	5.81	0.0E+00 BE79087	BE799873.1	EST_HUMAN	601567561F1 NIH MGC 7 Homo sepiens cDNA clone MACE:3941847 5
6467		32234	0.56	0.0E+00	0.0E+00 BE767955.1	EST_HUMAN	QV1-GN0065-140800-318-h02 GN0065 Homo sapiens cDNA
8467	19234	32235		0.0E+00	0.0E+00 BE767955.1	EST_HUMAN	QV1-GN0065-140800-318-h02 GN0065 Homo sepiens cDNA
6471		32238	96.8	0.0E+00 BE8881	BE889813.1	EST_HUMAN	601512058F1 NIH_MGC_71 Homo septens cDNA clone IMAGE:3913311 5
6471		32239	6.95	0.0E+00 BE8898	BE886813.1	EST HUMAN	801512058F1 NIH_MGC_71 Hamo septens cDNA dane IMAGE:3913311 5'
6480		32247	5.62	0.0E+00 L24493.	124483.1	NT	Human antigen CD27 gene, exons 1-2
6485	19262	32251	1.98	0.0E+00	0.0E+00 AL163204.2	TN	Homo seplens chromosome 21 segment HS210004
6485	19252	32252	1.98	0.0E+00	0.0E+00[AL163204.2	TN	Homo septens chromosome 21 segment HS21C004
6491	19258	32259	4.00	0.0E+00	LN 8865009	TN	Homo sepiens zone pellucida glycoprotein 3A (sperm receptor) (ZP3A), mRNA
6494	19290	32261	4.76	0.0E+00	0.0E+00 AI638412.1	EST_HUMAN	tts1f11.x1 NCI_CGAP_GG8 Homo sepiens dDNA clone IMAGE:2242413 3' similer to SW:WNT3_MOUSE P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR.
6495	19261	32262	1.36	0.0E+00 L32832.	_	N	Homo sepiens zinc finger homeodometra protein (ATBF1-A) mRNA, complete cds
6507	19272	32273	4.12	0.0E+00		EST_HUMAN	Zw52c03.r1 Sogres_total_fetus_Nb2HFB_9w Homo sapiens cDNA clone IMAGE:773668 5
6520			0.99	0.0E+00	0.1	EST_HUMAN	601885317F1 NIH_MGC_57 Hamo septens cDNA clone IMACE:4103693 57
6523	19289	32283	1.82	0.0E+00 BE92587	BE925875.1	EST HUMAN	QV3-BN0047-300800-278-c06 BN0047 Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed in Brain

Expn NO: ORF SEQ ID NO: Expression Signal Moet Similar PLAST E No. Top Hit No. Top Hit No. Top Hit No. 19468 32487 1.08 0.0E+00 11431474 19468 32480 0.6 0.0E+00 BE313075.1 19468 32487 1.08 0.0E+00 BE313075.1 19468 32487 0.6 0.0E+00 BE313075.1 19468 32487 0.6 0.0E+00 BE313075.1 19468 32573 2.06 0.0E+00 BE313075.1 19649 32574 3.62 0.0E+00 BE313075.1 19649 32574 3.62 0.0E+00 BE313075.1 17836 30573 3.62 0.0E+00 BE317775 17840 30576 0.74 0.0E+00 BE26778.1 17840 30576 0.74 0.0E+00 BE26778.1 17840 30576 0.78 0.0E+00 BE267737.1 17840 30571 0.58 0.0E+00 AL413909.1		
19468 32487 1.08 0.0E+00 11431474 19468 32490 0.6 0.0E+00 BE313075.1 19468 32490 0.6 0.0E+00 BE313075.1 19468 32491 0.6 0.0E+00 BE313075.1 19483 32505 2.89 0.0E+00 BF368905.1 19484 32573 2.32 0.0E+00 BF313075.1 19645 32574 3.62 0.0E+00 AF217289.1 17846 32575 1.18 0.0E+00 AF217289.1 17857 30571 3.2 0.0E+00 AF217289.1 17856 30571 3.2 0.0E+00 AI418059.1 17857 30574 0.74 0.0E+00 AI418059.1 17856 30574 0.74 0.0E+00 AI418059.1 17860 30574 0.74 0.0E+00 AI418059.1 17860 30574 0.74 0.0E+00 AI418059.1 17860 30521 2.25 0.		Top Hit Descriptor
19468 32490 0.6 0.0E+00 BE313076.1 19468 32491 0.6 0.0E+00 BE313075.1 19483 32505 2.89 0.0E+00 BE313075.1 19483 32573 2.32 0.0E+00 BF568905.1 19645 32574 3.62 0.0E+00 AF217289.1 19546 32574 3.52 0.0E+00 AF217289.1 17835 30571 3.2 0.0E+00 AF217289.1 17840 30572 0.74 0.0E+00 AR11869.1 17840 30573 0.74 0.0E+00 AR11869.1 17840 30574 3.2 0.0E+00 AR11869.1 17840 30574 3.2 0.0E+00 AR13069.1 17840 30574 0.74 0.0E+00 AR13069.1 17841 30574 0.74 0.0E+00 AR13069.1 17842 30574 0.74 0.0E+00 AR13069.1 17843 30521 2.25 0.0E+00	11431474 NT	Homo septens sodium channel, nonvoltage-gated 1, beta (Liddle syndrome) (SCNN1B), mRNA
19468 32491 0.6 0.0E+00 BE313075.1 19483 32505 2.89 0.0E+00 BF568905.1 19483 32505 2.89 0.0E+00 BF568905.1 19645 32573 3.62 0.0E+00 AF217289.1 19546 32574 3.62 0.0E+00 AF217289.1 17835 30571 3.2 0.0E+00 AF217289.1 17840 30573 0.74 0.0E+00 AR18699.1 17850 30574 3.2 0.0E+00 AR18699.1 17840 30574 0.74 0.0E+00 AR18699.1 17850 30574 0.74 0.0E+00 AR18699.1 17860 30574 0.0E+00 AR18699.1 17860 30518 8.08 0.0E+00 AR18699.1 17861 30521 1.05 0.0E+00 AR18699.1 17862 30521 2.28 0.0E+00 AR18699.1 17863 30521 3.28 0.0E+00 AR2	75.1 EST_HUMAN	601150662F1 NIH_MGC_19 Hamo sepiens dDNA clane IMAGE:3503391 5'
19483 32505 2.89 0.0E+00 BF568905.1 19483 32505 2.89 0.0E+00 BF568905.1 19499 3.2573 3.62 0.0E+00 AF217289.1 19546 3.2574 3.62 0.0E+00 AF217289.1 19549 3.2575 1.18 0.0E+00 AF217289.1 17835 3.0571 3.2 0.0E+00 AF217289.1 17840 3.0573 0.74 0.0E+00 AI418069.1 17850 3.0574 0.74 0.0E+00 AI418069.1 17840 3.0573 0.74 0.0E+00 AI418069.1 17850 3.0518 0.0E+00 AI418069.1 17861 3.0518 0.0E+00 AI418069.1 17862 3.0518 0.0E+00 AI418069.1 17861 3.0521 0.0E+00 AI418069.1 17862 3.0521 1.05 0.0E+00 AI418069.1 17863 3.0521 3.25 0.0E+00 AI418069.1 <td< td=""><td>75.1 EST HUMAN</td><td>601150662F1 NIH_MGC_19 Homo eapiens cDNA clone IMAGE:3503391 5'</td></td<>	75.1 EST HUMAN	601150662F1 NIH_MGC_19 Homo eapiens cDNA clone IMAGE:3503391 5'
19469 2.32 0.0E+00 J03069.1 19545 3.2573 3.62 0.0E+00 AF217289.1 19545 3.2574 3.62 0.0E+00 AF217289.1 19546 3.2574 3.52 0.0E+00 AF217289.1 17835 3.0572 0.74 0.0E+00 M38113.1 17840 3.0573 0.74 0.0E+00 AI419969.1 17850 3.0573 0.77 0.0E+00 AI419969.1 17860 3.0574 0.78 0.0E+00 AI419969.1 17860 3.0573 0.74 0.0E+00 AI419969.1 17860 3.0518 8.08 0.0E+00 AI419969.1 17861 3.0521 1.05 0.0E+00 AI41969.1 17862 3.0521 2.28 0.0E+00 AI41969.1 17863 3.0522 3.28 0.0E+00 AI53777.1 18863 3.0521 1.08 0.0E+00 AI41969.1 18843 3.0522 3.28 0.0E+00	5.1 EST_HUMAN	602185852F1 NIH_MGC_45 Homo sapiens dNA clone IMAGE:4310076 5'
19545 3.52 0.0E+00 AF217289.1 19545 3.2574 3.62 0.0E+00 AF217289.1 19546 3.2576 1.18 0.0E+00 M38113.1 17836 3.0571 3.2 0.0E+00 M38113.1 17840 3.0572 0.74 0.0E+00 M41999.1 17850 3.0573 0.74 0.0E+00 AI41999.1 17850 3.0573 0.77 0.0E+00 BE266708.1 17850 3.0518 0.0E+00 AI41999.1 17860 3.0518 0.0E+00 AU118478.1 17861 3.0518 0.0E+00 AU118478.1 17862 3.0518 0.0E+00 AI41999.1 17861 3.0521 2.28 0.0E+00 AI4199.85.1 17862 3.0518 2.28 0.0E+00 AI419478.1 17863 3.0521 3.28 0.0E+00 AI419478.1 18843 3.0522 3.28 0.0E+00 AI419478.1 18846 3.0522		Human MYCL2 gene, complete cds
19545 3.52 0.0E+00 AF217289.1 19646 3.2576 1.18 0.0E+00 M38113.1 17836 3.0572 0.74 0.0E+00 M38113.1 17836 3.0572 0.74 0.0E+00 M38113.1 17840 3.0573 0.74 0.0E+00 Al419969.1 17840 3.0576 0.78 0.0E+00 BE266708.1 17850 3.0546 0.58 0.0E+00 BE266708.1 17861 3.0518 8.08 0.0E+00 AL118478.1 17862 3.0518 8.08 0.0E+00 AL118478.1 17863 3.0518 8.08 0.0E+00 AL118478.1 17864 3.0521 2.28 0.0E+00 AS7876.1 17865 3.0521 3.28 0.0E+00 AS7877.1 1886 3.0522 3.28 0.0E+00 AS7877.0.1 1884 3.0522 3.28 0.0E+00 AS7877.0.1 1886 3.2897 0.0E+00 AS7806.1	39.1 NT	Homo saplens cadherin 20 (CDH20) mRNA, complete cds
19546 32576 1.18 0.0E+00 M38113.1 17835 30571 3.2 0.0E+00 A1419969.1 17836 30572 0.74 0.0E+00 A1419969.1 17840 30573 0.74 0.0E+00 A1419969.1 17840 30576 0.78 0.0E+00 BE256708.1 17850 30546 0.59 0.0E+00 BE266708.1 17861 30514 1.05 0.0E+00 BE266708.1 17862 30518 8.08 0.0E+00 AU116478.1 17863 30518 8.08 0.0E+00 BE26674.1 17864 30520 2.26 0.0E+00 BE26274.1 17865 30521 3.28 0.0E+00 AF267737.1 17870 30521 3.28 0.0E+00 AF267737.1 1884 32621 1.03 0.0E+00 AF267737.1 1884 32681 1.03 0.0E+00 AF267737.1 1885 32687 0.78 0.0	NT 1.08	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
17835 30571 3.2 0.0E+00 11420775 17836 30572 0.74 0.0E+00 Al419899.1 17836 30573 0.74 0.0E+00 Al419899.1 17840 30576 0.78 0.0E+00 BE256708.1 17850 30546 0.59 0.0E+00 BE266708.1 17860 30514 1.05 0.0E+00 BE26874.1 17861 30518 8.08 0.0E+00 AU116478.1 17862 30518 8.08 0.0E+00 AU116478.1 17863 30520 2.26 0.0E+00 Z37076.1 17864 30521 3.28 0.0E+00 Z37076.1 17865 30521 3.28 0.0E+00 AF267737.1 1867 32681 1.03 0.0E+00 AF267737.1 1868 32687 1.03 0.0E+00 AF267737.1 1868 3276 0.79 0.0E+00 AF367737.1 1868 32704 0.7 0.0E+00 </td <td>1 NT</td> <td>Human neurofibromatbeis type 1 gene, expn x8</td>	1 NT	Human neurofibromatbeis type 1 gene, expn x8
17836 30572 0.74 0.0E+00 Al419999.1 17836 30573 0.74 0.0E+00 Al419999.1 17840 30576 0.78 0.0E+00 BE256708.1 17850 30546 0.58 0.0E+00 BE266708.1 17860 30514 1.05 0.0E+00 AU118478.1 17861 30518 8.08 0.0E+00 AU118478.1 17862 30518 8.08 0.0E+00 AU118478.1 17863 30520 2.26 0.0E+00 Z7876.1 17864 30520 2.26 0.0E+00 Z78776.1 17865 30521 3.28 0.0E+00 Z78777.1 17870 30521 3.28 0.0E+00 AF267737.1 1884 32687 1.08 0.0E+00 BF362770.1 1885 32704 0.79 0.0E+00 AV862362.1 1886 32704 0.7 0.0E+00 AV862382.1 1888 32715 2.33 0.0E+00	11420775 NT	Homo sapiens melanoma antigen, family B, 2 (MAGEB2), mRNA
17836 30573 0.74 0.0E+00 Al418869.1 17940 30576 0.78 0.0E+00 BE256708.1 17960 30546 0.58 0.0E+00 BE256708.1 17960 30514 1.05 0.0E+00 AU118478.1 17964 30518 8.08 0.0E+00 AU118478.1 17964 30529 2.26 0.0E+00 E282041.1 17965 30521 2.26 0.0E+00 Z37976.1 17965 30527 1.06 0.0E+00 AF257737.1 17965 30527 1.06 0.0E+00 AF257737.1 17965 32581 1.05 0.0E+00 AF257737.1 19646 32692 4.53 0.0E+00 BF666005.1 19646 32692 0.79 0.0E+00 L01978.1 19656 32692 0.79 0.0E+00 AL039581.1 19658 32704 0.7 0.0E+00 AL039581.1 19666 32715 2.33 0	9.1 EST_HUMAN	tp53c06.x1 Soares_NPL_T_GBC_S1 Homo sapiens cDNA done IMAGE:2112490 3' similar to SW:OXYB_HUMAN P22059 OXYSTEROL-BINDING PROTEIN.;
17940 30576 0.78 0.0E+00 BE256708.1 17950 30546 0.58 0.0E+00 BE904955.1 17963 30518 8.08 0.0E+00 AU118478.1 17964 30519 2.26 0.0E+00 BE28241.1 17965 30520 2.26 0.0E+00 Z37976.1 17965 30521 3.26 0.0E+00 Z37976.1 17965 30527 1.06 0.0E+00 AF257737.1 17965 30527 1.06 0.0E+00 AF257737.1 17967 30527 1.06 0.0E+00 AF257737.1 19842 32881 1.03 0.0E+00 BF66006.1 19646 32887 2.37 0.0E+00 BF66006.1 19650 32897 0.79 0.0E+00 AL039581.1 19658 32704 0.7 0.0E+00 BF30606.1 19686 32715 2.33 0.0E+00 BF30606.1 19686 32715 2.33 0.0E+	9.1 EST HUMAN	ty53c08x1 Soarss_NFL_T_GBC_S1 Home asplens cDNA clone IMAGE:2112490 3' similar to SW:OXYB_HUMAN P22059 OXYSTEROL-BINDING PROTEIN.
17950 30546 0.58 0.0E+00 BE904955.1 17960 30514 1.05 0.0E+00 AU118478.1 17963 30518 8.08 0.0E+00 BE282941.1 17964 30519 2.28 0.0E+00 Z37976.1 17965 30521 3.28 0.0E+00 Z37976.1 17965 30527 1.06 0.0E+00 AF257737.1 17965 30527 1.06 0.0E+00 AF257737.1 19640 32681 1.03 0.0E+00 AF257737.1 19640 32682 4.53 0.0E+00 BF66006.1 19640 32692 4.53 0.0E+00 BF66006.1 19650 32697 0.79 0.0E+00 AL039581.1 19656 32704 0.7 0.0E+00 AL039581.1 19666 32715 0.7 0.0E+00 BF30606.1 19686 32715 2.33 0.0E+00 BF30606.1		601115515F1 NIH MGC 16 Homo sapiens cDNA clone IMAGE:3356330 5
17960 30514 1.05 0.0E+00 AU118478.1 17063 30518 8.08 0.0E+00 BE282941.1 17964 30518 2.26 0.0E+00 Z37976.1 17965 30520 2.26 0.0E+00 Z37976.1 17965 30521 3.28 0.0E+00 AF257737.1 17970 30527 1.06 0.0E+00 AF257737.1 19642 32681 1.03 0.0E+00 AF257737.1 19646 32692 4.53 0.0E+00 BF666005.1 19646 32692 4.53 0.0E+00 L01978.1 19650 32697 0.79 0.0E+00 AV802362.1 19658 32704 0.7 0.0E+00 AL039681.1 19666 32714 6.87 0.0E+00 AL039681.1 19686 32715 2.33 0.0E+00 BF306968.1		601496743F1 NIH_MGC_70 Homo septems cDNA clone IMAGE:3898739 5
17963 30518 8.08 0.0E+00 BE282641.1 17894 30519 2.28 0.0E+00 237976.1 17864 30520 2.26 0.0E+00 237976.1 17865 30521 3.28 0.0E+00 AF257737.1 17865 30527 1.06 0.0E+00 AF257737.1 17870 30527 1.06 0.0E+00 AF257737.1 19842 32881 1.03 0.0E+00 BF310105.1 19842 32887 2.37 0.0E+00 BF66906.1 19850 32897 0.79 0.0E+00 L01878.1 19858 32704 0.7 0.0E+00 AW802362.1 19858 32704 0.7 0.0E+00 AL39581.1 19866 32704 0.7 0.0E+00 AL39581.1 19866 32714 5.87 0.0E+00 AL390508.1	78.1 EST_HUMAN	AU118478 HEMBA1 Homo sepiens CDNA clone HEMBA1003879 5
17864 30519 2.28 0.0E+00 237976.1 17864 30520 2.26 0.0E+00 237976.1 17865 30521 3.28 0.0E+00 AF257737.1 17870 30527 1.06 0.0E+00 AF257737.1 17870 30527 1.06 0.0E+00 AF257737.1 19842 32887 2.37 0.0E+00 BF566005.1 19845 32897 2.37 0.0E+00 L01978.1 19850 32897 0.79 0.0E+00 L01978.1 19858 32704 0.7 0.0E+00 AW502362.1 19858 32704 0.7 0.0E+00 AL039581.1 19866 32714 6.87 0.0E+00 AL039581.1 19886 32715 0.0E+00 AL039581.1	1.1	801148954F1 NIH_MGC_19 Homo sapiens dDNA clone IMAGE:3501829 51
17864 30520 2.26 0.0E+00 237976.1 17965 30521 3.28 0.0E+00 AF257737.1 17970 30522 3.28 0.0E+00 AF257737.1 19642 32681 1.08 0.0E+00 BF310105.1 19642 32687 2.37 0.0E+00 BF66006.1 19650 32697 0.79 0.0E+00 L01978.1 19650 32697 0.79 0.0E+00 AW502362.1 19658 32704 0.7 0.0E+00 AL039581.1 19668 32704 0.7 0.0E+00 AL039581.1 19669 32704 0.7 0.0E+00 AL039581.1 19669 32714 5.87 0.0E+00 BF30606.1	1 NT	H.saplens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
17965 30521 3.28 0.0E+00 AF257737.1 17965 30522 3.28 0.0E+00 AF257737.1 17970 30527 1.06 0.0E+00 AF310105.1 19642 32681 1.03 0.0E+00 BF56606.1 19646 32687 2.37 0.0E+00 BF56606.1 19650 32692 4.53 0.0E+00 LD1978.1 19650 32697 0.79 0.0E+00 AW502362.1 19658 32704 0.7 0.0E+00 AL039581.1 19668 32704 0.7 0.0E+00 AL039581.1 19669 32704 0.7 0.0E+00 AL039581.1 19669 32704 0.7 0.0E+00 AL039581.1 1968 32704 0.7 0.0E+00 AL039581.1 1969 32716 2.33 0.0E+00 LA1302.1	1 NT	H.saplens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
17865 3.0522 3.28 0.0E+00 AF267737.1 17970 30527 1.06 0.0E+00 AF310105.1 19637 3.2881 1.03 0.0E+00 BF782770.1 19642 3.2887 2.37 0.0E+00 BF586006.1 19646 3.2692 4.53 0.0E+00 LD1978.1 19650 3.2697 0.79 0.0E+00 AW502362.1 19658 3.2704 0.7 0.0E+00 AL039581.1 19659 3.2705 0.7 0.0E+00 AL039581.1 19669 3.2716 0.7 0.0E+00 AL039581.1 1969 3.2715 0.3 0.0E+00 AL039581.1	37.1 NT	Homo saplens cillary dynein heavy chain 9 (DNAH9) mRNA, complete cds
17970 30527 1.06 0.0E+00 AF310105.1 19637 32681 1.03 0.0E+00 BE782770.1 19642 32687 2.37 0.0E+00 BF56906.1 19650 32692 4.53 0.0E+00 L01978.1 19650 32697 0.79 0.0E+00 AW502362.1 19658 32704 0.7 0.0E+00 AL039581.1 19658 32705 0.7 0.0E+00 AL039581.1 19669 32715 5.87 0.0E+00 BF30606.1 19699 32715 2.33 0.0E+00 U41302.1		Homo saplens ciliary dynein heavy chain 9 (DNA-H9) mRNA, complete cds
19637 32681 1.03 0.0E+00 BE762770.1 19642 32687 2.37 0.0E+00 BF56906.1 19646 32692 4.53 0.0E+00 L01978.1 19650 32696 0.79 0.0E+00 AW502362.1 19658 32704 0.7 0.0E+00 AL039581.1 19658 32705 0.7 0.0E+00 AL039581.1 19669 32711 5.87 0.0E+00 BF30606.1 19699 32715 2.33 0.0E+00 U41302.1	35.1 NT	Homo saptems NALP1 mRNA, complete cds
19642 32887 2.37 0.0E+00 BF569006.1 19646 32692 4.53 0.0E+00 L01978.1 19650 32696 0.79 0.0E+00 AW502362.1 19658 32704 0.7 0.0E+00 AW502362.1 19658 32705 0.7 0.0E+00 AL039581.1 19686 32711 5.87 0.0E+00 BF30606.1 19699 32715 2.33 0.0E+00 L41302.1		QV3-NT0022-140600-223-f01 NT0022 Hamo septens cDNA
19646 32692 4.53 0.0E+00 L01978.1 19650 32696 0.78 0.0E+00 AW502362.1 19658 32704 0.7 0.0E+00 AL039581.1 19658 32705 0.7 0.0E+00 AL039581.1 19686 32711 5.87 0.0E+00 BF306068.1 19699 32715 2.33 0.0E+00 U41302.1	16.1 EST_HUMAN	802/185852F1 NIH_MGC_45 Hamo sepiens dDNA clone IMAGE:4310076 5
19650 32696 0.78 0.0E+00 AW 502362.1 19650 32697 0.78 0.0E+00 AW 502362.1 19658 32704 0.7 0.0E+00 AL039581.1 19686 32705 0.7 0.0E+00 AL039581.1 19686 32711 5.87 0.0E+00 BF306006.1 19689 32715 2.33 0.0E+00 U41302.1		Human type IV, sodium channel alpha polypeptide (SCN4A) gene, excn 19
19850 32897 0.7e 0.0E+00 AW602362.1 19658 32704 0.7 0.0E+00 AL039581.1 19686 32705 0.7 0.0E+00 AL039581.1 19686 32711 6.87 0.0E+00 BF30606.1 19689 32715 2.33 0.0E+00 U41302.1	82.1 EST_HUMAN	UHIF-BROD-aka-d-10-0-UI.rl NIH_MGC_52 Hamo sepiens cDNA clane IMAGE:3076290 5'
19658 32704 0.7 0.0E+00 AL039581.1 19686 32711 6.87 0.0E+00 BF306906.1 19689 32715 2.33 0.0E+00 U41302.1	82.1 EST_HUMAN	UHF-BROD-aka-d-10-0-UI.rf NIH_MGC_52 Homo sepiens cDNA clone IMAGE:3076290 5'
19858 32705 0.7 0.0E+00 AL039581.1 19866 32711 6.87 0.0E+00 BF308906.1 1989 32715 2.33 0.0E+00 U41302.1	H.1 EST_HUMAN	DKFZp434D2211_r1 434 (synonym: htee3) Homo sepiens cDNA clone DKFZp434D2211 5'
1966 32711 6.87 0.0E+00 BF30698.1 1969 32715 2.33 0.0E+00 U41302.1		DKFZp434D2211_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D2211 5'
19899 32715 2.33 0.0E+00 U41302.1	8.1 EST_HUMAN	601889823F1 NIH_MGC_17 Hamo sepiems cDNA dane IMAGE:4123948 5
	- N	Human chromosome 16 creetine transporter (SLOSA8) and (CDM) peratogous genes, complete ods
19404 324/4 1.18 0.0E+00 AL049/84.1	14.1	Novel human gene mapping to chomosome 13
7008 19700 32754 0.65 0.0E+00 AB026893.1 N	33.1 NT	Homo sapiens mRNA for vescular cadherin-2, complete cds

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	SEQ ID	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acessian No.	Top Hit Detrabase Source	Top Hit Descriptor
7008	19700	32755	0.65		0.0E+00 AB026893.1	NT	Homo seplens mRNA for vascular cadherin-2, complete ods
7013	19705	32761	1.07	0.0E+00	0.0E+00 AU137738.1	EST_HUMAN	AU137738 PLACE1 Homo septiens cDNA clone PLACE1007120 5
7013	19705	32762	1.07	0.05+00	0.0E+00 AU137738.1	EST_HUMAN	AU137738 PLACE1 Hamo septens cDNA clone PLACE1007120 5
7019	19711	32768	1.2		0.0E+00 AW954806.1	EST_HUMAN	EST368876 MAGE resequences, MAGC Hamo sepiens cDNA
7020	19712	32769	6.0		0.0E+00 BE254103.1	EST_HUMAN	601113958F1 NIH_MGC_16 Hamo septens cDNA clane IMAGE:3354566 5'
7033	19725	32781	0.98	0.0E+00 L01973.1		N _T	Human type VI sodium channel alpha polypeptide (SCN4A) gene, exon 14
7041	19732	32791	,		5.1	¥	Homo sepiens mRNA for KIAA0408 protein, pertial cds
7041	19732	32792	0.64	0.0E+00 AB00793	5.1	NT TN	Homo sapiens mRNA for KIAA0405 protein, partial cds
7047	19738	32799			3.1	EST_HUMAN	AU133213 NT2RP4 Hamo septiens cDNA clone NT2RP4001558 5'
7062	19753	32818	0.95	00+30.0	11428081 NT		Homo saplens membrane protein CH1 (CH1), mRNA
7064	19755	32820	0.58		0.0E+00 AA312125.1	EST HUMAN	EST182818 Jurkat T-cells VI Homo septems cDNA 5' and
7069	19760		2.57		0.0E+00 AU143706.1	EST_HUMAN	AU143708 Y79AA1 Homo sepiens cDNA clone Y79AA1002365 51
0707	19761	32825	0.94		883		Homo sepiens netrin 1 (NTN1), mRNA
20707	19770	32834			0.0E+00 BE891286.1	EST HUMAN	601431819F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917164 5
7079	19770	32835		l	3.1	EST_HUMAN	601431819F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917164 5
7100	17981	30495	2.54	0.0E+00[AF13728	3.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
7100	17981	30496		0.0E+00 AF137286	1.1	TN	Homo sapiens keretin 12 (KRT12) gene, complete cds
7122	19810	32876	5.01	0.0E+00	11436690 NT	N	Homo sapiens witamin D (1,25- dihydroxywitamin D3) receptor (VDR), mRNA
7122	19810	32877	5.01	0.0E+00	11436899 NT	TN	Homo sapiens vitamin D (1,25- dihydroxyvitamin D3) receptor (VDR), mRNA
7137	19824	32891	0.55	0.0E+00 AF22774	13	F	Homo sabiens voltage-dependent calcium channel alpha 10 subunit isoform ac (CACNA10) mRNA, complete cds
7156	19843	32811	37.67	0.0E+00 A1128344	A1128344.1	EST HUMAN	qo87a07xt Scares_placenta_bto8weets_ZNbHP8tx8W Homo sapiens cDNA clone IMAGE:1714844 3' similar to SW:ARSD_HUMAN P51689 ARYLSULFATASE D PRECURSOR ;contains element HGR repetitive element;
							qc67a07xt Scares_placenta_8tc9weeks_2NbHP8tc9W Home sapiens cDNA clone IMAGE:1714644 3' similar to SW:ARSD_HUMAN P51689 ARYLSULFATASE D PRECURSOR; contains element HGR
138	19843	32912	"	0.0E+00 AI128344		I_HUMAN	repetitive element;
7158	19846	32914	0.08	0.0E+00	0.0E+00 AF227135.1	LN	Homo sapiens candidate taste receptor T2R9 gene, complete cds
7158	19845	32915	0.00	0.0E+00	0.0E+00 AF227135.1	۲	Homo sapiene candidate taste receptor T2R9 gene, complete cds
7181	19848	32918	39'4	0.0E+00	11426392 NT		Homo sapiens myosin, heavy polypeptide 8, skoletal muscle, perhatal (MYH8), mRNA
7161	19848	32919	4.66	0.0E+00	11426392 NT		Homo sapiens mycsin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
7163	19850		15.23	0.0E+00	0.0E+00 BF337375.1	EST_HUMAN	602035089F1 NCI_CGAP_Bm64 Home sepiens cDNA clone IMAGE:4182839 51
7165	19852	32921	2.85	0.0E+00 AA128453	5		zn60f09.r1 Stratagene musche 937209 Homo sapiens cDNA clone IMAGE:562601 5' stratiar to TR:Ge06562 G906562 NEBUI.N.;
1							

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Table 4
Single Exon Probes Expressed in Brain

Probe SEQ ID	Exan SEQ ID	ORF SEQ	Expression	Most Similar (Top) Hit	8	Top Hit	Single Exon Probes Expressed in Brain Top Hit Descriptor
NO:		Ö. Ö.	Signal	BLAST E Vætue	No.	Source	
7460	20133	33224	4.16	0.0E+00	0.0E+00 AI752581.1	EST_HUMAN	cn17d05.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn17d05 random
7535	20205	33301	1.83	0.0E+00	0.0E+00 AF064205.1	LN	Homo sapiens dynactin 1 (DCTN1) gene, alternatively spiloed products, exons 7 through 32 and complete ods
7535	20205	33302	1.83	0.0E+00	0.0E+00 AF064205.1	H	Homo saplens dynactin 1 (DCTN1) gene, etternatively spliced products, exons 7 through 32 and complete ode.
7543		33313	1.14	0.0E+00	0.0E+00 U74315.1	EST_HUMAN	HSU74315 Human chromosome 14 Homo sapiens oDNA clone 1-4
7557	20227	3330	1.1	0.0E+00	11417342 NT	Ę	Homo septens seme domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplesmic domain, (semaphorin) 5A (SEMA5A), mRNA
7570	20239	33343	2.28	0.05+00	0.0E+00 AW672785.1	EST_HUMAN	be01e06.11 NIH_MGC_7 Hamo septens aDNA done IMAGE:2823106 5' similar to SW:P101_PIG 002898 PHOSPHATIDYLINOSITOL 3-KINASE REGULATORY SUBUNIT;
7570	20238	33344	2.28	0.0E+00	0.0E+00 AW672785.1	EST_HUMAN	ba01e06.17 NIH MGC_7 Homo septens CDNA clone IMACE:2823106 5' similar to SW:P101_PIG C02896 PHOSPHATIDYLINOSITOL 3-KINASE REGULATORY SUBUNIT;
7586	20264	33360	1.97	0.0E+00	0.0E+00 AI825504.1	EST_HUMAN	wb17g05x1 NCI_CGAP_GC8 Homo saplens cDNA done IMAQE;2305676 3' similar to TR:075363 075363 ABC1.
7586	20254	33361	18.1	0.0E+00	0.0E+00 AI825504.1	EST_HUMAN	wb17g05.x1 NCI_CGAP_GC8 Homo sapiens cDNA done IMAGE:2305976 3' similar to TR:075363 075363 ABC1;
7594		33370	1.51	0.0E+00	6912735 NT	Z L	Homo saplens transient receptor potential channel 5 (TRPC5), mRNA
7599		33373	1.09	0.0E+00	0.0E+00 N78128.1	EST HUMAN	za88e05.s1 Scenes, fetal_king_NbHL19W Homo saptens cDNA clone IMAGE:289456 3'
7604			5.87	0.0E+00	0.0E+00 BF217905.1	EST_HUMAN	601885465F1 NIH_MGC_67 Homo septems cDNA clame IMAGE:4103729 5
7613	20279		5.41	0.0E+00	0.0E+00 AU129822.1		AU129622 NT2RP2 Homo sepiens cDNA clone NT2RP2005913 5
7633		ŀ	0.97	0.0E+00	0.0E+00 AW069274.1	П	042e09.x1 Jia bone marrow stroma Homo sepiens cDNA clone HBMSC_0742e09.31
7833	25117	33407	76.0	0.0E+00	0.0E+00 AW069274.1	T HUMAN	ar42e09.x1 Jie bane merrow strome Homo sepiens aDNA clane HBMSC_ar42e09.3°
7636	20301	33409	6.28	0.0E+00	4501848 NT	N.	Homo saptens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
7643	20308	33416	1.13	0.0E+00	0.0E+00 AV758467.1	EST_HUMAN	AV758467 BM Homo saplens cDNA clone BMFBGG05 5
7645	20309	33417	6.31	0.0E+00	0.0E+00 BE739870.1	EST_HUMAN	601593156F1 NIH_MGC_9 Hamo sepiens cDNA done INAGE:3947385 5
7645	20309	33418	6.31	0.0E+00	0.0E+00 BE739870.1	Γ	601593136F1 NIH_MGC_9 Homo saplens cDNA clone MAGE:3947385 5
7646	20310	33419	1.18	0.0E+00	6912461 NT	F	Homo sapiens atrophin-1 interacting protein 1; activin receptor interacting protein 1 (KIAA0705), mRNA
7646	20310	33420	1.18	0.05+00	6912461 NT		Homo sepiens atrophin-1 Interacting protein 1; activin recoptor inferacting protein 1 (KJAA0705); mRNA
7647	20311	33421	0.71	0.0E+00	0.0E+00 AU120424.1	T_HUMAN	AU120424 HEMBB1 Homo sepiens cDNA clone HEMBB1000655 5'
7847	20311	33422	0.71	0.0E+00	4.1		AU120424 HEMBB1 Homo sepiens aDNA clone HEMBB1000655 5'
7680	20344	33456	1.81	0.0E+00 BE78761	BE787610.1	EST_HUMAN	601481713F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884258 5

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	Top Hit Descriptor	601481713F1 NIH_MGC_88 Homo sepiens cDNA clone IMAGE:3884258 5	zcsorio.ri Pencreetto Islet Homo septens cDNA clone IMAGE:338443 5	UI-HF-BK0-eat-b-08-0-UI.r1 NIH_MGC_38 Hamo sapiens cDNA clane IMAGE:3053915 5	nz13808.s1 NCI_CGAP_GCB1 Hamo sapiens cDNA clone IMAGE:1287638 3' similar to gb:U01828 MICROTUBULE-ASSOCIATED PROTEIN 2 (HUMAN);	riz13e08.s1 NCI_CGAP_GCB1 Homo septens cDNA clone IMAGE:1287638 3' similar to gb:U01828	MICACI UBOLE-NOSCOCIA LE LA TICO LESSA A COMPANA MICACIA SE MICACI	13310/ NIZATA FALID SQUARE CONTROL TO THE TANCES SANDED E	601150347F1 NIH MGC_19 Home saperts curve crore Inventional Victorial And Additional And MgG-1984410 5	2001c06.rt Stratagene colon (#637204) monte esperia cultum colon minos	601672310F1 NIH MGC 20 Homo septems CUNA Ciche IMAGE 3903131 d	2833H08.r1 Sources retina N224HR Homo sepiens CUNA Crone IMPACE:350631 3	601305658F1 NIH_MGC_39 Homo eaplens cDNA clone IMAGE:3839903 5	Human amykold-beta protein (APP) gena, exon 11	Human amyloid-beta protein (APP) gene, excn 11	bb34d02.y1 NIH_MGC_10 Homo sapiens dDNA clone IMAGE:2985123 5' similar to 1 K:064632' 064632	F17K2.24 PROTEIN.;	bi34d02.y1 NIH_MGC_10 Homo sepiens cDNA clone IMAGE:2885123 5 similar to 1 R:004d52 004d52 F17X2.26 PROTEIN. :	Jan 1907 of Strategies and Strategies (2004) And Strategies (2004) Anno series (2004) Anno series (2004)	G300482 POL-REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);	MR0-ST0031-061000-003-e11 ST0031 Hamp sepiens CLINA	Homo septens mRNA for KIAA0884 protein, pertiel cds	AU142402 Y79AA1 Homo septems cDNA clone Y79AA1000277 6	601285550F1 NIH_MGC_44 Hamo septens aDNA clane IMAGE:3607237 5	601285550F1 NIH_MGC_44 Hamo septens aDNA clane IMAGE:3607237 5	ze05d01.r1 Sogree_fetal_heart_NbHH19W Homo septens cDNA clone IMAGE:338081 5	ze05d01,r1 Sogres_fetal_heart_NbHH19W Homo sepiens cDNA clone IMAGE:338081 5	602153008F1 NIH_MGC_81 Hamo septems aDNA clame IMAGE:4294128 5	AU134114 OVARC1 Homo sepiens dDNA done OVARC1001298 6	602069632F1 NCI_CGAP_Bm64 Hamo sepiens cDNA clone IMAGE:4212727 5	602069632F1 NCI_CGAP_Bm64 Hamo sepiens cDNA clone IMAGE:4212/2/5	DKFZp761P092_r1 761 (synonym: hamy2) Homo sepiens cDNA clone DKFZp761P092 5	DKFZp761P092_r1 761 (synonym: hamyz) Homo sapiens cunna done Unitzp761F01F092.5
	Top Hit Detabase Source	EST_HUMAN 0	EST HUMAN Z	EST HUMAN U		1		Т	T	╗	П		EST_HUMAN 6	INT IN	IN TN	<u>a</u>	EST_HUMAN F	DEST HIMAN	Т		EST HUMAN	± N	EST_HUMAN /	EST_HUMAN 6		EST HUMAN 2	EST_HUMAN A	EST_HUMAN C	EST_HUMAN /	EST_HUMAN (EST HUMAN	\Box	EST HUMAN
	Top Hit Acession No.	0.1		32.1			1	1.5				0.0E+00 AA017021.1	0.0E+00 BE736046.1	1	1		0.0E+00 AW674581.1	0 05400 AW674884 1	1.100-1011	0.0E+00 AA397551.1	AW387131.1	AB020691.1	0.0E+00 AU142402.1	BE388421.1	BE388421.1	0.0E+00 W95278.1	0.0E+00 W96278.1	BF673096.1	AU134114.1	0.0E+00 BF526634.1	0.0E+00 BF525534.1	0.0E+00 AL120124.1	0.0E+00 AL120124.1
	Most Similar (Top) Hit BLAST E Value	0.0E+00 BE78761	0.0E+00 W52673.	0.0E+00/	00-400		0.0E+00 AA76069	0.0E+00/	0.0E+00 BE31301	0.0E+00/	0.05+00	0.0E+00	0.0E+00	0.0E+00 M34872.	0.0E+00 M34872		0.0E+00	200	32.0	0.0E+00	0.0E+00 AW3871	0.0E+00 AB02066	0.0E+00	0.0E+00 BE3884;	0.0E+00 BE38842	0.0E+00	0.0E+00	0.0E+00 BF57305	0.0E+00 AU1341	0.0E+00	0.0E+00	0.0E+00	0.0E+00
	Expression Signal	1.81	0.63	95.0	97.0		0.78	0.64	0.82	1.13	0.84	0.45	2.31	10.48	10.46		0.74	72.0	6/3	3.9	1.4.1	0.73	7.02	1.83	1.63	1.8	8.	6.80	0.67	98'0	0,95	1.50	1.59
-	ORF SEQ ID NO:	33457			20 74 74		33516	33572	33630	33645	33650	33672	33688	33703			33734		3/3	33741	33742		33744					L		33782			33814
	Exam SEQ ID NO:	20344	20384	20308				20448	20507	20519	ı	1			20576		20804	1	2002	20611		L	Ŀ	L	L	L	<u>i </u>		1	L	1		20687
	Probe SEO 10 NO:	0892	2	1		3	7735	7762	7812	7824	7837	7849	7886	788	1884		2002		808/ 2	7916	7018	7027	7922	7828	7028	7942	7942	784	78	7962	7062	7992	7982

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similer (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Detabese Source	Top Hit Descriptor
8035			1.32	0.0E+00	0.0E+00 BE877693.1	EST_HUMAN	601485254F1 NIH_MGC_69 Homo saplens cDNA clone IMAGE:3887773 51
8057		33882	2.48		0.0E+00 AW500549.1	EST_HUMAN	UI-HF-BNO-akj4-01-0-UI.r1 NIH_MGC_50 Homo saplens cDNA clone IMAGE:3077496 5
8065	20759	33888	16.05		0.0E+00 AW157233.1	EST HUMAN	au83b08.x1 Schneider fetal brain 00004 Homo saplens oDNA clone IMAGE:2783799 3' similar to TR:0e0463 060463 TYPE-2 PHOSPHATIDIC ACID PHOSPHOHYDROLASE. [1];
8082	20778	33906	89.0	0.0E+00	0.0E+00 AW 072395.1	EST HUMAN	xe07d12x1 Soures, NRL_T_GBC_S1 Homo sepiens cDNA done IMAGE:2967639 3' similar to contains element OFR repetitive element;
8089		33924	1.09		22	L.	Homo sepiens centrosomel protein 2 (CEP2), mRNA
8102	l	33927	1.07	0.0E+00 W01818	-	EST_HUMAN	za36d05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294633 51
8104					1.7	EST HUMAN	601578195F1 NIH_MGC_9 Hamo septens aDNA clane IMAGE:3926998 5'
8104		33830	1.22		7.1	EST_HUMAN	601578195F1 NIH_MGC_9 Hamo sepiens aDNA clane IMAGE:3926998 5'
8115	20802	33943	1.46	0.0E+00	2.1	LN	Homo sapiens Xq pseudoautosomal region; segment 1/2
8154	20848	33980	0.95	0.0E+00	0.0E+00 Al367350.1	EST_HUMAN	qv05c12.x1 NCI_CGAP_Ut2 Homo septens cDNA clone IMAGE:1989334 3' similar to TR:C14673 Q14673 KIAA0164 PROTEIN.;
8166	20859	33001	2.63	0.0E+00 BE67415	7.1	EST_HUMAN	7d70a04.x1 NCI_CGAP_Lu24 Home saplens cDNA clone IMAGE:3278862 3' similar to TR:095783 095793 STAUFEN PROTEIN;
8167	20861	33983	1.19	0.0E+00 Al885671		EST HUMAN	WISOB10.x1 NCI_CGAP_BIN25 Homo septems cDNA clone IMAGE:2429275 3' similar to SW:COGT_HUMAN P50281 MATRIX METALLOPROTEINASE-14 PRECURSOR:
8180			1.07	0.0E+00 BE56365		EST_HUMAN	601334790F1 NIH_MGC_39 Homo saplens cDNA clone IMAQE:3888655 51
8180	20874	34010	1.07	0.0E+00	0.0E+00 BE563650.1	EST_HUMAN	601334790F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688655 51
8189	20883	34020	1.63	0.0E+00	11427235 NT	Z	Homo sepiens Chediak-Higashi syndrome 1 (CHS1), mRNA
8189	20883	34021	1.63	0.0E+00	11427235 NT	Z	Homo sapiens Chedlak-Higashi syndrome 1 (CHS1), mRNA
8191	20885	34023	3.2	0.0E+00	0.0E+00 AA403192.1	EST HUMAN	zv69f02.r1 Soares, total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMACE:758619 5' similar to TR:G1304132 G1304132 TPRD.;
8191	20885	34024	3.2	0.0E+00		EST HUMAN	zv6002.r1 Sceres, total_fetus_Nb2HF8_9w Homo sepiens cDNA clone IMAGE:758619 5' similer to TR:G1304132 G1304132 TPRD.;
8231	20926		4.63	0.0E+00 AA39861	-	EST HUMAN	zf3s08.s1 Soeres lestis NHT Homo sapiens cDNA done IMAGE:727958 3' similar to gb:S85855 PROHIBITIN (HUMAN);
8240	20834	34071	0,55	0.0E+00 BE8375g	3.1	EST HUMAN	RC2-FN0094-120600-013-h07 FN0094 Homo sepiens cDNA
8241	20835	34072	1.17	0.0E+00 AW36487	1.4	}	QV3-DT0045-221299-048-c07 DT0045 Homo sapiens cDNA
8241		34073	1.17	0.0E+00 AW36487	4.1	EST_HUMAN	QV3-DT0045-221299-046-c07 DT0045 Homo sapiene cDNA
8260		34092	1.88	0.0E+00 BE61258	3.1	EST_HUMAN	601452412F1 NIH_MGC_86 Homo sepiens cDNA clone INAGE:3856179 5
8260		34083	1.88	0.0E+00 BE61258		EST_HUMAN	601452412F1 NIH_MGC_66 Hamo septens cDNA clane IMAGE:3856179 5
8275			1.52	0.0E+00	0.0E+00 AL163209.2	NT	Homo saplens chromosome 21 segment HS21C009
8275	L I	34111	1.52	0.0E+00		NT	Homo saplens chromosome 21 segment HS21C009

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Table 4
Single Exon Probee Expressed in Brain

			j		5	אסו ביוועש פולי	Single Lyon Flores Explement III Didnii
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Velue	Top Hit Acession No.	Top Hit Databese Source	Top Hit Descriptor
8238	20980	34120	1.3	0.0E+00 A1884477	A1884477.1	EST_HUMAN	wm33a11x1 NCI_CGAP_Uk4 Homo septens cDNA clone IMAGE:2437724 3' similar to TR:075457 075457 CYTOSOLIC PHOSPHOLIPASE A2-GAMMA.;
8293	20987	34128	1.27	0.0E+00	0.0E+00 AA502294.1	EST_HUMAN	ne26410.s1 NCI_CGAP_Co3 Homo sepiens dDNA done IMAGE:882259.3' striller to TR:G1136434 G1136434 KIAA0187 PROTEIN.;
8238	20802		0.59	0.0E+00	11416799 NT	NT.	Homo sapiens protocacherin beta 3 (PCDHB3), mRNA
8305	20899	34137	1.02	0.0E+00 A1580780	AI580780.1	EST_HUMAN	tat04f11.x1 Sogres_pregnant_uterus_NbHPU Homo sapiens cDNA clone IVAGE:2043117.3
8308	21002		1.84	0.01100	0.0E+00 BE890797.1	EST_HUMAN	601431238F1 NIH_MGC_72 Homo sepiens cONA clone IMAGE:3916569 5'
8334		34163			AW245765.1	EST_HUMAN	2822701.5prime NIH_MGC_7 Hamo sapiens cDNA clone IMAGE:2822701 5'
8334	21027	34164	0.72		AW246785.1	EST_HUMAN	2822701.5pttme NIH_MGC_7 Homo sepiens cDNA clone IMAGE:2822701 5
8335					4758095 NT	TN	Homo sapiens mitogen-ectivated protein kinase kinase kinase 13 (MAP3K13), mRNA
8335		34166			4758995 NT	N	Homo sapiens mitogen-activated protein kinase kinase kinase 13 (MAP3K13), mRNA
8339	21032	34169	69'0	0.0E+00 U88084.		TN	Human zinc finger protein (ZNF165), gene, exons 2 and 3
8339	21032	34170	65.0	0.0E+00 U88084.		ĮN.	Human zinc finger protein (ZNF166), gene, exons 2 and 3
8404	21097	34233	99'0		0.0E+00 AJ251760.1	TN	Horno sapiens NESP55, GNAS1 antisense (partial) and XLalphas (partial) genes
8409	21102	34239	2.63	0.0E+00 X98922.1		NT	H.sepiens mRNA for gamma-glutamytransferase
8409	21102	34240	2.63	0.0E+00 X98922.1		TN	H.sapiens mRNA for gamma-glutamy/transferase
8409	21102	34241	2.63	0.0E+00 X98922.		IN	H.sepiens mRNA for gamma-glutamytransferase
8424	1	34255				N.	Human immunoglobulin-like transcript-3 mRNA, complete cds
8465	21157	34300	88.0		0.0E+00 AF022655.1	ΤN	Homo sapiens cep250 centrosome sesociated protein mRNA, complete ods
8465	21157		88.0	0.0E+00	0.0E+00 AF022655.1	TN	Homo sapiens cep250 centrosome associated protein mRNA, complete cds
8468	21160	34303	2.28	0.0E+00 AU13167	1.1	EST_HUMAN	AU131671 NT2RP3 Hamo septens cDNA clone NT2RP3003016 5
8483	21175	34320	0.65	0.0E+00	11426572 NT	NT	Homo sepiens immunoglobulin superfamily, member 2 (IGSF2), mRNA
8487	21179		1.92	0.0E+00 AW 5135	AW513513.1	EST_HUMAN	2046e01.x1 NCI_CGAP_Ut1 Homo septens cDNA clone IMAGE:2707032 3' similær to gb:M14123_cds4 RETROVIRUS-RELATED POL POLYPROTEIN (HUMAN);
							HUM084002B Clortech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-084002
8489	21181	34323	14.65	0.0E+00 D52650.	D52650.1	EST HUMAN	io
8520			404		5.1	EST_HUMAN	601236488F1 NIH_MGC_44 Hamo septems cDNA clane IMAGE:3608709 5'
8528		34390			5.1	EST_HUMAN	#32e04.r1 Soares overy furnor NDHOT Homo septens cDNA clone IMAGE:724062 51
8228	21220		19.2	0.0E+00 BF31394	BF313946.1	EST HUMAN	601900571F1 NIH_MGC_19 Homo septens cONA clane IMAGE:4129744 5
							Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3
8535	21227	34369	0.52	0.0E+00	11424387 NT		(LILRB3), mRNA
8540		34374		0.0E+00 AW 1396	73.1		UI-H-BI1-ect0-12-0-UI.s1 NCI_CGAP_Sub3 Homo sepiens cDNA clone IMAGE:2717687 31
8540	21232		1.46	0.0E+00	73.1	EST_HUMAN	UI-H-Bi1-ed0-12-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717687 3'
	i						

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Single Exon Probes Expressed in Brain

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Detabase Source	Top Hit Descriptor
8645	24237		0.49	0.05+00	0.0E+00 AI640150.1	EST_HUMAN	ws30b10.x1 NCI_CGAP_Kid11 Homo saplens cDNA clone IMAGE:2299579 3' similær to TR:015044 015044 KIAA0335: ;
8564	21256	34383	0.76	0.0E+00	0.0E+00 BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
8574	21266		0.59	0.0E+00	0.0E+00 AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
8580	21272		6.80	0.0E+00 BE2802	BE280272.1	EST_HUMAN	601150051F1 NIH_MGC_19 Hamo septens cDNA clane IMAGE:3502836 5'
8585	21277	34414	2.51	0.0E+00	0.0E+00 BF700165.1	EST_HUMAN	602127664F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284542 5
8585	21277			0.0E+00	0.0E+00 BF700165.1	EST_HUMAN	602127664F1 NIH_MGC_56 Hamo sepiens aDNA clane IMAGE:4284542 5
8585	21277		2.51	0.0E+00	0.0E+00 BF700165.1	EST_HUMAN	602127664F1 NIH_MGC_56 Hamo sepiens cDNA clane IMAGE:4284542 5'
8800	21292		0.53		0.0E+00 A/458722.1	EST_HUMAN	tk13h11x1 NCI_CGAP_Lu24 Homo septens cDNA clone INAGE:2150949 3'
8626	21318	34460			0.0E+00 AL449770.1	EST_HUMAN	AL449770 Homo sapiens fetal brain (Stavides GS) Homo sapiens cDNA
863	24232	24464	ķ	00000	0.05400 4.8082827.4	NALM BY FOR	or80g02.s1 NCI_CGAP_Lu5 Homo saplens cDNA clone IMAGE:1602194 3' similar to gb:M36072.60S PIROSOMAI PROTEIN 7A (HIMAAN)
8637	21328			0.0E+00	10947037 NT	L	Homo sapiens ankorin 1. endinocytic (ANK1), transcript varient 1. mRNA
8637	21320			0.0E+00	10947037 NT	ĽΖ	Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript variant 1, mRNA
88	21352			0.0E+00 Y11107.3	Y11107.3	F	Homo sapiens ITGB4 gane for Integrin beta 4 subunit, exons 3-41
8662	21354	34501	1.62	0.0E+00 BE2789*	BE278917.1	EST_HUMAN	801158330F1 NIH_MGC_21 Homo sepiens cDNA clone IMAGE:3139734 5'
8672	21364		1.01	0.0E+00 AV7183	AV718377.1	EST_HUMAN	AV718377 FHTB Home sepiens cDNA clone FHTBAAF11 5'
02.98	24374	34548	2 22	000	0.05-00 0.00337377 4	NAVE TO FOR	xw73c07.x1 NCI_CGAP_Pan1 Home saplens cDNA done IMAGE:2833644 3' similar to gb:X53587
158	21377				0.0E+00 AU124051.1	EST HUMAN	AU124051 NT2RM2 Homo septems CDNA clone NT2RM2001575 5'
8761	21453			1	0.0E+00 AU140704.1	EST HUMAN	AU140704 PLACE4 Homo sapiens cDNA clone PLACE4000089 5
87771	21463		98.0	0.0E+00	0.0E+00 AB007923.1	Z	Homo sapiens mRNA for KIAA0454 protein, periled cds
8778	21468		0.54	0.0E+00 R17132	R17132.1	EST_HUMAN	yg09e09.r1 Source Infant brain 1NIB Homo septens cDNA clone IMAGE:31674 5'
8778	21468	34615	0.54	0.0E+00 R17132	R17132.1	EST_HUMAN	yg08e09.r1 Soures Infant brain 1NIB Homo sapiens cDNA clone IMAGE:31674 6
8780	21472		4.43	0.0E+00	0.0E+00 AW 592233.1	EST_HUMAN	Hf48a09.x1 Soeres_NFL_T_GBC_S1 Harro sepiens cDNA done IMAGE:2835096 3'
8780	21472		4.43	0.0E+00	0.0E+00 AW 592233.1	EST_HUMAN	H48a09.x1 Scarre_NFL_T_GBC_91 Homo septems cDNA clone IMAGE:2835096 3'
8815	21507	34652	0.47	0.0E+00	0.0E+00 AU128804.1	EST HUMAN	AU128804 NT2RP2 Homo sapiens cDNA clone NT2RP2004245 5'
8827	21519	34664	1.04	0.0E+00	0.0E+00 AV714784.1	EST_HUMAN	AV714764 DCB Homo septens cDNA clone DCBAUA06 5"
8843	21535	34679		0.0E+00	AL040428.1	EST HUMAN	DKFZp434C1814_s1 434 (synonym: https3) Hamo sapiens cDNA clane DKFZp434C1814 3'
8843	21535	34680	2.79	0.0E+00	0.0E+00 AL040428.1	EST_HUMAN	DKFZp434C1814_s1 434 (synonym: htes3) Hamo sapiens cDNA clone DKFZp434C1814 3'
8840	21540	34686	1.17	0.0E+00	0.0E+00 AF133901.1	L	Homo sapiens killer inhibitory receptor 2-2-1 (KIR221) and killer inhibitory receptor 2-2-2 (KIR222) genes, pertial cds
8851	21542	L		0.0E+00 AB04094	AB040945.1	¥	Homo saplens mRNA for KIAA1512 protein, partial cds
8858	21549		0.65	0.0E+00	0.0E+00 BF675505.1	EST_HUMAN	802138483F1 NIH_MGC_83 Homo sepiens cDNA done IMAGE:4274708 5

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Proba SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession 'No.	Top Hit Database Source	Top Hit Descriptor
0988	21551		0.8		0.0E+00 BF058289.1	EST_HUMAN	7K29b03.x1 NCI_CGAP_Ov18 Homo sepiens cDNA done IMAGE:3476892.3' similar to TR:036448 039448 S GAG.;
8889	21580	34720	3.97	0.0E+00	11422857 NT	닐	Homo sapiens tumor protein p73 (TP73), mRNA
8888		34729	1.19	0.0E+00 K01241	K01241.1	NT	Human Ig rearranged H-chain epsitor-3 pseudogene, constant region
8905		34737	4.27	0.0E+00 AB02063		ΙN	Homo seplens mRNA for KIAA0823 protein, partial cds
9068	21596	34738	4.27	0.05+00	0.0E+00 AB020630.1	TN	Homo saplens mRNA for KIAA0823 protein, pertial cds
0168	21601	34744	1.79	0.0E+00	0.0E+00 AV660739.1	EST_HUMAN	AV660739 GLC Homo seplens oDNA done GLCGKG123'
8916	21607	34750	2.88	00+30°0	TN08638 NT	NT	Homo sapiens polycystin-L (PKDL), mRNA
1288	21812	34755	0.5	0.0E+00 BE7933;	BE793328.1	EST_HUMAN	801588304F1 NIH_MGC_7 Homo septens cDNA clone IMAGE:3942553 51
8922	21613	34756	67.0	0.0E+00 AB0330	AB033077.1	TN	Homo saplens mRNA for KIAA1251 protein, partial cds
8022	21613	34757	0.73	0.0E+00 AB03307	AB033077.1	NT	Homo sapiens mRNA for KIAA1251 protein, pertial cds
8934	21625		0.91	0.0E+00 H73937	+	EST_HUMAN	yu03h08.r1 Soares fetal fiver apleen 1NFLS Homo septens cDNA clone IMAGE:232767 5
8944		34779	4.57	0.0E+00 BE31540	BE315402.1	EST_HUMAN	601141119F1 NIH_MGC_9 Homo sepiens cDNA clone IMAGE,3140740 5
9044	21635	34780	4.57	0.0E+00	0.0E+00 BE315402.1	EST_HUMAN	601141119F1 NIH_MGC_9 Homo septens cDNA clone IMAGE:3140740 51
8954			0.48	0.0E+00	0.0E+00 BE612721.1	EST_HUMAN	601452582F1 NIH_MGC_66 Homo saplens cDNA clone IMAGE:3856100 5'
8954		34798	0.48	0.0E+00 BE61272	BE612721.1	EST_HUMAN	601452682F1 NIH_MGC_66 Homo septems cDNA clone IMAGE:3856100 5'
8957			0.45	. '	M89986.1	NT	Human polymorphic loci in Xq28
8969		34800	3.66	0.0E+00 X14768.		LN	Human mRNA for GABA-A receptor, aigha 1 subunit
8880	21670	34820	2.03	0.0E+00	0.0E+00 Al0 0 1395.1	EST HUMAN	an 29e04.x1 Gessler Wilms furnor Homo sapiens cDNA clone IMAGE;170009437
8085	24675	34824	Ą	0 0F+00 A195480	AIOSARN7 4	EST HIMAN	wq34s12x1 NCI_CGAP_GC9 Homo sepiens cDNA clone IMAGE:2473150 3' similer to SW:MGB3_HUMAN 015480 MFI ANOMA-ASSOCIATED ANTIGEN R3
8968	L.	34828	4.85	0.0E+00		LΝ	Homo saplens protocadharin alpha 8 (PCDHA8), mRNA
0006	Ш	34840	1.42	0.0E+00 AW9583	11.1	EST_HUMAN	EST370381 MAGE resequences, MAGE Hamo sepiens cONA
1106	21701	34851	248	0.0E+00	9635487		Human endogencus retrovirus, complete genome
8020	21716	34869	1.53	0.0E+00[AU1428	AU142862.1	HUMAN	AU142862 Y79AA1 Homo sapiens cDNA clone Y79AA1000678 5'
8042		34887	1.78	0.0E+00	11436965 NT		Homo saplens MAP-kinase activating death domain (MADD), mRNA
9043	21733		1.18	0.0E+00	0.0E+00 BE410788.1	EST_HUMAN	601301676F1 NIH_MGC_21 Homo septens cDNA clane IMAGE:3636163 5'
							7g97h12x1 NCI_CGAP_Co18 Homo septens cDNA done IMAGE:3314471 3' similar to TR:09UH62
B	_[34904	1.83	0.0E+00	1	HOMAN	GRUHEZ HYPOTHETICAL 42.8 KD PROTEIN.
9070	- (34920	=	0.0E+00.	٦	Į.	Homo sapiens mRNA for KIAA0578 protein, perfee cds
9071	- (34021	7.72	0.0E+00		HUMAN	601589294F1 NIH_MGC_7 Hamo septems cDNA dans IMAGE:3943463 5'
9075	- [34828	0.99	0.0E+00			RC3-PT0151-280600-011-c05 PT0151 Hamo sapiens cDNA
9075		34927	0.99	0.05+00	0.0E+00 BE810282.1		RC3-PT0151-290600-011-c05 PT0151 Hamo sepiens cDNA
8206	21767	34830	2.83	0.0E+00)	0.0E+00 AU138229.1	EST_HUMAN	AU136229 PLACE1 Homo seplens cDNA clone PLACE1003804 5

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Probe SEQ ID NO:	Exam SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8083	21772	34935	1.27	0.0E+00	0.0E+00 BE883843.1	EST_HUMAN	801510247F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911986 5'
8083	21772	34936	1.27	0.05+00	0.0E+00 BE883843.1	EST_HUMAN	601510247F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911986 5
9102	21790	34953	0.62	0.05+00	0.0E+00 AB011168.1	LN	Homo saplens mRNA for KIAA0584 protein, partial cds
9108	21794	34957	4.1	0.0E+00	0.0E+00 AA344601.1	EST_HUMAN	EST50505 Gall bladder I Homo saplens cDNA 6' end
9106	21704	34058	4.4	0.0E+00	0.0E+00 AA344601.1	EST_HUMAN	EST50505 Gall bladder I Homo saplens cDNA 5' end
9184	21834	34998	1.13		0.0E+00 AW673459.1	EST_HUMAN	ba54d08.y3 NIH_MGC_10 Homo sapiens cDNA done IMAGE:2900367 5' similar to TR:060275 060275 KIAA0622 PROTEIN;
9 20	21834	34999			0.0E+00 AW673469.1	EST_HUMAN	be34d08.y3 NIH_MGC_10 Homo sepiens cDNA done IMAGE:2900367 5 similar to TR:060276 060275 KIAA0522 PROTEIN;
9 88	21867	35031	1.62	0.0E+00	0.0E+00 BE207063.1	EST_HUMAN	be09f05.y1 NIH_MGC_7 Homo septiens cDNA clone IMAGE:2823873 5' shriller to gb:L35049 Mus musculus Bct-vL mRNA, complete cds (MOUSE);
92	21867	35032	1.62	0.0E+00	0.0E+00 BE207063.1	EST HUMAN	be09005.y1 NIH_MGC_7 Homo septens cONA clone IMAGE:2823873 5' similar to gb:1.35049 Mus musculus Bd-x1 mRNA, complete cds (MOUSE);
6023	22088	35280		0.0E+00	0.0E+00 BF348013.1	EST HUMAN	802023150F1 NCI_CGAP_Bm67 Homo septens cDNA clone IMAGE:4158300 5
8244	21823	l		0.05+00	0.0E+00 BE712515.1	EST_HUMAN	QV2-HT0698-250700-282-b08 HT0698 Hano sepiens cDNA
21728	22031	35201	0.88		0.0E+00 BF034377.1	EST_HUMAN	801455116F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3859035 5'
2227	22031	35202	88.0		0.0E+00 BF034377.1	EST_HUMAN	601455118F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3859035 5'
8283	22037	35209	0.5		0.0E+00 AI906351.1	EST_HUMAN	RC-BT108-040399-032 BT108 Homo septens oDNA
9828	22040	35211	0.81	0.0E+00	IN 6900089	Ę	Homo sepiens ieukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 5 (LILRB5), mRNA
888	22040	35212	18.0	0.0E+00	TN 6905089	Þ	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domeins), member 5 (LILRBS), mRNA
9628				0.0E+00	0.0E+00 AL042278.1	EST HUMAN	DKFZp434L0120_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L0120 5
9331	21998	35171	1.28		0.0E+00 AI088043.1	EST_HUMAN	ow80h01x1 Soarse_NSF_F8_9W_OT_PA_P_S1 Homo sepiens oDNA done IMAGE:1651249 3' s£nilar to TR:014677 Q14677 KIAA0171 PROTEIN :
8338	20409	33524	0.72		0.0E+00 BF309982.1	EST_HUMAN	601802245F1 NIH_MGC_17 Homo sepiens cDNA clone IMAGE:4138068 5
9340	20411	33527	2.51	0.0E+00	11580151 NT	1.	Homo sapiens hypothetical C2H2 zino finger protein FLJ22504 (FLJ22504), mRNA
9340	20411	33528		0.0E+00	11560151 NT	뉟	Homo sapiens hypothetical CZH2 zinc finger protein FLJ22504 (FLJ22504), mRNA
9342	20413	33531	98'6	0.0E+00	0.0E+00 AI290809.1	EST_HUMAN	qm09a08x1 NCI_CGAP_Lu5 Hamo sapiens cDNA clone IMAGE:1881298 3' similer to SW:RL2B_HUMAN P28316 60S RIBOSOMAL PROTEIN L23A.;
8342	20413	33532	88.6	0.0E+00	0.0E+00 AI290909.1	EST HUMAN	qm09a08.xt NCI_CGAP_Lu5 Homo saplens cDNA clone !MAGE:1881298 3' similer to SW:RL28_HUMAN P29316 60S RIBOSOMAL PROTEIN L23A.;
88. 8.43	20414		1.98	0.0E+00	6.1	EST_HUMAN	EST368028 MAGE resequences, MAGC Homo sepiens cDNA
9370	21945	35117	3.07	0.0E+00	3.1	Ŋ	Homo sapiens polycystic kidney disease 2-like protein (PKD2L) gene, exon 8

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Prabe SEQ ID NO:	Exen SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Velue	Top Hit Acession No.	Top Hit Dertabase Source	Top Hit Descriptor
2396	22304	35499	2.23	0.0E+00 S78466	S78466.1	NT	AIGF=androgen-induced growth factor AIGF [human, placenta, Genomic/mRNA, 498 nt, segment 5 of 5]
29952	22304	35500	2.28	0.0E+00 S78466	S78466.1	LN	AIGF=endrogen-induced growth factor AIGF [humen, placenta, Genomic/mRNA, 498 nt, segment 5 of 5]
9992	L	35505	2.83	0.0E+00 BE5633;	BE563320.1	EST_HUMAN	601334803F1 NIH_MGC_39 Homo saplens cDNA clane IMAGE:388880 5'
9674			1.64	0.0E+00 AW363	AW363135.1	EST_HUMAN	CM2-CT0311-301199-043-h11 CT0311 Homo sepiens cDNA
2662		35537	0.46	0.0E+00	11436432 NT	TN	Homo sapiens multimentn (MMRN), mRNA
2808	22344	35538	0.51	0.0E+00	11424387 NT	ΙN	Homo sepiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3 (LILRB3), mRNA
9702	22353	35548	0.54	0.0E+00 BE2067	BE206710.1	EST_HUMAN	bb28c01.x1 NIH_MGC_5 Home septions oDNA clone MAGE:2864000 3'
8719	22370	35568	2.57	0.0E+00 AU1323	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Hamo septens cDNA clane NT2RP3004260 5"
8719	07822	35569	2.57	0.0E+00 AU1323	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cONA clone NT2RP3004280 5'
8228	22379	35581	0.77	0.05+00	0.0E+00 AW 500836.1	EST HUMAN	UI-HF-BP0p-air-f-05-0-UI.r1 NIH_MGC_61 Homo septens cDNA clone IMAGE:3072897 5
8733	22384	35586	80.08	0.0E+00	0.0E+00 BE740490.1	EST_HUMAN	601595558F1 NIH_MGC_9 Hamo sepiens cDNA done IMAGE:3948383 5'
9733	22384	35587	80.6	0.0E+00	0.0E+00 BE740490.1	EST_HUMAN	601595558F1 NIH_MGC_9 Homo sepiens cDNA done IMAGE:3949383 5'
9734	22385	35588	0.48	0.0E+00	0.0E+00 AB033057.1	TN	Homo sapiens mRNA for KIAA1231 protein, pertial cds
9734	22385	35580	0.48	0.0E+00	0.0E+00 AB033057.1	NT	Homo sapiens mRNA for KIAA1231 protein, persial cds
9747	22398	35603	1.73	0.0E+00	7882087 NT	NT	Homo sapiens KIAA0345 gene product (KIAA0345), mRNA
9785	22418	35623	1.59	0.0E+00 AL042Z1	AL042278.1	EST HUMAN	DKFZp434L0120_r1 434 (synonym: https://domo.sapiens.cDNA.clane.DKFZp434L0120 51
0770	12422	35629	1.53	0.0E+00	0.0E+00 AL041084.2	EST_HUMAN	DKFZp434B2416_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434B2416 5
9780	22431	35636	2.54	0.0E+00	0.0E+00 AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5
9781	22432	35637	2.37	0.0E+00	0.0E+00 AF152308.1	IN	Homo saplens protocadherin alpha 12 (PCDH-alpha12) mRNA, complete cds
8080	22450	35664	2.63	0.0E+00 AF00922	AF009220.1	NT	Homo sapiens leucocyte immunoglobulin-like receptor-1 mRNA, complete cds
888	22459	35885	2.63	0.0E+00	0.0E+00 AF009220.1	NT	Homo sapiens leucocyte Immunoglobulin-tike receptor-1 mRNA, complete cds
9824	22475	35678	1.81	0.0E+00	0.0E+00 BF092898.1	EST HUMAN	MR4-TN0114-110900-101-e04 TN0114 Homo saplens cDNA
9854	22504	35704	2.41	0.0E+00	0.0E+00 BE280793.1	EST_HUMAN	601155227F1 NIH_MGC_21 Homo septens cDNA done IMAGE:3138799 57
9864	22514	35710	0.86	0.0E+00	0.0E+00 BE388700.1	EST_HUMAN	601286351F1 NIH_MGC_44 Hamp septens cDNA dane IMAGE:3613045 5
9964	22514	35711	0.83	0.0E+00	0.0E+00 BE388700.1	EST_HUMAN	801286351F1 NIH_MGC_44 Homo septems cDNA clone IMAGE:3613045 5
- 5	-	-					xn72b01 x1 NOI_CGAP_CML1 Home sapiens cDNA clone IMAGE:2899977 3' similar to gb:X02152_cds1 L-
88	22523	35717	3.8	0.0E+00		EST HUMAN	LACTATE DEHYDROGENASE M CHAIN (HUMAN);
8674 478	22524	35718	1.06	0.0E+00	5.1	EST HUMAN	EST46740 Fetal kidney II Hamo sapiens cDNA 5' end
8	22653	35748	0.97	0.0E+00 AW9641	AW964113.1	EST_HUMAN	EST376186 MAGE resequences, MAGH Homo septens cDNA
9915	22564	35769	7.01	0.0E+00 AU14387	AU143673.1		AU143673 Y79AA1 Hamo saplens cDNA clane Y79AA1002307 5'
9915	22564	35760	7.01	0.0E+00	0.0E+00 AU143673.1	EST HUMAN	AU143873 Y79AA1 Hamo saplens cDNA clone Y79AA1002307 5'

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Single Exon Probes Expressed in Brain

טווווון ווייבים באטוורן ווייבים באטוורן	Source Source Similar Top Hit Acession Source Source	0.0E+00 AF072408.1 NT Homo saplens killer cell inhibitory receptor KIRCI gene, exons 2, 3, and 4	0E+00 (1421001 NT Home sapiens HEF like Protein (HEFL), mRNA	0E+00 11421001 NT Homo sapiens HEF like Protein (HEFL), mRNA	0.0E+00 AU139837.1 EST_HUMAN AU138637 PLACE1 Homo sapiens cDNA clone PLACE1004737 5	0.0E+00 AU130837.1 EST_HUMAN AU136837 PLACE1 Homo septens cDNA clone PLACE1004737 5	TN	0.0E+00(AJ295844.1 NT Homo sapiens partial RANBP7 gene for RanBP7/Importin? and partial ZNF143 gene	EST_HUMAN	0.0E+00 AV885712.1 EST_HUMAN AV885712 GKC Homo explene cDNA clone GKCDXA07 5	NT	0.0E+00 AA196387.1 EST_HUMAN 2297h11.r1 Strategene muscle 937209 Homo sapiens CDNA clone IMAGE:028197 5	EST_HUMAN	EST_HUMAN	N.	EST HUMAN	EST_HUMAN	EST_HUMAN	13.1 EST HUMAN	1.1	EST_HUMAN	EST HUMAN	0.0E+00 AA311024.1 EST HUMAN EST182353 Jurkat T-celle VI Homo expiens cDNA 67 and	4758827 NT	BE891113.1 EST_HUMAN	1560151 NT	TN	EST_HUMAN	0.0E+00 BE304522.1 EST_HUMAN 601105459F1 NIH_MGC_15 Homo sepiens cDNA clone IMAGE:2987918 57	FN	0.0E+00 AB008590.1 NT Homo sapiens mRNA for estrogen receptor bets, complete ods	2/19b08.s1 Soares fetal liver spleen 1NFLS S1 Homo sepiens cDNA cione IMAGE:450707 3' striiler to 0.0E+00 AA704457.1 EST HUMAN gb:M14123 cds1 RETROVIRUS-RELATED GAG POLYPROTEIN (HUMAN);	Z	1.1 EST HUMAN
BISHIS	Acession 6.		11421001 NT	11421001 NT												Г				1.1				4758827	3.1	11560151 NT						,		=
ľ	Most Similar (Top) Hit BLAST E Value	0.0E+00	0.05	0.0E+00	0.0E+00.0	0.0E+00.0	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00/	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00	0.0E+00/	0.0E+00/	0.0E+00/	0.0E+00	0.0E+00
	Expression Signal	2.98	2.75	2.75	8	8	2.08	2.08	1.04	1.04	0.74	3.11	1	1	1.44	0.92	6.22	6.22	76.0	0.87	0.87	0.68	0.67	1.01	0.67	1.13	1.72	0.48	0.48	8.02	6.02	1.06	0.74	5.45
	ORF SEQ ID NO:	35763	39298	32786	35809	35810	35824	32822	35832	35833	35840	35843	S2873	35874	35922	35964	35972	35973			35980	36007	36020	38021	36032	36035	36041	38042	36043	36048	36040	36056	36057	38060
	SEQ ID	22587	22569	22569	22604	22604	li		22825	22022		22833	22059	L	22704	22749			22765	22775	22775			- 1		22817	22827	22828	22828	22835	96822	22841	ı	
ſ	Probe SEQ ID NO:	9918	9921	9821	9968	8858	9972	9972	7265	2268	5863	3866	10011	10011	10058	10101	10112	10112	10117	10127	10127	10144	10154	1935	10166	10169	10179	10180	10180	10187	10187	10193	10195	10187

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Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
10197			5.45	0.0E+00	0.0E+00 BF340331.1	EST_HUMAN	602037045F1 NCI_CGAP_Bm64 Hamo septens cDNA clone IMAGE:4184939 61
10222	22870	36082	86°0	0.0E+00	0.0E+00 BE897149.1	EST_HUMAN	601439713F1 NIH_MGC_72 Hamo septens cDNA dane IMAGE:3824578 5'
10222	22870	36083	28 '0	0.0E+00	0.0E+00 BE897149.1	EST_HUMAN	601439713F1 NIH_MGC_72 Homo septens cDNA clone IMAGE:3924578 5
10252	22900	36110	0.55	0.0E+00 AV7162	AV716271.1	EST_HUMAN	AV716271 DCB Homo sepiens dDNA done DCBBDC09 5'
10252	22900	36111	99'0	0.0E+00 AV71627	AV716271.1	EST_HUMAN	AV716271 DCB Homo sepiens cDNA clone DCBBDC09 5"
10282	22830	36143	2.36	0.0E+00 AI63181	Al631818.1	EST_HUMAN	ws38e03.x1 NCI_CGAP_Kid11 Homo seplens cDNA clone IMAGE:2300188 3' similar to TR:Q61204 Q61204 NOTCH2-LIKE;
10282	22830	36144	2.36	0.0E+00 AI63181	Al631818.1	EST HUMAN	wa38e03.x1 NC_CGAP_Kid11 Homo sapiens cDNA clone IMAGE.2300188 3' similar to TR.Q61204 Q61204 NOTCH2-LIKE;
10288	22836	36149	0.49	0.0E+00	11545730 NT	Ę	Homo sapiens Gigazonin (GAN), mRNA
10298	22945	36159		0.0E+00 T03078.	T03078.1	EST_HUMAN	FB23A4 Fetal brain, Stratagene Homo sepiens cDNA clone FB23A4 3 and
10323	22970	36190	0.84	0.0E+00 AU1224	29.1	EST_HUMAN	AU122429 MAMMA1 Homo seplens cDNA clone MAMMA1002368 5
10329	22976	36196	0.48	0.0E+00	6005921	Þ	Homo septens triple functional domain (PTPRF Interacting) (TRIO), mRNA
10348	22995	36214	2.5	0.0E+00 BF4362	BF436218.1	EST HUMAN	nab45e12x1 Scares_NSF_F8_9W_OT_PA_P_S1 Homo septens cDNA clone IMAGE:3286271 3
10349	22996		26'0	0.0E+00 AV6647	AV664786.1	EST_HUMAN	AV654765 GLC Hamo sapiens aDNA clane GLCDZC07 3'
10360	23015	36234	27.6	0.0110.0	0.0E+00 AW517090 t	NAMI'H TRA	xu74b01x1 NCI_CGAP_Kid8 Homo sepiene cDNA clone IMAGE:2807401 3' similar to gb:M89066 MOESIN (HUMAN):
10374	1_	L	8.82	0.0E+00 BE5482	BE548213.1	EST HUMAN	601078764F1 NIH MGC 12 Homo saplens cDNA clone IMAGE 3464703 5
10389	L	L	0.75	0.0E+00	11436005 NT	Ę	Homo saplens hypothetical protein DKFZp761P1010 (DKFZp761P1010), mRNA
10414	L		279	0.0E+00 BE78174	BE781742.1	EST_HUMAN	801467419F1 NIH_MGC_67 Homo sepiens oDNA clone IMAGE:3870700 5
10435	23081	36307	o. L	0.0E+00 BE0827;	BE082720.1	EST_HUMAN	RC2-8T0642-150200-012-d03 BT0642 Homo sepiens cDNA
10435	23081	36308	1.9	0.0E+00 BE0827	BE082720.1	EST_HUMAN	RC2-BT0642-150200-012-d03 BT0642 Homo saplens cDNA
10442		36316	99.0	0.0E+00 Y08032	Y08032.1	NT	Human endogenous retrovirus-K, LTR U6 and gag gene
10448				0.0E+00	0.0E+00 AI658890.1	EST HUMAN	tt54e07.x1 NCL_CGAP_GC6 Hamo suplens cDNA dane IMAGE:2244612.3'
10454	23100	36331	1.33	0.0E+00 BE7432	BE743215.1	EST HUMAN	801573895F1 NIH_MGC_9 Hamo sepiens cDNA clone IMAGE:3835198 5'
10454	23100		1.33	0.0E+00 BE7432	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Hamo septens cDNA clone IMAGE:3835198 57
10459				0.0E+00	0.0E+00 BE617655.1	EST_HUMAN	601441723T1 NIH_MGC_65 Hamo septens cDNA done IMAGE:3845858 3'
10459			249	0.0E+00	0.0E+00 BE617855.1	EST_HUMAN	601441723T1 NIH_MGC_65 Home sapiens cDNA clone IMAGE:3845956 3'
10481	23127	38355	<i>1</i> 5'0	0.0E+00 H39805	H39905.1	EST_HUMAN	yp01e10.r1 Sogres breast 3NbHBst Homo septens cDNA clone IMAGE:186138 5
10508		36380	1.01	0.0E+00 D87675	1	LN	Homo sepiens DNA for emyloid precursor protein, complete cds
10510		36382	0.45	0.0E+00 AF08136	AF081364.1	NT	Synthetic construct CD30 ligand-excitadin A fusion protein (CD30L-ETA fusion) mRNA, partial cds
10519			1.02	0.0E+00	0.0E+00 BE172254.1	EST_HUMAN	MR0-HT0559-270300-008-e12 HT0559 Homo sepiens cDNA
10519	23165		1.02	0.0E+00	0.0E+00 BE172254.1	EST_HUMAN	MR0-HT0559-270300-008-e12 HT0559 Homo seplens cDNA
10532	_1	38463	2.76	0.0E+00 AV71107	AV711075.1	EST_HUMAN	AV711075 Ou Homo saplens cONA clone CuAAKG05 5

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acessian No.	Top Hit Detabase Source	Top Hit Descriptor
10532	23220	36464	2.78	0.0E+00	0.0E+00 AV711075.1	EST_HUMAN	AV711075 Cu Homo sepiens cDNA clone CuAAKG05 51
10534	23231		2.13	0.0E+00	0.0E+00 AW813783.1	EST_HUMAN	RC3-ST0197-120200-015-e03 ST0197 Homo septens cDNA
10542	23238	36472	7.02	0.0E+00	0.0E+00 AW963563.1	EST_HUMAN	EST378636 MAGE resequences, MAGH Hamo sapiens cDNA
105555	23251	36487	3.19	0.0E+00	11431124 NT	FX	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
105555	23251	36488	3.19	0.0E+00	11431124 NT	LN.	Homo sepiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
10530	23255	36492	2.09	0.0E+00	0.0E+00 AW057821.1	EST HUMAN	wy61f09.x1 Soures_NSF_F8_9W_OT_PA_P_S1 Hamo sapiens cDNA done IMAGE:2553085 3' similar to TR:Qe0568 Qe0568 VDX;
							TCAAP3D0917 Pediatric acute myelogenous laukemia cell (FAB M1) Baykor-HGSC project=TCAA Homo
10567	23262	36489	1.6	0.0E+00	0.0E+00 BE243270.1	EST HUMAN	sepiens cDNA clone TCAAP0917
10568	23263	36500	2.85	0.0E+00	0.0E+00 AI652239.1	EST HUMAN	wb28s12x1 NCI_CGAP_GC9 Homo sepiens cDNA clone IMAGE:2306974 3' similiar to contains element MSR1 MSR1 repetitive element;
							wb28a12x1 NCI_CGAP_GC8 Homo septems cDNA clone IMAGE:2306974 3' strullar to contains element
10508	23263	36501	2.85	0.0€+00	0.0E+00 AIO52239.1	EST HUMAN	MSR1 MSR1 reportitive element;
10573	23268	36506	1.54	0.0E+00	0.0E+00 BF306642.1	EST_HUMAN	601888704F1 NIH_MGC_17 Homo sepiene cDNA clone IMAGE:4122649 5
10580	23275	36512	90'9	0.0E+00	11545911 NT	IN	Homo saplens NOD2 protein (NOD2), mRNA
10580	23275	36513		0.0E+00	11545911 NT	TN	Homo sapiens NOD2 protein (NOD2), mRNA
10508	23290	36528	1.98	00+30'0	AW40476	EST_HUMAN	UI-HF-BL0-acm-d-04-0-UI.r1 NIH_MGC_37 Homo sepiens cDNA clone IMAGE:3059383 5'
10900	23294	36533	3.17	0.0E+00	11424829 NT	TN	Homo sapiens hypothetical protein FLJ20079 (FLJ20079), mRNA
10601	23295	36534	7.47	0.0E+00	4504536 NT	IN	Homo eaplens 5-hydroxydryptamine (serotonin) receptor 1E (HTR1E) mRNA
10601	23205	36535	7.47	0.0E+00	4504536 NT	TN	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E) mRNA
10802	23298	36536	3.68	0.0E+00	0.0E+00 Al991827.1	EST_HUMAN	wu32b08.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:25217153'
10605	23289	36540	4.48	0.0E+00	0.0E+00 BE882109.1	EST_HUMAN	601505204F2 NIH_MGC_71 Homo septems cDNA clone IMAGE:3906865 5
10609	23303	36542	8.24	0.0E+00	0.0E+00 BEB91630.1	EST_HUMAN	801434522F1 NIH_MGC_72 Homo septems aDNA done IMAGE:3919636 5
10612	23306	36544	1.98	0.0E+00	8923939 NT	IN	Homo sapiens myosin, heavy potypeptide 2, skeletai muscle, adult (MYH2), mRNA
10612	23306	36545	1.06	0.0E+00	IN 6623339 NT	INT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
10619	23312	36551	4.1	0.0E+00	0.0E+00 AB014608.1	NT	Homo sapiens mRNA for KIAA0708 protein, pertial ods
10619	23312	38662	7 .	0.0E+00	0.0E+00 AB014808.1	N	Homo sapiens mRNA for KIAA0708 protein, peritial cds
10628	23321	36559	1.31	0.0E+00	0.0E+00 BE903304.1	EST HUMAN	601674332F1 NIH_MGC_21 Hamo septems cDNA dane IMAGE:3957343 5
10634	78787	24403	, 78	00490	0.05+00.44.05008.4	NOW! IN LOS	2955011.1 Strategere muscle 937209 Homo sepiens oDNA done IMAGE:627933 5' similar to gb:X03740 MYOSIN HEAVY CHAIN SKELFTAL MILISCI F (HUMAN):
108.5	23.63	1858	5	001100		EST HIMAN	601588829F1 NIH MGC 7 Homo septens cDNA clone IMAGF:3943015 5
7000	2000	10000	2000	30.10		MANUEL FOR	MATERIAL INTO TO LIGHT AND A CONTROL MATERIAL OF THE CONTROL OF TH
2000	10882	8800	8/1	0.05+00	<u>.</u>	EST HUMAN	SOURCESOCRET INITIALISE OF THE SELECTION SELECTION OF THE SECTION
0000	1000	36585		0.0=+00	<u>.</u>	ESI HUMAN	OU TOXOGO-FI THIN MOC. TO THING SEPTEND CUTTOR TO THE TOXOGO O
10661	23352	36590	33.99	0.0=+00	0.0E+00 AV727362.1	ES! HUMAN	AV72/302 FILC Homo sapiens alina dane fill Cautho 3

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Table 4
Single Exon Probes Expressed in Brain

Single Exon Probes Expressed in Brain	Most Similar Top Hit Acession (Top) Hit Top Hit Acession Signal BLASTE 'No. Source Source	352 38591 33.99 0.0E+00/AV727382.1 EST_HUMAN AV727382 HTC Hamo septens CDNA clone HTCAQH08 5'	36008 8.59 0.0E+00 AW516055.1 EST HUMAN	36813 3.18 0.0E+00 AU135741.1 EST_HUMAN	36617 3.41 0.0E+00 AW68333.1 EST_HUMAN	36518 3.41 0.0E+00 AW59333.1 EST HUMAN	36519 3.41 0.0E+00 AW59333.1 EST HUMAN	36820 1.89 0.0E+00 234897.1 NT	36621 2.97 0.0E+00 F13069.1 EST_HUMAN	36629 1.79 0.0E+00 D10083.1 NT	39634 1.33 0.0E+00 4758281 NT	96 38835 1.33 0.0E+00 4758281 NT Homo sapiens EphA7 (EPHA7) mRNA	36648 2.13 0.0E+00 AW338094.1 EST HUMAN CHAIN C REGION (HUMAN);	36849 4.62 0.0E+00 AW451230.1 EST HUMAN	36650 4.62 0.0E+00 AW451230.1 EST_HUMAN	11.67 0.0E+00 4508632 NT	36652 2.53 0.0E+00 AB014567.1 NT	39670 1.98 0.0E+00[BE298449.1 EST_HUMAN	36883 2.04 0.0E+00 AB011117.1 NT	1.71 0.0E+00 AU124106.1 EST_HUMAN	36697 1.45 0.0E+00/AB029040.1 INT	36698 1.45 0.0E+00 AB029040.1 NT	36702 4.04 0.0E+00 BE792165.1 EST_HUMAN	59.14 0.0E+00 BF684061.1 EST_HUMAN	36703 1.3 0.0E+00 BE269288.1 EST_HUMAN	36706 5.6 0.0E+00 AU118386.1 EST_HUMAN	36710 8.53 0.0E+00 AI149809.1 EST_HUMAN	36711 6.53 0.0E+00 AI149809.1 EST HUMAN	70 36712 3.04 0.0E+00 AW391937.1 EST_HUMAN QV4-ST0234-121199-032-506 ST0234 Homo sepiens cDNA
	ORF SEQ ID NO:			36613	30617	36618	36619	36820	36621	36629	39834	38635	36648	39649	36650		36652	39670	36883		36697	36698	38702		36703	36706	36710	36711	36712
	SEQ ID NO:	23352	23365	23371	23377	77882	77.552	23379	23380	23391	23396	23396	23407	23408	23408	13021	23411	23425	23430	23447	23454	23454	23459	23460	23461	23464	23469	23469	23470
	Probe SEG ID NO:	10681	10674	10680	10686	10686	10686	10688	10689	10700	10708	10706	10718	10719	10719	10721	10723	10738	10754	10763	10771	10771	10778	10777	10778	10781	10786	10788	10787

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Expression Signal Moet Similar Top Hit Accession Signal Top Hit Top Hit Accession Source Surce Signal Top Hit Top Hit Accession Source S							
23481 36721 4.39 0.0E+00 AF223391.1 NT 23481 36722 4.39 0.0E+00 AF223391.1 NT 23480 36726 9.67 0.0E+00 AV804516.1 EST HUMAN 23480 36726 9.67 0.0E+00 AV804516.1 EST HUMAN 23480 36724 1.42 0.0E+00 BED31209.1 EST HUMAN 23480 36726 1.6 0.0E+00 AR804516.1 EST HUMAN 23500 36734 1.6 0.0E+00 AR80500.1 INT 23501 36746 1.66 0.0E+00 AR80500.1 EST HUMAN 2351 36779 1.55 0.0E+00 BE773030.1 EST HUMAN 23520 36782 1.56 0.0E+00 BE773030.1 EST HUMAN 23520 36782 1.54 0.0E+00 BA740782.1 EST HUMAN 23520 36782 1.54 0.0E+00 BA740782.1 EST HUMAN 23520 36806 <t< th=""><th></th><th></th><th>Expression Signal</th><th>Most Similar (Top) Hit BLAST E Value</th><th>Top Hit Acession No.</th><th></th><th>Top Hit Descriptor</th></t<>			Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.		Top Hit Descriptor
23481 36722 4.39 0.0E+00 AF223381.1 NT 23480 36726 9.57 0.0E+00 AF223381.1 NT 23480 36726 1.42 0.0E+00 AV804516.1 EST HUMAN 23480 36734 1.42 0.0E+00 BF340308.1 EST HUMAN 23480 36736 1.69 0.0E+00 BE241208.1 EST HUMAN 23500 36736 1.69 0.0E+00 BE26403.1 NT 23501 36736 1.69 0.0E+00 BE26403.1 NT 23510 36736 1.69 0.0E+00 BE26403.1 NT 23510 36776 1.69 0.0E+00 BE27308.1 NT 23527 36780 1.55 0.0E+00 BE773038.1 EST HUMAN 23527 36780 2.91 0.0E+00 BA740782.1 EST HUMAN 23529 36806 7.34 0.0E+00 BA740827.1 EST HUMAN 23576 36816 2.31 <				0.05+00	AF223391.1	F	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
23490 36728 9.67 0.0E+00 11424728 INT 23497 36733 1.42 0.0E+00 AW804516.1 EST_HUMAN 23497 36734 1.42 0.0E+00 BF340308.1 EST_HUMAN 23409 36736 1.6 0.0E+00 BF340308.1 EST_HUMAN 23500 36736 1.6 0.0E+00 BF340308.1 EST_HUMAN 23501 36746 1.69 0.0E+00 BF30303.1 INT 23514 36755 1.65 0.0E+00 BF03303.1 INT 23520 36776 3.47 0.0E+00 BE773036.1 EST_HUMAN 23521 36778 1.36.91 0.0E+00 BF73038.1 EST_HUMAN 23520 36780 2.91 0.0E+00 W21828.1 EST_HUMAN 23527 36780 2.91 0.0E+00 CA740782.1 EST_HUMAN 23527 36780 2.31 0.0E+00 AA740787.1 EST_HUMAN 23547 36826 36816				0.0E+00	AF223391.1	Į.	Homo septens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial ods, alternatively spliced
23497 36733 1,42 0.0E+00 AW804516.1 EST HUMAN 23496 36734 1,42 0.0E+00 BF340308.1 EST HUMAN 23406 36736 52.84 0.0E+00 BE261209.1 EST HUMAN 23500 36738 52.84 0.0E+00 BE261209.1 EST HUMAN 23504 36746 1.69 0.0E+00 BE261209.1 EST HUMAN 23510 36746 1.69 0.0E+00 BE26040.1 NT 23514 36756 1.69 0.0E+00 BE773036.1 EST HUMAN 23520 36762 1.47 0.0E+00 BE773036.1 EST HUMAN 23520 36782 1.55 0.0E+00 BE773036.1 EST HUMAN 23520 36782 1.47 0.0E+00 BV21825.1 EST HUMAN 23520 36782 1.47 0.0E+00 AV48822.1 EST HUMAN 23568 36806 7.34 0.0E+00 AV48822.1 EST HUMAN 23568 36815 2.31 0.0E+00 AV48375.1 EST HUMAN 23569 36826 3.74				0.0E+00	11424728	N	Homo sapiens insulin receptor (INSR), mRNA
23497 36734 1,42 0.0E+00 BF340308.1 EST HUMAN 23408 36736 1.8 0.0E+00 BF340308.1 EST HUMAN 23500 36738 52.84 0.0E+00 BE281209.1 EST HUMAN 23504 36746 1.69 0.0E+00 J80730.1 NT 23510 36736 1.69 0.0E+00 J80730.1 NT 23514 36756 1.55 0.0E+00 J80730.1 NT 23514 36756 1.55 0.0E+00 J80730.1 EST HUMAN 23520 36762 1.55 0.0E+00 J8773036.1 EST HUMAN 23520 36762 1.47 0.0E+00 J871803.1 EST HUMAN 23520 36762 1.47 0.0E+00 J871803.1 EST HUMAN 23568 36806 7.34 0.0E+00 J872403.1 EST HUMAN 23568 36815 2.31 0.0E+00 J8748376.1 EST HUMAN 23568 36816 2.31 0.0E+00 J8748376.1 EST HUMAN 23569 36826 3.74 0.0E+00 J876803.1 ES				0.0E+00	AW804516.1	EST_HUMAN	QV0-UM0063-170400-191-d06 UM0063 Homo sepiens cDNA
23498 36736 1.6 0.0E+00 BF340308.1 EST HUMAN 23500 36738 52.94 0.0E+00 BE281209.1 EST HUMAN 23504 36740 1.69 0.0E+00 AB007832.1 NT 23510 36746 1.69 0.0E+00 BE773036.1 NT 23514 36750 1.55 0.0E+00 BE773036.1 EST HUMAN 23514 36756 1.55 0.0E+00 BE773036.1 EST HUMAN 23520 36762 1.47 0.0E+00 BE773036.1 EST HUMAN 23537 36762 1.47 0.0E+00 BE773036.1 EST HUMAN 23540 0.0E+00 MZ1625.1 EST HUMAN EST HUMAN 23650 36816 2.31 0.0E+00 AA746375.1 EST HUMAN 23671 36826 3.74 0.0E+00 AA746375.1 EST HUMAN 23671 36826 3.74 0.0E+00 AA746375.1 EST HUMAN 23671 36826 3.74 <td></td> <td></td> <td></td> <td>0.0E+00</td> <td>AW804516.1</td> <td>EST_HUMAN</td> <td>QV0-UM0083-170400-191-406 UM0083 Homo sapiens cDNA</td>				0.0E+00	AW804516.1	EST_HUMAN	QV0-UM0083-170400-191-406 UM0083 Homo sapiens cDNA
23500 36738 52.94 0.0E+00 BE261209.1 EST HUMAN 23504 36743 2.37 0.0E+00 AB023040.1 NT 23510 36756 1.69 0.0E+00 BE07303.1 NT 23514 36756 1.55 0.0E+00 BE773030.1 EST HUMAN 23520 36776 1.55 0.0E+00 BE773030.1 EST HUMAN 23530 36779 1.55 0.0E+00 MA740782.1 EST HUMAN 23531 36783 2.91 0.0E+00 AA740782.1 EST HUMAN 23543 36784 2.31 0.0E+00 AA740782.1 EST HUMAN 23656 36815 2.31 0.0E+00 AA74082.1 EST HUMAN 23668 36816 2.31 0.0E+00 AA7408376.1 EST HUMAN 23676 36826 3.74 0.0E+00 AA7408376.1 EST HUMAN 23678 36826 3.74 0.0E+00 AA740836.1 EST HUMAN 23678 36826 <td></td> <td></td> <td></td> <td>0.0E+00</td> <td>BF340308.1</td> <td>EST_HUMAN</td> <td>602037014F1 NCI_CGAP_Bm64 Homo saplens cDNA clone IMAGE:4184979 51</td>				0.0E+00	BF340308.1	EST_HUMAN	602037014F1 NCI_CGAP_Bm64 Homo saplens cDNA clone IMAGE:4184979 51
23504 36743 2.37 0.0E+00 AB029040.1 NT 23507 36746 1.69 0.0E+00 AB007932.1 NT 23514 36750 1.55 0.0E+00 BE773036.1 EST_HUMAN 23514 36756 1.55 0.0E+00 BE773036.1 EST_HUMAN 23520 36762 1.47 0.0E+00 BE773036.1 EST_HUMAN 23531 36779 1.36.01 0.0E+00 BE773036.1 EST_HUMAN 23532 36783 2.05 0.0E+00 BE773036.1 EST_HUMAN 23543 36789 2.91 0.0E+00 BE773036.1 EST_HUMAN 23569 36806 7.34 0.0E+00 BA746375.1 EST_HUMAN 23576 36815 2.31 0.0E+00 BA746375.1 EST_HUMAN 23576 36826 3.74 0.0E+00 BA746375.1 EST_HUMAN 23576 36826 3.74 0.0E+00 BA746375.1 EST_HUMAN 23577 36826 3.74 0.0E+00 BA76836.1 EST_HUMAN 23604 36826 3.74 0.0E+00 BA76836.1				0.0E+00	BE261209.1	EST_HUMAN	601148357F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163310 5'
23507 36746 1.69 0.0E+00 AB0079321 INT 23510 36750 3.47 0.0E+00 U50328.1 INT 23514 36755 1.55 0.0E+00 BE773036.1 EST_HUMAN 23520 36762 1.55 0.0E+00 W21826.1 EST_HUMAN 23531 36762 1.47 0.0E+00 W21826.1 EST_HUMAN 23532 36783 2.05 0.0E+00 AA740782.1 EST_HUMAN 23543 36780 2.91 0.0E+00 AA746822.1 EST_HUMAN 23560 36806 7.34 0.0E+00 AA746375.1 EST_HUMAN 23561 36815 2.31 0.0E+00 AA746375.1 EST_HUMAN 23576 36826 3.74 0.0E+00 AA746375.1 EST_HUMAN 23576 36826 3.74 0.0E+00 AA746375.1 EST_HUMAN 23576 36826 3.74 0.0E+00 AA746375.1 EST_HUMAN 23577 36826 3.74 0.0E+00 AA746376.1 EST_HUMAN 23604 36836 1.64 0.0E+00 AV66368.1	_			0.0E+00	AB023040.1	NT	Homo saplens mRNA for KIAA1117 protein, pertial ods
23510 36750 3.47 0.0E+00 U50328.1 NT 23514 36755 1.55 0.0E+00 BE773036.1 EST_HUMAN 23520 36756 1.55 0.0E+00 W21828.1 EST_HUMAN 23531 36779 1.47 0.0E+00 W21828.1 EST_HUMAN 23532 36779 2.91 0.0E+00 A740782.1 EST_HUMAN 23543 36780 2.91 0.0E+00 A746852.1 EST_HUMAN 23560 36806 7.34 0.0E+00 A746875.1 EST_HUMAN 23561 36815 2.31 0.0E+00 A746875.1 EST_HUMAN 23576 36826 3.74 0.0E+00 A746875.1 EST_HUMAN 23576 36826 3.74 0.0E+00 A746875.1 EST_HUMAN 23576 36826 3.74 0.0E+00 A746875.1 EST_HUMAN 23576 36826 3.74 0.0E+00 A76608.1 EST_HUMAN 23604 36836 5.81 0.0E+00 A76608.1 EST_HUMAN 23604 36862 2.09 0.0E+00 A76608.1				0.0E+00	AB007932.1	NT	Homo saplens mRNA for KIAA0463 protein, pertial cds
23514 36755 1.55 0.0E+00 BE773036.1 EST_HUMAN 23520 36756 1.55 0.0E+00 W21828.1 EST_HUMAN 23521 36762 1.47 0.0E+00 W21828.1 EST_HUMAN 23532 36779 136.01 0.0E+00 AA740782.1 EST_HUMAN 23543 36780 2.91 0.0E+00 AA746822.1 EST_HUMAN 23569 36806 7.34 0.0E+00 AA746375.1 EST_HUMAN 23569 36815 2.31 0.0E+00 AA746375.1 EST_HUMAN 23576 36826 3.74 0.0E+00 AA746375.1 EST_HUMAN 23576 36826 3.74 0.0E+00 AA746375.1 EST_HUMAN 23576 36826 3.74 0.0E+00 AA746375.1 EST_HUMAN 23577 36826 3.74 0.0E+00 AA746375.1 EST_HUMAN 23604 36828 3.74 0.0E+00 AA76636.1 EST_HUMAN 23604 <td< td=""><td></td><td></td><td></td><td>0.0E+00</td><td>U50326.1</td><td>۲</td><td>Human profein kinase C substrate 80K-H (PRKCSH) gene, exon 15-17</td></td<>				0.0E+00	U50326.1	۲	Human profein kinase C substrate 80K-H (PRKCSH) gene, exon 15-17
23614 36756 1.55 0.0E+00 BE773038.1 EST HUMAN 23620 36762 1.47 0.0E+00 W21828.1 EST HUMAN 23634 36779 136.01 0.0E+00 AA740782.1 EST HUMAN 23543 36783 2.05 0.0E+00 AA746822.1 EST HUMAN 23569 36806 7.34 0.0E+00 AA746375.1 EST HUMAN 23568 36815 2.31 0.0E+00 AA746375.1 EST HUMAN 23676 36826 3.74 0.0E+00 AA746375.1 EST HUMAN 23676 36826 3.74 0.0E+00 AA746375.1 EST HUMAN 23676 36826 3.74 0.0E+00 AA746375.1 EST HUMAN 23676 36826 3.74 0.0E+00 AA746375.1 EST HUMAN 23677 36826 3.74 0.0E+00 AA746375.1 EST HUMAN 23604 36836 5.81 0.0E+00 AA6803658.1 EST HUMAN 23604	L			0.0E+00	BE773036.1	EST_HUMAN	RC1-FT0134-170700-012-f07 FT0134 Homo aspiens aDNA
23520 36762 1.47 0.0E+00 W21828.1 EST_HUMAN 23634 36779 136.01 0.0E+00 AA740782.1 EST_HUMAN 23543 36783 2.05 0.0E+00 AA746782.1 EST_HUMAN 23569 36806 7.34 0.0E+00 AA746375.1 EST_HUMAN 23568 36815 2.31 0.0E+00 AA746375.1 EST_HUMAN 23676 36826 3.74 0.0E+00 AA746375.1 EST_HUMAN 23676 36826 3.74 0.0E+00 AA746375.1 EST_HUMAN 23676 36826 3.74 0.0E+00 AA746375.1 EST_HUMAN 23676 36826 3.74 0.0E+00 AA746375.1 EST_HUMAN 23677 36826 3.74 0.0E+00 AL157608.1 EST_HUMAN 23604 36836 5.81 0.0E+00 AV683658.1 EST_HUMAN 23604 36862 2.09 0.0E+00 AV683658.1 EST_HUMAN 23639		L.		0.0E+00	BE773036.1	EST_HUMAN	RC1-FT0134-170700-012-f07 FT0134 Homo sapiens cDNA
23634 36779 136.01 0.0E+00 AA740782.1 EST_HUMAN 23537 36783 2.05 0.0E+00 AW468622.1 EST_HUMAN 23543 36780 2.91 0.0E+00 AF262303.1 NT 23569 36806 7.34 0.0E+00 CD5085.1 EST_HUMAN 23568 36815 2.31 0.0E+00 AA746375.1 EST_HUMAN 23576 36826 3.74 0.0E+00 AA746375.1 EST_HUMAN 23576 36826 3.74 0.0E+00 AA746375.1 EST_HUMAN 23576 36826 3.74 0.0E+00 AA746375.1 EST_HUMAN 23576 36826 3.74 0.0E+00 AL157608.1 EST_HUMAN 23604 36836 5.81 0.0E+00 AV683658.1 EST_HUMAN 23604 36862 2.09 0.0E+00 AV683658.1 EST_HUMAN 23604 31312 2.73 0.0E+00 AV683658.1 EST_HUMAN 23636 368				0.0E+00	W21826.1	EST_HUMAN	57E10 Human retina cDNA Tsp508Holeawed sublibrary Homo saplens cDNA not directional
23534 36779 136.01 0.0E+00 AA740782.1 EST HUMAN 23537 36783 2.05 0.0E+00 AW466822.1 EST HUMAN 23543 36906 7.34 0.0E+00 AF252303.1 NT 23560 36806 7.34 0.0E+00 AF262303.1 NT 23566 36815 2.31 0.0E+00 AA746375.1 EST HUMAN 23576 36826 3.74 0.0E+00 AA746375.1 EST HUMAN 23576 36826 3.74 0.0E+00 AA746375.1 EST HUMAN 23576 36826 3.74 0.0E+00 AA746375.1 EST HUMAN 23577 3682 0.0E+00 AA746375.1 EST HUMAN 23578 3682 0.0E+00 AA763526.1 EST HUMAN 23604 36836 1.64 0.0E+00 AV663658.1 EST HUMAN 23604 31312 2.73 0.0E+00 BE182360.1 EST HUMAN 23636 36888 2.64 0.0E+00 BE182360.1 EST HUMAN 23637 36888 2.64 0.0E+00 BE182360.1 EST HUMAN	 						db32e07.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325412.3' similar to contains element
23537 36783 2.05 0.0E+00 AW466622.1 EST HUMAN 23543 36790 2.91 0.0E+00 AF262303.1 NT 2356 36806 7.34 0.0E+00 CO5089.1 EST HUMAN 2356 36815 2.31 0.0E+00 AA746375.1 EST HUMAN 23576 36826 3.74 0.0E+00 AA746375.1 EST HUMAN 23576 36826 3.74 0.0E+00 AA746375.1 EST HUMAN 23576 36826 3.74 0.0E+00 AA746375.1 EST HUMAN 23576 36826 3.74 0.0E+00 AA746375.1 EST HUMAN 23577 3682 0.0E+00 AA746375.1 EST HUMAN 23604 36836 5.81 0.0E+00 AA7635.1 EST HUMAN 23604 36836 5.81 0.0E+00 BE36563.1 EST HUMAN 23604 31312 2.73 0.0E+00 BE182360.1 EST HUMAN 23636 31312 2.73 0.0E+00 BE182360.1 EST HUMAN 23636 36888 2.64 0.0E+00 BE182360.1 EST HU				0.0E+00		EST HUMAN	MSR1 repetitive element:
23543 36790 2.91 0.0E+00 AF262303.1 NT 23569 36806 7.34 0.0E+00 CO5089.1 EST HUMAN 23566 36815 2.31 0.0E+00 AA746375.1 EST HUMAN 23576 36826 3.74 0.0E+00 AA746375.1 EST HUMAN 23576 36826 3.74 0.0E+00 AA746375.1 EST HUMAN 23576 36826 3.74 0.0E+00 AA746375.1 EST HUMAN 23576 36826 3.74 0.0E+00 AL157608.1 EST HUMAN 23590 36836 5.81 0.0E+00 AU16988.1 EST HUMAN 23604 36852 2.09 0.0E+00 AV663658.1 EST HUMAN 18399 31311 2.73 0.0E+00 AV663658.1 IT 23636 36887 2.64 0.0E+00 AB635268.1 IT 23637 36888 2.64 0.0E+00 BE182360.1 EST HUMAN 22636 36888 <	Ц			0.0E+00	2.1	EST_HUMAN	ha04h04.x1 NCI_CGAP_Kid12 Homo saplens cDNA clone IMAGE:2872759 3'
23569 36806 7.34 0.0E+00 CO5089.1 EST HUMAN 23568 36814 2.31 0.0E+00 AA746375.1 EST HUMAN 2356 36826 3.74 0.0E+00 AA746375.1 EST HUMAN 23576 36826 3.74 0.0E+00 M78448.1 EST HUMAN 23576 36826 3.74 0.0E+00 AL157608.1 EST HUMAN 23590 36836 5.81 0.0E+00 AL157608.1 EST HUMAN 23604 36853 1.64 0.0E+00 AV683658.1 EST HUMAN 23604 36862 2.09 0.0E+00 BF386563.1 EST HUMAN 18399 31311 2.73 0.0E+00 BF386563.1 IT 23636 31812 2.73 0.0E+00 BE182360.1 IT 23636 36888 2.64 0.0E+00 BE182360.1 EST HUMAN 23637 36888 2.64 0.0E+00 BE182360.1 EST HUMAN 23637 36888				0.0E+00	3.1	N	Homo seplens signaling lymphocytic activation molecule (SLAM) gene, exon 2
23568 36814 2.31 0.0E+00 AA746375.1 EST_HUMAN 23566 36815 2.31 0.0E+00 AA746375.1 EST_HUMAN 23576 36826 3.74 0.0E+00 M78448.1 EST_HUMAN 23578 36827 6.82 0.0E+00 M78448.1 EST_HUMAN 23590 36836 5.81 0.0E+00 AL157608.1 EST_HUMAN 23604 36836 5.81 0.0E+00 AV863658.1 EST_HUMAN 23612 36862 2.09 0.0E+00 BF38658.1 EST_HUMAN 18399 31311 2.73 0.0E+00 BF38658.1 IT_HUMAN 18399 31312 2.73 0.0E+00 BE182360.1 IT_HUMAN 23636 36887 2.64 0.0E+00 BE182360.1 EST_HUMAN 22636 36888 2.64 0.0E+00 BE182360.1 EST_HUMAN 22636 36888 2.64 0.0E+00 BE182360.1 EST_HUMAN 22636 36808 2.64 0.0E+00 BE182360.1 EST_HUMAN 22653 36808 2.64 0.0E+00 BE182				0.0E+00	CD5089.1	EST_HUMAN	C05089 Human heart cDNA (YNakamura) Homo saplens cDNA clone 3NHC4817
2356 36815 2.31 0.0E+00 AA746375.1 EST HUMAN 23576 36826 3.74 0.0E+00 M78448.1 EST HUMAN 23576 36826 3.74 0.0E+00 M78448.1 EST HUMAN 23590 36836 5.81 0.0E+00 AL157608.1 EST HUMAN 23604 36853 1.64 0.0E+00 AV683658.1 EST HUMAN 23612 36862 2.09 0.0E+00 BF386563.1 EST HUMAN 18399 31311 2.73 0.0E+00 AB635286.1 NT 18399 31312 2.73 0.0E+00 AB635286.1 NT 23636 36887 2.84 0.0E+00 BE182360.1 EST HUMAN 23637 36888 2.04 0.0E+00 BE182360.1 EST HUMAN 23636 36868 2.04 0.0E+00 BE182360.1 EST HUMAN 23637 36868 2.04 0.0E+00 BE182360.1 EST HUMAN 23637 36869	L			0.0E+00	AA746375.1	EST_HUMAN	pa56h01.r1 NCI_CGAP_GCB1 Homo sapiens cDNA done IMAGE:1309009 5'
23575 36825 3.74 0.0E+00 M78448:1 EST_HUMAN 23576 36826 3.74 0.0E+00 M78448:1 EST_HUMAN 23590 36836 5.81 0.0E+00 AL157608:1 EST_HUMAN 23604 36853 1.64 0.0E+00 AV683658:1 EST_HUMAN 23612 36862 2.09 0.0E+00 BF386563:1 EST_HUMAN 18399 31311 2.73 0.0E+00 ABG35286:1 NT 18390 31312 2.73 0.0E+00 ABG35286:1 NT 23636 36887 2.64 0.0E+00 BE182360:1 EST_HUMAN 23636 36888 2.64 0.0E+00 BE182360:1 EST_HUMAN 23637 36888 2.64 0.0E+00 BE182360:1 EST_HUMAN 23637 36868 2.64 0.0E+00 BE182360:1 EST_HUMAN 23655 36908 4.07 0.0E+00 BC182363:1 EST_HUMAN 23655 36908				0.0E+00	AA746375.1	EST_HUMAN	oa66h01.r1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1309009 5'
23576 36826 3.74 0.0E+00 M78448.1 EST HUMAN 23578 36827 6.82 0.0E+00 AL157608.1 EST HUMAN 23590 36836 5.81 0.0E+00 AU18988.1 EST HUMAN 23604 36853 1.64 0.0E+00 AV683658.1 EST HUMAN 23612 36862 2.09 0.0E+00 BF36563.1 EST HUMAN 18399 31311 2.73 0.0E+00 AB635266.1 NT 18390 31312 2.73 0.0E+00 BE182360.1 EST HUMAN 23636 36887 2.64 0.0E+00 BE182360.1 EST HUMAN 23637 0.0E+00 BE182360.1 EST HUMAN EST HUMAN 23637 0.0E+00 BE182360.1 EST HUMAN 23637 0.0E+00 BE182360.1 EST HUMAN 23637 0.0E+00 BE182360.1 EST HUMAN 23637 0.0E+00 BE182360.1 EST HUMAN 23655 36908 4.07 0.0E+00 BE896423.1 EST HUMAN	L.,			0.0E+00	M78448.1	EST_HUMAN	EST00598 Fetal brain, Strategone (cat#836208) Homo septens cDNA clone HFBCC28
23578 36827 6.82 0.0E+00 AL157608.1 EST HUMAN 23590 36836 5.81 0.0E+00 AU16988.1 EST HUMAN 23604 36853 1.64 0.0E+00 AV683658.1 EST HUMAN 23612 36862 2.09 0.0E+00 BF36653.1 EST HUMAN 18399 31311 2.73 0.0E+00 ABG35266.1 NT 18390 31312 2.73 0.0E+00 ABG35266.1 NT 23636 36887 2.64 0.0E+00 BE182360.1 EST HUMAN 23637 36888 2.64 0.0E+00 BE182360.1 EST HUMAN 23637 0.0E+00 BE182360.1 EST HUMAN 23638 2.64 0.0E+00 BE182360.1 EST HUMAN 23637 1.4 0.0E+00 BE182360.1 EST HUMAN 23655 36908 4.07 0.0E+00 BE896423.1 EST HUMAN				0.0E+00	M78448.1	EST_HUMAN	EST00596 Fetal brain, Stratagene (cat#636206) Homo sapiens cDNA clone HFBCC26
23590 36836 5.81 0.0E+00 AU118988.1 EST_HUMAN 23604 36863 1.64 0.0E+00 AV683658.1 EST_HUMAN 23612 36862 2.09 0.0E+00 BF36658.1 EST_HUMAN 18399 31311 2.73 0.0E+00 ABC35266.1 NT 18390 31312 2.73 0.0E+00 ABC35266.1 NT 23636 36887 2.64 0.0E+00 BE182360.1 EST_HUMAN 23636 36888 2.64 0.0E+00 BE182360.1 EST_HUMAN 23637 1.4 0.0E+00 AV701162.1 EST_HUMAN 23655 36908 4.07 0.0E+00 BE896423.1 EST_HUMAN	1		6.82	0.0E+00	AL157608.1	EST HUMAN	DKFZp761J2116_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761J2116 5
23604 36863 1.64 0.0E+00 AV603656.1 EST HUMAN 23612 36862 2.09 0.0E+00 BF36563.1 EST HUMAN 18399 31311 2.73 0.0E+00 AB035266.1 NT 18390 31312 2.73 0.0E+00 AB035266.1 NT 23636 36887 2.64 0.0E+00 BE182360.1 EST HUMAN 23636 36888 2.64 0.0E+00 BE182360.1 EST HUMAN 23637 1.4 0.0E+00 BE182360.1 EST HUMAN 23655 36908 4.07 0.0E+00 BE86423.1 EST HUMAN	l			0.0E+00	AU116988.1	EST_HUMAN	AU116988 HEMBA1 Homo sepiens cDNA done HEMBA1000424 67
23612 36862 2.09 0.0E+00 BF386563.1 EST HUMAN 18399 31311 2.73 0.0E+00 AB035266.1 NT 18390 31312 2.73 0.0E+00 AB035266.1 NT 23630 36887 2.64 0.0E+00 BE182360.1 EST HUMAN 23636 36888 2.64 0.0E+00 BE182360.1 EST HUMAN 23637 1.4 0.0E+00 AV701162.1 EST HUMAN 23655 36908 4.07 0.0E+00 BE869423.1 EST HUMAN	L			0.0E+00	AV603658.1	EST HUMAN	4V693656 GKC Homo septens dDNA clane GKCCNC03 5
18399 31311 2.73 0.0E+00 AB035206.1 NT 18390 31312 2.73 0.0E+00 AB035208.1 NT 23630 36887 2.64 0.0E+00 BE182300.1 EST HUMAN 23636 36888 2.64 0.0E+00 BE182300.1 EST HUMAN 23637 1.4 0.0E+00 AV701162.1 EST HUMAN 23656 36908 4.07 0.0E+00 BE86423.1 EST HUMAN				0.0E+00	BF366553.1	EST HUMAN	1.3-NT0104-200500-143-A07 NT0104 Homo sepiens cDNA
18390 31312 2.73 0.0E+00 AB035288:1 NT 23636 36887 2.64 0.0E+00 BE182360:1 EST HUMAN 23636 36888 2.64 0.0E+00 BE182360:1 EST HUMAN 23637 1.4 0.0E+00 AV701162:1 EST HUMAN 23656 36908 4.07 0.0E+00 BE86423:1 EST HUMAN				0.0E+00	AB035266.1	F	Homo sapiens mRNA for neuravin II, complete cds
23636 36887 2.64 0.0E+00 BE182360.1 EST HUMAN 23636 36888 2.64 0.0E+00 BE182360.1 EST HUMAN 23637 1.4 0.0E+00 AV701162.1 EST HUMAN 23656 36908 4.07 0.0E+00 BE869423.1 EST HUMAN				0.0E+00	AB035268.1	¥	Homo sapiens mRNA for neuredn II, complete cds
23636 36888 2.64 0.0E+00 BE182360.1 EST HUMAN 23637 1.4 0.0E+00 AV701162.1 EST HUMAN 23656 36908 4.07 0.0E+00 BE86423.1 EST HUMAN				0.0E+00	BE182360.1	EST_HUMAN	PM0-HT0845-060500-002-E05 HT0845 Hamp sepiens cDNA
23637 1.4 0.0E+00 AV701152.1 EST HUMAN 23955 3999 4.07 0.0E+00 BE898423.1 EST HUMAN				0.0E+00	BE182360.1	EST_HUMAN	PM0-HT0845-060500-002-E05 HT0845 Homo sepiens cDNA
23655 36908 4.07 0.0E+00 BE896423.1 EST HUMAN		837	1.4	0.0E+00	AV701152.1		4V701152 ADA Homo sapiens cDNA clone ADAAAD06 5
		36908	4.07	0.0E+00	BE896423.1	EST_HUMAN	601439092F1 NIH_MGC_72 Homo septems cDNA dome IMAGE:3924142 5

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Protect Earn Single Exon Probes Expressed in Brain Top-Hit Aceasion Top-Hit Descriptor Top-Hit Descrip
11008 23788 37044 2.69 0.0E+00 BE206846.1 EST_HUMAN 65NDA-ASSOCIATED PROTEIN.; 11110 23780 37055 1.9 0.0E+00 11628409 NT Homo septiens KIAA0428 gene product (KIAA0428), mRNA 11124 23783 37059 1.52 0.0E+00 11024711 NT Homo septiens myosin, heavy polyapside 4, skeletal muscle (MYH4), mRNA 11131 23789 37074 3.84 0.0E+00 BE148076.1 EST_HUMAN RC3-HT0230-040500-110-ho4 HT0230 Homo septiens cDNA 11131 23789 37075 3.84 0.0E+00 BE148076.1 EST_HUMAN RC3-HT0230-040500-110-ho4 HT0230 Homo septiens cDNA 11131 23789 37075 3.84 0.0E+00 BE148076.1 EST_HUMAN RC3-HT0230-040500-110-ho4 HT0230 Homo septiens cDNA 11134 2382i 37101 1.56 0.0E+00 AW673489.1 EST_HUMAN KIAA0522 PROTEIN;
23768 37044 2.69 0.0E+00 BE206846.1 EST_HUMAN 23780 37055 1.9 0.0E+00 11628406 NT 23783 37069 1.52 0.0E+00 11024711 NT 23789 37074 3.84 0.0E+00 BE148076.1 EST_HUMAN 23789 37075 3.84 0.0E+00 BE148076.1 EST_HUMAN
23768 37044 2.69 0.0E+00 BE206846.1 EST_HUMAN 23780 37055 1.9 0.0E+00 11628406 NT 23783 37069 1.52 0.0E+00 11024711 NT 23789 37074 3.84 0.0E+00 BE148076.1 EST_HUMAN 23789 37075 3.84 0.0E+00 BE148076.1 EST_HUMAN
23768 37044 2.69 0.0E+00 BE206846.1 EST_HUMAN 23780 37055 1.9 0.0E+00 11628409 NT 23783 37069 1.52 0.0E+00 11024711 NT 23789 37074 3.84 0.0E+00 BE148076.1 EST_HUMAN
23768 37044 2.69 0.0E+00 BE206846.1 EST_HUMAN 23780 37055 1.9 0.0E+00 11628409 NT 23783 37059 1.52 0.0E+00 11024711 NT 20052 33133 1.6 0.0E+00 32882.1 NT
23768 37044 2.89 0.0E+00 BE206848.1 EST_HUMAN 23780 37065 1.9 0.0E+00 11628409 NT 23783 37069 1.52 0.0E+00 11024711 NT
23768 37044 2.69 0.0E+00 BE206846.1 EST_HUMAN 23780 37055 1.9 0.0E+00 11628409 NT
23788 37044 2.69 0.0E+00 BE206846.1 EST_HUMAN
23788 37043 2.69 0.0E+00 BE206846.1 EST_HUMAN
23786 37041 4.23 0.0E+00 AB018280.1 INT
23766 37040 4.23 0.0E+00[AB018260.1 NT
23761 37036 12.22 0.0E+00 AW 207734.1 EST_HUMAN
23756 37032 2.67 0.0E+00 BF206561.1 EST_HUMAN
23755 37031 3.98 0.0E+00 4758827 NT
23763 37028 1.61 0.0E+00 10880982 NT
23721 36992 2.76 0.0E+00/AL042278.1 EST_HUMAN
23708 36978 1.89 0.0E+00 AM59545.1 EST_HUMAN
23708 38977 1.89 0.0E+00 AH59546.1 EST HUMAN
23706 36974 8.73 0.0E+00 BE897953.1 EST_HUMAN
23705 36973 1.53 0.0E+00 4758281 NT
26133 36965 1.27 0.0E+00 AW387786.1 EST HUMAN
25133 36864 1.27 0.0E+00 AW387786.1 EST_HUMAN
23688 36951 1.77 0.0E+00 BF528907.1 EST_HUMAN
23688 36960 1.77 0.0E+00 BF628907.1 EST_HUMAN
23688 36949 1.77 0.0E+00 BF628907.1 EST_HUMAN
23600 36923 2.39 0.0E+00 BE018293.1 EST_HUMAN
bb78604.y1 NIH_MGC_10 Home expiers aDNA done IMAGE:3048486 6' similer to gb:Y00345_cde1 POLYADENYLATE-BINDING PROTEIN (HUMAN); db:X86563 M.muscalus mRNA for polyA) binding
23863 36920 1.85 0.0E+00 AW500307.1 EST_HUMAN
COLOR OF THE COLOR
23683 38919 1.85 0.0F+00 AW5003071 FST HIMAN
NO: ID NO: Signer BLASTE: No. Source
Exon ORF SEQ Expression (Top)Hit Top Hit Accession Detabase
Single Exon Probes Expressed in Brain

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Single Exult Flobes Expressed in Brain	Exam ORF SEQ Expression (Top) Hit Top Hit Acession No. Signal BLASTE No. Source Source	24018 37321 4.02 0.0E+00 BE206846.1 EST_HUMAN 55KDA-ASSOCIATED PROTEIN.;	24018 37322 4.02 0.0E+00 BE206846.1 EST HUMAN 55KDA-AS9OCIATED PROTEIN.:	128.1	3.06 0.0E+00/AA568707.1 EST HUMAN	30623 3.84 0.0E+00 AK34954.1 EST HUMAN	37330 7.45 0.0E+00 AW327895.1 EST_HUMAN	37348 1.89 0.0E+00 AW292776.1 EST_HUMAN	38401 2.2 0.0E+00 4758827 NT	37276 1.73 0.0E+00 BE264068.1 EST_HUMAN	37278 1.74 0.0E+00 BE965909.2 EST_HUMAN	EST HUMAN	37280 4.52 0.0E+00 BE186858.1 EST HUMAN	1.29 0.0E+00 BF513980.1 EST_HUMAN	37294 7.81 0.0E+00 AL046540.1 EST_HUMAN	23983 37286 7.81 0.0E+00 AL046540.1 EST_HUMAN DKFZp434G178_r1 434 (synonym: httes3) Homo septens cDNA clone DKFZp434G178 5	24003 37308 5.89 0.0E+00 AI923116.1 EST_HUMAN RECEPTOR (HUMAN);	24050 37353 3.42 0.0E+00 AA780913.1 EST HUMAN Q13988 ALKB HOMOLOG PROTEIN.:		37380 1.94 0.0E+00 BE910646.1 EST HUMAN		Т	SOTION 1.78 U.UE+UUIBEG15008.1 ESI HUMAN	38417 1.79 0.0E+00 BE615686.1 EST HUMAN	38424 1.81 0.0E+00 AV757420.1 EST_HUMAN	37367 1.52 0.0E+00 Y18800.1 NT	37370 10.31 0.0E+00[L39691.1 NT	37371 10.31 0.0E+00 L39891.1 NT	1.1 EST_HUMAN
	SEQ ID NO:									_ }					┙	┙	1			1_1	İ	- 1		_	_			.	- 1
	Probe SEQ ID NO:	11327	11327	11329	11334	11335	11336	11355	11362	11368	11371	11371	11372	11373	11387	11387	11397	11401	11401	11408		44440		11419	11428	11457	1461	11461	11478

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Single Exon Probes Expressed in Brain

Probe SEQ ID NO:	Exan SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Debabese Source	Top Hit Descriptor
11401		37404	1.92	0.0E+00	0.0E+00 BE622317.1	EST_HUMAN	601441096F1 NIH_MGC_72 Hamo septens cDNA clane IMAGE:3916270 5'
11518	24118	37428	1.42	0.0E+00	0.0E+00 Alg39834.1	EST_HUMAN	tm94c10.x5 NCI_CGAP_Bm25 Home septems oDNA done IMAGE:2165778 3
11529	24129	37434	13.79	0.0E+00	0.0E+00 BE748899.1	EST HUMAN	801572186T1 NIH MGC_56 Hano septens cONA clane IMAGE:3839012.3
11529	24129	37435	13.79	0.0E+00	0.0E+00 BE748899.1	EST HUMAN	601572180T1 NIH MGC 55 Hamo sablens cDNA clane IMAGE:3839012.3
11630	24139	37447	1.81	0.0E+00	0.0E+00 AU141882.1	EST HUMAN	AU141882 THYRO1 Homo septens cDNA clone THYRO1001398 5
11539	24139	37448	1.81	0.0E+00	0.0E+00 AU141882.1	EST_HUMAN	AU141882 THYRO1 Homo sepiens cDNA clone THYRO1001398 5
11542	24142	37451	2.08	0.0E+00	0.0E+00 AW008022.1	EST HUMAN	w291h01.x1 NCI_CGAP_Bm25 Homo septens cDNA done IMAGE:2569225 3' similar to WP:F53H10.2 CE11040 ZINC FINGER_C2H2 TYPE:
.,							7h22b10.x1 NCI_CGAP_Co16 Homo sepiens cDNA done IMAGE:3316699 3' striller to TR:Q13458 Q13458
11346	25135	37455	3.49	0.0E+00	Σ.	EST HUMAN	TRIO.;
11571	2413	37485	2.88	0.0E+00	6.1	EST HUMAN	MR4-ST0118-261089-012-b03 ST0118 Hano sapiens cDNA
11571	24170	37486	2.88	0.0E+00	0.0E+00 AW387778.1	EST HUMAN	MR4-ST0118-261069-012-b03 ST0118 Homo sepiens cDNA
11582	24181	·	2.41	0.0E+00	0.0E+00 AW863777.1	EST_HUMAN	MR3-SN0010-310300-107-h03 SN0010 Homo septens cDNA
11601	24200	37521	4.76	0.0E+00	11435244 NT	۲	Homo sapiens KIAA0247 gene product (KIAA0247), mRNA
11601	24200	37522	4.78	0.0E+00	11435244 NT	NT	Homo saplens KIAA0247 gene product (KIAA0247), mRNA
11908	24208	37529	5.87	0.0E+00 U36253.1	U36253.1	NT	Human beta-prime adaptin (BAM22) gene, exon 5
11812	24210	37533	2.29	0.0E+00 BE379254	BE379254.1	EST_HUMAN	601237691F1 NIH_MGC_44 Homo septens cDNA clone IMAGE:3809623 51
11612	24210	37534	2.29	0.05+00	0.0E+00 BE379254.1	EST HUMAN	601237691F1 NIH_MGC_44 Homo septens cDNA clone IMAGE:3809623 5
11632	24229	37553	222	0.0E+00	0.0E+00 BE794758.1	EST HUMAN	801580588F1 NIH_MGC_7 Homo septens cDNA clone IMAGE:3944708 5'
11634	24231	37554	45.09	0.0E+00	0.0E+00 BE879633.1	EST_HUMAN	601491821F1 NIH_MGC_69 Homo sepiens cDNA olone IMAGE:3894220 5'
11840	24237	37560	1.62	0.0E+00	4758827 NT	L	Homo sapiens neuredn III (NRXN3) mRNA
1108	24237	37501	1.62	0.0E+00	4758827 NT	¥	Homo sapiens neurech III (NRXN3) mRNA
104	24241	37565	1.65	0.0E+00)	0.0E+00 AF053543.1	N.	Homo saplens glutathione transferase zata 1 (GSTZ1) gene, exons 6 and 7
11848	24243		1.56	0.0E+00	0.0E+00 AL163204.2	INT	Hamo seplens chranosome 21 segment HS21C004
11053	24250	37572	14.08	0.05+00	0.0E+00 BE409933.1	EST_HUMAN	801289403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3829544 5'
1654	24251	37673	1.46	0.0E+00	0.0E+00 BE148650.1	EST_HUMAN	MR0-HT0241-150500-011-f02 HT0241 Homo sepiens cDNA
11855	24252	37574	2.69	0.0E+00 AF223391	-	k	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and pertial cds, alternatively spliced
11656	24252	37575	2.69	0.0E+00 AF223391	<u>-</u>	¥	Homo septens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11857	18187	30878	1.20	0.0E+00 D26635.1		Ę	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
11057	18187	30879	1.29	0.0E+00 D28535.1		Ν	Human gene for ditydrolipoamide succinyltransferase, complete cds (exon 1-15)
11658	24254	37578	5.6	0.0E+00 BF881641	.1	EST HUMAN	602155722F1 NIH_MGC_83 Homo septens cDNA clone IMAGE:4296725 5
11668	24264	37577	5.8	0.0E+00 BF681641	3F681641.1	EST_HUMAN	802155722F1 NIH_MGC_83 Homo saplens cONA clone IMAGE:4286725 5'

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Table 4
Sindle Exon Probes Expressed in

					THO I	Jie Exoli Pio	Single Exon Probes Expressed in Brain
Probe SEQ ID NO:	Eon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Defabese Source	Top Hit Descriptor
11662	24258		1.93	0.0E+00	8008002 NT	LN LN	Homo sepiens glutamate receptor, lonotropic, N-methyl D-espartale 24 (GRIN2A) mRNA
11864		30683	1.5	0.0E+00	83.1	F	Homo sepiens gephyrin mRNA, complete cds
11667		37588	1.71	0.0E+00 AU1329		EST HUMAN	AU132940 NT2RP4 Hamo septens cDNA clane NT2RP4000929 5
11670	24265	37588	1.35	0.0E+00	0.0E+00 BE903372.1	EST_HUMAN	601676357F1 NIH_MGC_21 Hamp septens cDNA clane IMAGE:3858935 5'
11687	24282	37604	2.5	0.0E+00	0.0E+00 X51755.1	N	Humen lembdie-Immunoglobulin constant region complex (germiline)
11687	24282	37605	2.5	0.0E+00 X51755	-	Ę	Human lambda-immunoglobulin constant region complex (germline)
11728			15.74	0.0E+00 BF3091	20.1	EST_HUMAN	601690534F1 NIH_MGC_17 Homo septens cDNA clone IMAGE:4131416 5'
11737		37854	11.96	0.0E+00	5.1	EST HUMAN	801177407F1 NIH_MGC_17 Hamo septens cDNA clone IMAGE:3532368 5'
11751	24342	37671	1.3	0.0E+00 BE74431		EST_HUMAN	601576625F1 NIH_MGC_9 Hamo saplene cDNA clane IMAGE:3837222 5
11751	24342	37672	1.3	0.0€+00	0.0E+00 BE744311.1	EST_HUMAN	601576525F1 NIH_MGC_9 Homo septens cDNA clone IMAGE:3837222 5
11757	24348	37878	1.43	0.0E+00		EST_HUMAN	601113009F1 NIH_MGC_16 Homo septens cDNA clone IMAGE:3353378 5
11757	24348	37879	1.43	0.0€+00	0.0E+00 BE257812.1	EST_HUMAN	601113009F1 NIH_MGC_16 Homo septens cDNA clone IMAGE:3353378 5
11785	24375	37705	1.69	0.0E+00		EST HUMAN	801114240F1 NIH_MGC_16 Homo septens CDNA clone IMAGE:3354872 5
11790	24380	37710	1.68	0.0E+00	84.1	EST_HUMAN	PM1-BT0348-151289-001-c11 BT0348 Homo sepiens cDNA
11790	24380	37711	1.68	0.0E+00 AW749		EST_HUMAN	PM1-8T0348-151209-001-c11 BT0348 Homo sapiens cDNA
11792	24382	37713	2.23	0.0E+00		EST_HUMAN	MR0-HT0166-271199-005-003 HT0166 Homo septens cDNA
11702	24382	37714	2.23	0.0€+00.0		EST_HUMAN	MR0-HT0166-271199-005-003 HT0166 Homo septens cDNA
11797	24387	37720	2.46	0.0€+00		EST HUMAN	AU117974 HEMBA1 Homo sepiens cDNA clone HEMBA1002612 6
11797	24387	37721	2,46	0.0E+00∫	74.1	EST_HUMAN	AU117974 HEMBA1 Homo septens dans HEMBA1002612 5
11808	14948		1.31	0.0E+00 U36264		NT	Human beta-prime-edaptin (BAM22) gene, exon 16
11821	!	31859	2.45	0.0€+00		NT	Human beta2-chimeerin mRNA, complete cds
11822	24407	37741	5.54	0.0E+00 Z31706.1		NT	H.sapiens GLAST1 gene for gällel gutamate transporter, exon6
11835	24419	37760	2.28	0.05+00	0.0E+00 Al866185,1	EST HUMAN	t38f02x1 NCI_CGAP_GC8 Homo saplens cDNA clone IMAGE:2243067 3' similar to SW:CG2G_HUMAN P51959 G2MITOTIC-SPECIFIC CYCLIN G1.
11837	24421	37762	2.31	0.0E+00 AU1323		EST HUMAN	AU132394 NT2RP3 Hamo sepiens aDNA clone NT2RP3004339 5
11879	25300	30800	227	0.0E+00.	0.0E+00 BE312542.1	EST HUMAN	601150023F1 NIH_MGC_19 Hamo septens cDNA clane IMAGE:3503020 5
11863	26267		3.80	0.05+00.		EST_HUMAN	qe17b12.x1 Soares_fetal_lung_NbHL19W Homo sepiens cDNA clone IMAGE:1739231 3'
11902	24408		1.6	0.0E+00	0.0E+00 AB011399.1	Ę	Homo sapiens gene for AF-8, complete cds
11921	24482		4.9	0.0€+00	0.0E+00 AL163246.2	L	Homo sapiens chromosome 21 segment HS21C046
11829	24488	-	4.1	0.0E+00	11417862 NT	5	Homo saplens calcineurin binding protein 1 (KIAA0330), mRNA
11947	24501		3.05	0.0E+00	5802973 NT	Ę	Homo sapiens antioddart protein 1 (AOP1), nuclear gene encoding mitochondrial protein, mRNA
11082	25218	30816	2.50	0.05+00		IN	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
11993	25226		5.39	0.0E+00		EST_HUMAN	DKFZp434K0819_r1 434 (synonym: https:// Hamo sapiens.cDNA clane DKFZp434K0819.57
!	 						

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Olingia Evolutiones Expressed III Digili	ORF SEQ Expression (T ID NO: Signal BL	25369 3.12 0.0E+00 11418318/NT Homo saplens G-2 and S-phase expressed 1 (GTSE1), mRNA	24551 0.0E+00/AL046544.1 EST HUMAN DKFZp434G218 r1 434 (synonym: hises3) Homo septiens cDNA clone DKFZp434G218 5	:1 EST HUMAN	28390 1.52 0.0E+00 N64484.1 EST HUMAN SW-POL BAEVM P10272 POL POLYPROTEN.	0.0E+00(AF106658.1	28262 3.39 0.0E+00 4507500 NT	0.0E+00 4507500 NT	2.21 0.0E+00 10092587 NT Homo septens nucleer factor of activated T-cells, cytoplasmic, celcineurin-dependent 2 (NFATC2), mRNA	Homo sepiens X-linked anhidrotific ectodermal dysplessia protein gene (EDA), exon 2 and flanking repeat regions 2.04 0.0E+00 AF003528.1 NT regions	EST HUMAN	1.34 0.0E+00 BE090210.1 EST_HUMAN	4.43 0.0E+00 AF068757.1 INT	3.36 0.0E+00 9835487 NT	2.41 0.0E+00 AI204914.1 EST HUMAN	1.68 0.0E+00 AISO4646.1 EST HUMAN		Z7437 1.51 0.0E+00 6912457 NT	31039 2.08 0.0E+00 AF0363e5.1 NT Homo septens careolin-3 (CAV3) mRNA, complete cds	14424 27119 2,76 0.0E+00 H30132.1 EST_HUMAN GAMMA-GLUTAMYLTRANSPEPTIDASE 5 PRECURSOR (HUMAN);	14424 Z7120 2.76 0.0E+00 H30132.1 EST HUMAN GAMMA-GLUTAMYLTRANSPEPTIDASE 5 PRECURSOR (HUMAN):	10.66 0.0E+00 D50659.1 NT		24818 31021 2.51 0.0E+00 11418189 NT Homo septens thyroid autoentigen 70kD (Ku entigen) (G22P-1), mRNA	27549 1.53 0.0E+00 4758489 NT	1.5 0.0E+00 AW884898.1 EST HUMAN	26017 2.09 0.0E+00 8922563 NT	1.88 0.0E+00 11528291 NT	16089 28718 4.24 0.0E+00 4885312 Hamo sapiens G protein-coupled receptor 24 (GPR24), mRNA
		99	:51	:81	8	48		L	25	18		8	88	32	52	78				.		18				20			
	- W		12023 245	12037 252	12076 2538	12089 245		12092 1356	12100 2526	12129 1331	12218 2516	12229 2524	12273 2525						12423 247B	12435 1442	12435 1442			12448 2481			ļ		12588 1606
1	Proba SEQ II NO:	7	1,	12	4	12	12	12	7	12	2	12	2	12	12	12	12	12	2	12	12	ĮŽĮ	12	12	12	12	5	힏	젔

Page 536 of 536 Table 4 Single Exon Probes Expressed in Brain

Top Hit Descriptor	od protein 2 (LRP2), mRNA	ulfotrænsferase, excm 1, 2, 3, 4, 5	Homo sepiens cleavage and polyadenylation specific factor 1, 160kD subunit (CPSF1), mRNA	5210046	od protein 2 (LRP2), mRNA	(KIAA0330), mRNA	(FZP434P211), mRNA	wu83c07x1 NCI_CGAP_Kid3 Home sepiens cDNA clone IMAGE:2527596 3' struiter to TR:Q12844 Q12844 BREAKPOINT CI IISTER REGION PROTEIN ************************************	nd frame 3 (C12ORF3), mRNA	ha 2 subunit (CACNAZD1) gene, exon 8
	Homo saplens low density lipoprotein-related protein 2 (LRP2), mRNA	Homo sapiens CST gene for cerebroside sulfotransferase, excn 1, 2, 3, 4, 5	Homo sepiens cleavage and polyadenylati	Homo sepiens chramosame 21 segment HS21C046	Homo sapiens low density ilpoprotein-related protein 2 (LRP2), mRNA	Homo sepiens calcineurin binding protein 1 (KIAA0330), mRNA	Homo sepiens DKFZp434P211 protein (DKFZP434P211), mRNA	W483c07 x1 NCI_CGAP_KG3 Homo sepi	Homo sabiens chromosome 12 open reading frame 3 (C12ORF3), mRNA	Homo saplens dhydropyridine receptor alpha 2 subunit (CACNA2D1) gene, exon 8
Top Hit Database Source	Ę	¥	F	N	7	7	ΥT	EST HIMAN		Į.
Top Hit Acession No.	D806918 NT	0.1	9558724 NT	5.2	6806918 NT	11417862 NT	7657020 NT	AW025032 4	9966844	2
Most Similar (Top) Hit BLAST E Value	0.0E+00	0.0E+00 AB02900	0.0E+00	0.0E+00 AL16324	0.0E+00	0.0E+00	0.0E+00	00=30		0.0E+00 AF08382
Expression Signal	3.05	2.12	2.06	2.66	277	1.5	*	1.78	137	1.30
ORF SEQ ID NO:	30592		31009		26021	30972		30967	28550	
Probe Exan SEQ ID SEQ ID NO: NO:	17905	24905	24927	25410	13300	24999	25004	25042	13890	25251
Probe SEQ ID NO:	12576	12582	12622	12648	12664	12729	12735	12790	12808	12818

1/10

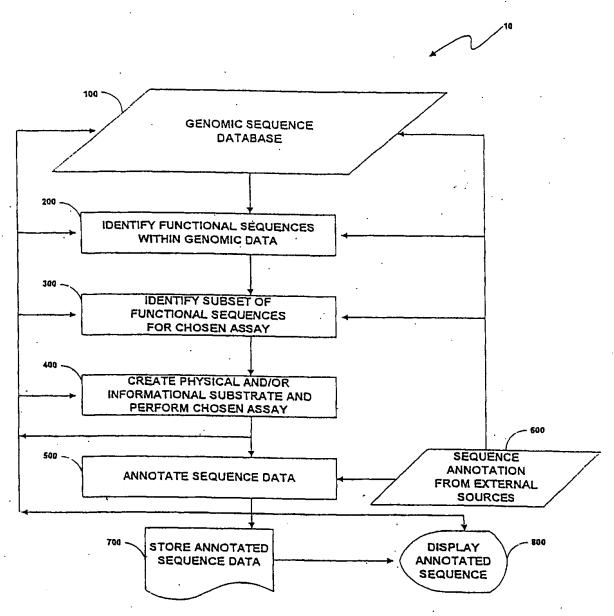


Fig. 1

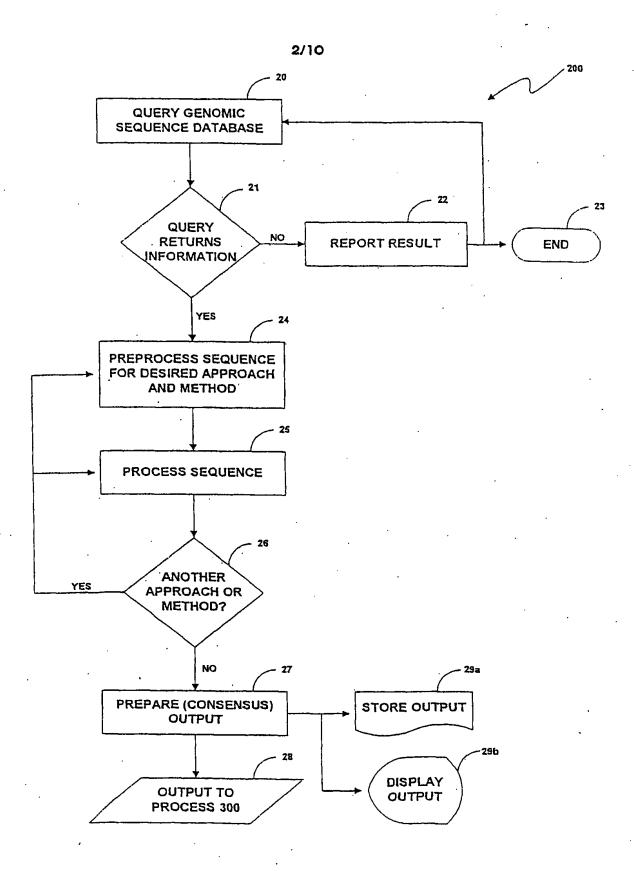


Fig. 2

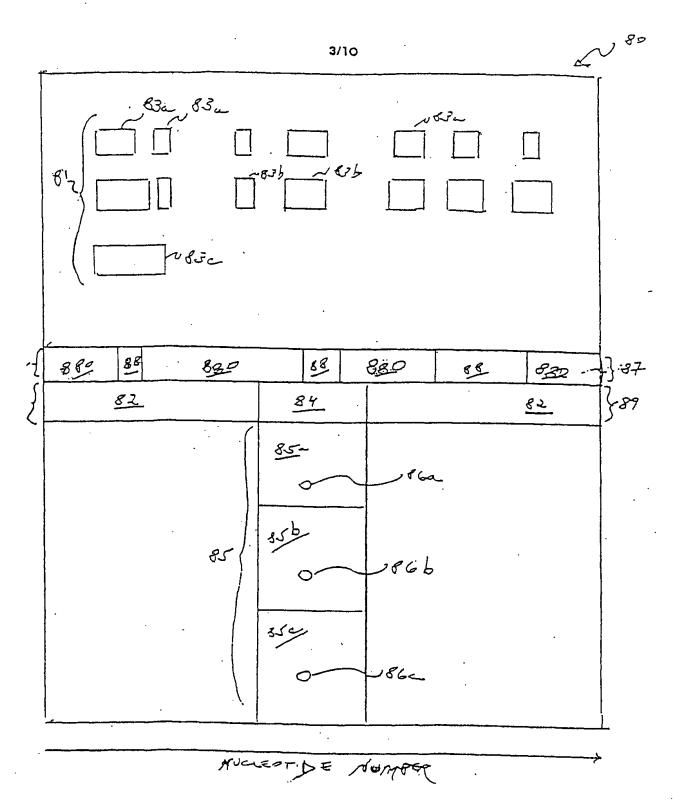


Fig. 3

4/10

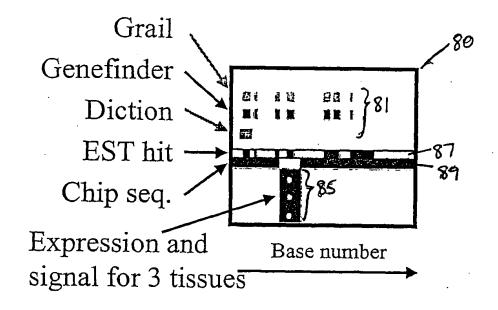


Fig. 4

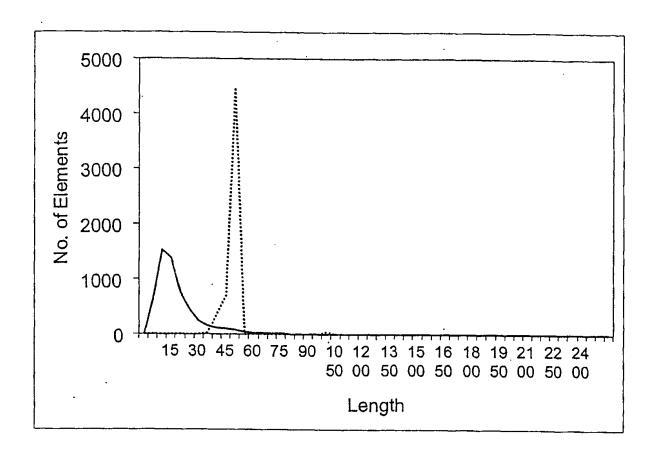


Fig. 5

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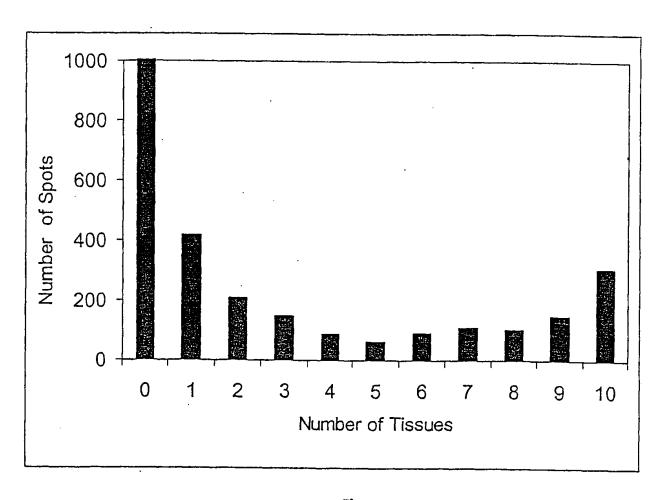
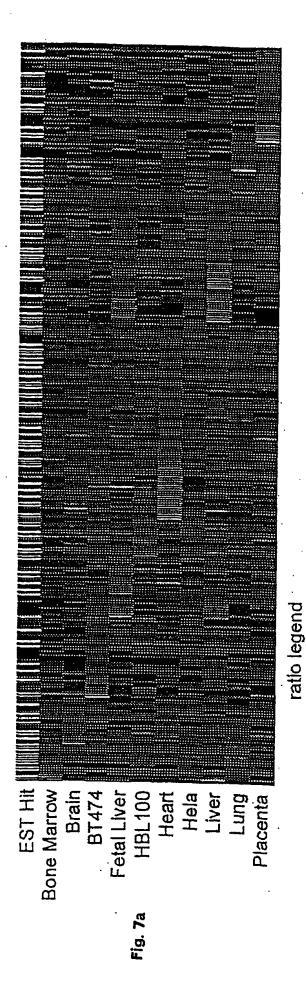
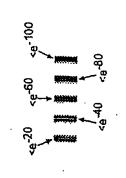
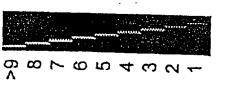


Fig. 6







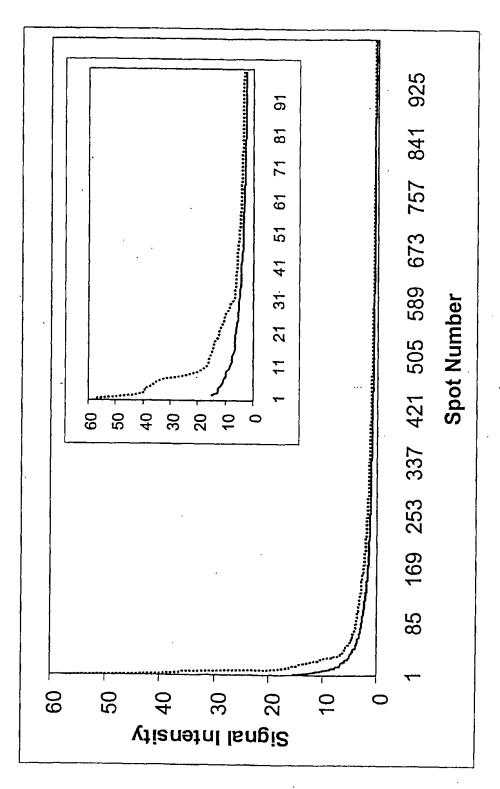
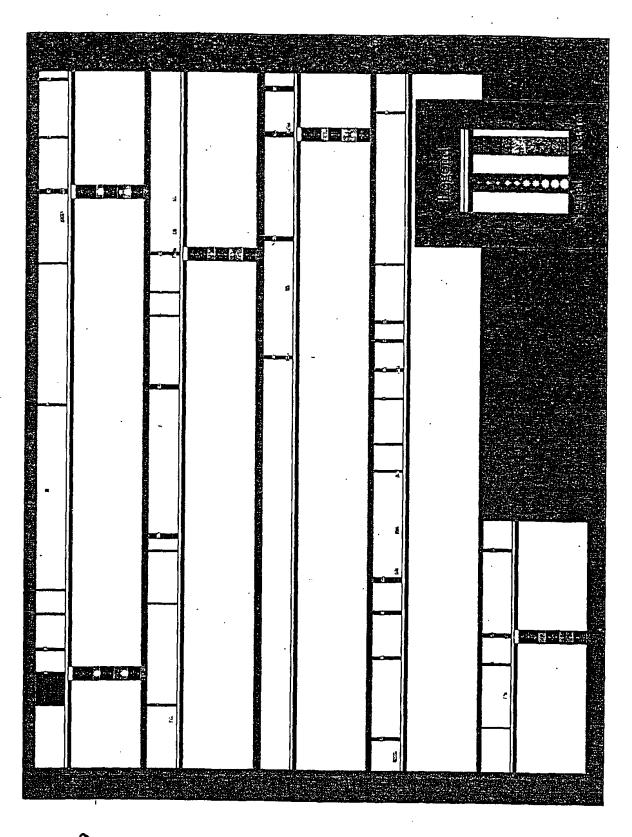
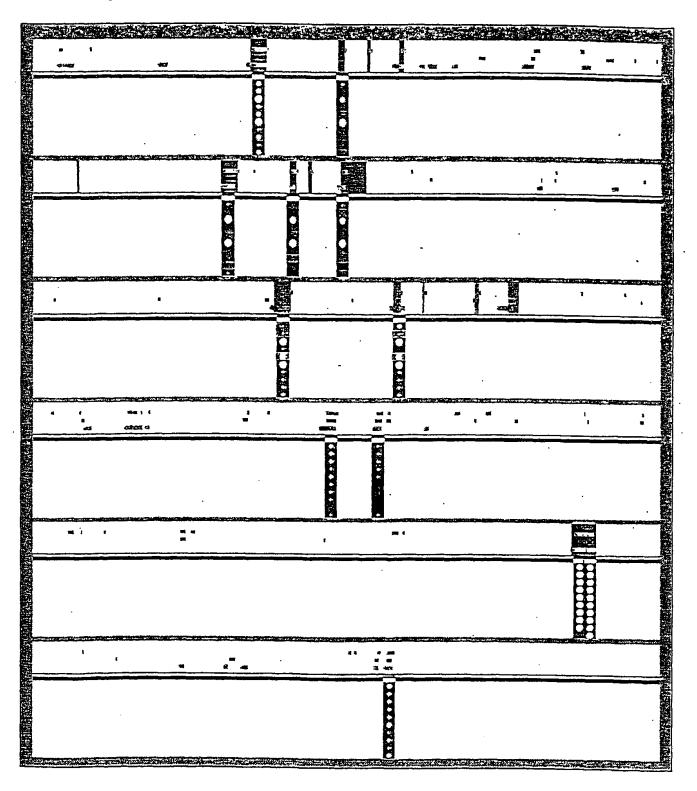


Fig. 8



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Fig. 10



(19) World Intellectual Property Organization International Bureau





(43) International Publication Date 9 August 2001 (09.08.2001)

PCT

(10) International Publication Number WO 01/057275 A3

(51) International Patent Classification⁷: C1 G06F 19/00, C07K 14/47

C12Q 1/68,

(21) International Application Number: PCT/US01/00667

(22) International Filing Date: 30 January 2001 (30.01.2001)

(25) Filing Language:

English

(26) Publication Language:

English

(30) Priority Data:

60/180,312	4 February 2000 (04.02.2000)	US
60/207,456	26 May 2000 (26.05.2000)	US
09/608,408	30 June 2000 (30.06.2000)	US
09/632,366	3 August 2000 (03.08.2000)	US
60/234,687	21 September 2000 (21.09.2000)	US
60/236,359	27 September 2000 (27.09.2000)	US
0024263.6	4 October 2000 (04.10.2000)	GB

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(72) Inventors; and

(75) Inventors/Applicants (for US only): PENN, Sharron, G. [GB/US]; 617 South Delaware Street, San Mateo, CA 94402 (US). HANZEL, David, K. [US/US]; 988 Loma Verde Avenue, Palo Alto, CA 94303 (US). CHEN, Wensheng [CN/US]; 210 Easy Street #25, Mountain View, CA 94043 (US). RANK, David, R. [US/US]; 117 El Dorado Commons, Fremont, CA 94539 (US).

(74) Agent: RONNING, Royal, N., Jr.; Amersham Pharmacia Biotech, Inc., 800 Centennial Avenue, Piscataway, NJ 08855 (US).

(81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:

with international search report

(88) Date of publication of the international search report: 17 April 2003

(15) Information about Correction:

Previous Correction:

see PCT Gazette No. 42/2002 of 17 October 2002, Section II

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

11/057275 A3

(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN BRAIN

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human brain is described. Also described are single exon nucleic acid probes expressed in the brain and their use in methods for detecting gene expression.

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C12Q1/68 G06F19/00 C07K14/47

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

 $\begin{array}{ll} \mbox{MinImum documentation searched (classification system followed by classification symbols)} \\ \mbox{IPC 7} & \mbox{C12Q} & \mbox{C07K} \end{array}$

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, PAJ, MEDLINE, EMBASE, CHEM ABS Data, EMBL, BIOSIS, INSPEC

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE EMBL 'Online! ID:AC007372, April 1999 (1999-04) DICKHOFF ET AL.: "Homo sapiens chromosome 14 BAC containing gene for type 2 iodothyronine deiodinase (DIO2) gene" XP002186078	13-21,25
Y	abstract	1-12, 22-24, 26,27
Х	DATABASE EMBL 'Online! ID:CNS0000F, 11 May 1999 (1999-05-11) HEILIG ET AL.: "Sequencing of the human chromosome 14" XP002186079	13-21,25
Y	abstract	1-12, 22-24, 26,27

Further documents are listed in the continuation of box C.	Patent family members are listed in annex.
Special categories of cited documents: "A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier document but published on or after the international filling date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filling date but later than the priority date claimed Date of the actual completion of the international search	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art. "&" document member of the same patent family
26 September 2002	Date of malling of the international search report 0 8 10 2002
Name and mailing address of the ISA European Patent Office, P.B. 5818 Patentlaan 2 NL. – 2280 HV Rijswijk Tel. (+31–70) 340–2040, Tx. 31 651 epo nl, Fax: (+31–70) 340–3016	Authorized officer Hagenmaier, S

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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT Category * Citation of document with indication where appropriate of the relevant passages. Relevant to state No.				
Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.		
х	DATABASE EMBL 'Online! ID: AQ750225, 20 July 1999 (1999-07-20) MAHAIRAS ET AL.: "Construction of a Characterized Clone Resource for Genomic Sequencing" XP002186080	13-21,25		
Y	abstract	1-12, 22-24, 26,27		
'	WO 98 30722 A (MACK DAVID H) 16 July 1998 (1998-07-16) the whole document	1-12, 22-24, 26,27		
Y	WO 99 67422 A (SMITHKLINE BEECHAM CORP; LEARY JEFFREY J (US); TAL SINGER RUTH (US) 29 December 1999 (1999-12-29) the whole document	1-12, 22-24, 26,27		
Y	BURGE C ET AL: "Prediction of complete gene structure in human genomic DNA" JOURNAL OF MOLECULAR BIOLOGY, LONDON, GB, vol. 268, no. 1, 25 April 1997 (1997-04-25), pages 78-94, XP002109301 ISSN: 0022-2836 the whole document	1-12, 22-24, 26,27		
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PCT/US 01/00667

		PC1/US 01/0066/
	ation) DOCUMENTS CONSIDERED TO BE RELEVANT	
Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	YASOJIMA K ET AL: "TANGLED AREAS OF ALZHEIMER BRAIN HAVE UPREGULATED LEVELS OF EXON 10 CONTAINING TAU MRNA" BRAIN RESEARCH, AMSTERDAM, NL, vol. 831, no. 1/2, 1999, pages 301-305, XP000929899 ISSN: 0006-8993 the whole document	1-12, 22-24
Y	ERMAK G ET AL: "RESTRICTED PATTERNS OF CD44 VARIANT EXON EXPRESSION IN HUMAN PAPILLARY THYROID CARCINOMA" CANCER RESEARCH, AMERICAN ASSOCIATION FOR CANCER RESEARCH, BALTIMORE, MD, US, vol. 56, no. 1, 1 March 1996 (1996-03-01), pages 1037-1042, XP002063388 ISSN: 0008-5472 the whole document	1-12, 22-24
	40 /	

INTERNATIONAL SEARCH REPORT

Box I	Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)
This Inte	ernational Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:
1.	Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:
2. X	Claims Nos.: 1-24,26 (partially) because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful international Search can be carried out, specifically: see FURTHER INFORMATION sheet PCT/ISA/210
3.	Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).
Box II	Observations where unity of invention is lacking (Continuation of item 2 of first sheet)
This Inte	rnational Searching Authority found multiple inventions in this international application, as follows:
	see additional sheet
1.	As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2.	As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
з. χ	As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.: 1-27 (all partially)
4.	No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
Remark	on Protest The additional search fees were accompanied by the applicant's protest. X No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

Claims Nos.: 1-24,26 (partially)

The following statements about the impossibility of performing a meaningful search according to Art. 17(2) PCT are made for the subject matter for which a search has been performed and identified as the first invention in form 206 PCT. If additional fees are paid for the (one or more) as yet unsearched inventions, similar statements about incomplete searches could be issued.

Present claims 1-12 and 22-24 relate to an extremely large number of possible sets of nucleic acid probes comprising Seq.Id. 1 or 2 as well as microarrays comprising said sets. In fact, the claims contain so many possible permutations that a lack of clarity and conciseness within the meaning of Article 6 PCT arises to such an extent as to render a meaningful search of the claims impossible. Consequently, the search for the sets of probes comprising Seq. Id. 1 or 2 has been limited to the Seq. Id as such.

Claims 1-3, 5, 6, 8-15 and 18-24 relate to portions or fragments of nucleic acids defined by Seq. Id. 1 or 2. The length or other similar characterizing features of the portions or fragments is not disclosed, bringing the total number of possible prior art sequences to exceptionally high numbers. The shorter the length, the higher the possibility that an overflow of, in principle unrelated, sequences are retrieved, making the establishment of a meaningful International Search Report impossible. For this reason the search has been limited to portions or fragments of Seq. Id. 1 or 2 having a significant minimum length and being supported by the description, namely at least 15 contiguous nucleotides (see claim 16).

Claims 15-21 relate to an extremely large number of nucleic acid probes. The probes are defined solely by their potential to code for peptide Seq. Id. 25443. However, due to the degeneracy of the genetic code, every peptide is potentially coded by an extremely high number of nucleic acid sequences. In fact, the claims contain so many potential nucleic acid sequences that a lack of clarity and conciseness within the meaning of Article 6 PCT arises to such an extent as to render a meaningful search over the whole scope of the claims impossible. The search has therefore been carried out for those parts of the claims which do appear to be clear and concise, namely the nucleic acid sequences disclosed in the application and identified as encoding the referred peptide in table 4 (Seq. Ids. 1 or 2 and 12830).

Likewise, claim 26, which refers to peptides encoded by Seq. Ids. 1 or 2 and 12830, encompasses a high and undefined number of possible peptides. Besides three possible reading frames deriving from the encoding nucleic acid strand, as well as three additional reading frames deriving from the complementary nucleic acid strand, every possible fragment of these is being covered by the claim. This is due to the potential presence of stop codons within any of the six possible reading frames which can not be established a priori. Thus, claim 26 contains so many potential peptide

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

sequences that a lack of clarity and conciseness within the meaning of Article 6 PCT arises to such an extent as to render a meaningful search over the whole scope of the claim impossible. Consequently, the search has been carried out for those parts of the claim which do appear to be clear and concise, namely the peptide disclosed, identified by Seq. Id. 25443.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

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			WO	9830722	A1	16-07-1998
			US	2002028454	A1	07-03-2002
			US	2002039739	A1	04-04-2002
WO 9967422	A	29-12-1999	CA	2330731	A1	29-12-1999
			ΕP	1090144	A1	11-04-2001
			JP		T	25-06-2002
			WO	9967422	A1	29-12-1999